

New York University School of Medicine
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No Blast Hits ()

FEATURES

Location/Qualifiers

source

/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exoerythrocytic malaria parasites does not require host
cells', (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BD Biosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
pGEM vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN

Query Match 5.8%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 1.4e-36;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY 571 GCTGACATTTATATCCCGAAGATCAGGTTAATGGCTTTTGTGTCATTTTCGG 630
Db 496 GCTGACATTTATATCCCGAAGATCAGGTTAATGGCTTTTGTGTCATTTTCGG 437
QY 631 GTGGCTGAGATCAGGATCTTCCCGGATACCGGAGACCGGACACTGGCCATATCGGT 690
Db 436 GTGGCTGAGATCAGGATCTTCCCGGATACCGGAGACCGGACACTGGCCATATCGGT 377
QY 691 GGTATATGCGGACGCTTATCCCGGATATGACACCGGATAGTTTACGGGAGAC 750
Db 376 GGTATATGCGGACGCTTATCCCGGATATGACACCGGATAGTTTACGGGAGAC 317
QY 751 TTTATCTGACAGCAGCTGCTGCGGAGGGGATCACCATCGTCCGCGGGGGTGTTC 810
Db 316 TTTATCTGACAGCAGCTGCTGCGGAGGGGATCACCATCGTCCGCGGGGGTGTTC 257
QY 811 AATAATATCATCTCTTATCATCCACAAACAG--ACGATAACGGCTCTCTTTTATAGGTG 868
Db 256 AATAAGATCATCTCTTATCATCCACAAACAG--ACGATAACGGCTCTCTTTTATAGGTG 197
QY 869 TAAACCTTAAACTGCATTTTC 888
Db 196 AAACCTTAAACCTGTTTC 177

RESULT 15
AG000791
LOCUS AG000791 724 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
survey sequence.
ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 724)

AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan [E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561]

FEATURES

Location/Qualifiers

source

1. 724
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="64E11X4"

ORIGIN

Query Match 5.6%; Score 264.4; DB 29; Length 724;
Best Local Similarity 98.6%; Pred. No. 2.8e-35;
Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 847 ACGGCTCTCTCTTTTATAGGTGTAACCC-TTAAACTGCAATTCACGAGTCCCTGTTCG 905
Db 27 ACGGCTCTCTCTTTTATAGGTGTAACCC-TTAAACTGCAATTCACGAGTCCCTGTTCG 86
QY 906 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGACCTCAGCCATCCCTTCCTGATTT 965
Db 87 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGACCTCAGCCATCCCTTCCTGATTT 146
QY 966 TCCGCTTTCCAGCGTTCCGGCAGCAGACGAGCGGCTTCATTCTGATGTTGTGCTTACC 1025
Db 147 TCCGCTTTCCAGCGTTCCGGCAGCAGACGAGCGGCTTCATTCTGATGTTGTGCTTACC 206
QY 1026 AGACCGGAGATTTGACATCATATATGCTTTGAGCAACTGATAGCTGCTGCTCAACTG 1085
Db 207 AGACCGGAGATTTGACATC--ATATGCTTTGAGCAACTGATAGCTGCTGCTCAACTG 264
QY 1086 TCAGTGAATACGCTGCTTCATAGCAGACACCTCTTTTGGACATACTTCCGGTA 1137
Db 265 TCAGTGAATACGCTGCTTCATAGCAGACACCTCTTTTGGACATACTTCCGGTA 316

Search completed: May 9, 2004, 21:55:54
Job time : 7263.7 secs

COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.	
	Location/Qualifiers 1. .337 /organism="Ipomoea nil" /mol_type="mRNA" /cultivar="Tokyo-tokei standard" /db_xref="taxon:35883" /clone="Jm18n08" /tissue_type="mixture of flower and flower bud" /clone_lib="Ipomoea nil mixture of flower and flower bud"	
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RESULT 13 CF469981/c LOCUS DEFINITION	CF469981 1068 bp mRNA linear EST 05-SEP-2003 P7-E11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii yoelii cDNA, mRNA sequence.	
	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	
CF469981 VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	CF469981.1 GI:34487353 EST. Plasmodium yoelii yoelii Plasmodium yoelii yoelii Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 1068) Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V. and Bhanot, P. Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture Unpublished (2003) Contact: Bhanot P Department of Pathology New York University School of Medicine 550 First Avenue, MSB 131, New York, NY 10016, USA Tel: 212 263 5346 Fax: 212 263 8179 Email: bhanop01@med.nyu.edu similar to NR GI-23483806 hypothetical protein [Plasmodium yoelii yoelii] (e-108).	
CF469119/c LOCUS DEFINITION	CF469119 1037 bp mRNA linear EST 05-SEP-2003 P1688 Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii yoelii cDNA, mRNA sequence.	
	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	
CF469119 VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	CF469119.1 GI:34486491 EST. Plasmodium yoelii yoelii Plasmodium yoelii yoelii Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 1037) Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V. and Bhanot, P. Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture Unpublished (2003) Contact: Bhanot P Department of Pathology	

philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1. .384
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/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmCDNA"
/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauvers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.3%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 4.2e-48;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 101 TAAAAACAGACTACATACTAGTAAACACACACATATCCAGTCACTATGAATCAACTA 160
Db 32 TAATACAGAGTACATATCTGTAAACACACACATATCCAGTCACTATGAATCAACTA 91

QY 161 CTTAGATGGTATTAGTACCTGTAGTCGACGAGCCTTCCAAATGTTCTTCGGGTGAT 220
Db 92 CTTAGATGGTATTAGTACCTGTAGTCGACGAGCCTTCCAAATGTTCTTCGGGTGAT 151

QY 221 GCTGCCAATCTAGTCGACGAGCCTTCCAAATGTTCTTCGAAACGGAATCGTGTAT 280
Db 152 GCTGCCAATCTAGTCGACGAGCCTTCCAAATGTTCTTCGAAACGGAATCGTGTAT 211

QY 281 CAGGCTACTCGTATTGCTCCTCAATGCGGTATTAAATCATATAAAGAAATAGAAAG 340
Db 212 CCACTACTCGGTATTGCTCCTCAATGCGGTATTAAATCATATAAAGAAATAGAAAG 271

QY 341 AGTGGGAGCCTCTTTTGTGTGACAAATAAATAAATCTACTATTTCATATACGCTAG 400
Db 272 AGTGGGAGCCTCTTTTGTGTGACAAATAAATAAATCTACTATTTCATATACGCTAG 331

QY 401 TGTCTATGCTGAAATCATCTGCAATCAAGAAACAATTCACAACTCTTATAC 453
Db 332 TGTCTATGCTGAAATCATCTGCAATCAAGAAACAATTCACAACTCTTATAC 384

RESULT 11
BI174407/c 384 bp mRNA linear EST 09-JUL-2001
LOCUS OSTF043E11.1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to
DEFINITION Fl1F1.5, mRNA sequence.

ACCESSION BI174407
VERSION BI174407.1 GI:14640210
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 384)
AUTHORS Reboul, J., Vaglio, P., Tzallas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucet-Stamm, L., Hartley, J. L., Temple, G. F., Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
TITLE Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE 21135099
PUBMED 11242119

COMMENT Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact Jerome.Reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu

POLYA=No.

FEATURES

source

Location/Qualifiers

1. .384

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/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

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/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauvers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

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Best Local Similarity 98.2%; Pred. No. 1.4e-45;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3496 TGTCTTGTAGTACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGTAT 3555
Db 366 TGTCTTGTAGTACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAT 307

QY 3556 TTTTATTTTGTACACAAAAAGAGCTCGACCTCTTTTCTTATTTCTTTTATGATT 3615
Db 306 TTTTATTTTGTACACAAAAAGAGCTCGACCTCTTTTCTTATTTCTTTTATGATT 247

QY 3616 TAATACGGCATTCAGGACCAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGAAGAA 3675
Db 246 TAATACGGCATTCAGGACCAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGAAGAA 187

QY 3676 CATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGC 3735
Db 186 CATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGC 127

QY 3736 TGTGCGTGCAGTACAGGTCACTAATACCATTAAGTAGTTGATTCTATAGTACGTGATAT 3795
Db 126 TGTGCGTGCAGTACAGGTCACTAATACCATTAAGTAGTTGATTCTATAGTACGTGATAT 67

QY 3796 GTTGTGTTTTACAGTATTATGTAGTCTGTTTTTA 3830
Db 66 GTTGTGTTTTACAGTATTATGTAGTCTGTTATTA 32

RESULT 12

BI555980

LOCUS

DEFINITION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BI555980 337 bp mRNA linear EST 18-DEC-2002
LOCUS BI555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil
DEFINITION cDNA clone jmln08 5', mRNA sequence.
KEYWORDS EST.
SOURCE BI555980.1 GI:27237800
ORGANISM Ipomoea nil (Japanese morning glory)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoea.
REFERENCE 1 (bases 1 to 337)
AUTHORS Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaoka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.
TITLE ESTs of Japanese morning glory
JOURNAL Unpublished (2002)


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QY 786 TCACCATCGTCGCCGCGCGTGTCAATAATATCACTCTGTACATCCCAACAGCAGAT 845
Db 263 TCACCATCGTCGCCGCGCGTGTCAATAATATCACTCTGTACATCCCAACAGCAGAT 322
QY 846 AACGGCTCTCTTTATAGAGTAAACCTTAAACTGATTTACAGTCCCTGTCG 905
Db 323 AACGGCTCTCTC-TTTATAGAGTAAACCTTAAACTGATTTACCAACCCCTGTCG 381
QY 906 TCAGCAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTAGCCATCC-TTCCTGATT 964
Db 382 TCAGCAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTAGCCATCCCTTTCGATT 441
QY 965 TTCGCTTTCAGCGTTCGGACGCGAGCAG 996
Db 442 TTTGCGTTTCCAGCGTTTCGGCGACGCCAGAC 473

RESULT 7
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LOCUS AG000763 722 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES
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Best Local Similarity 92.2%; Pred. No. 3.8e-58;
Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 601 GTTAATGGCTTTTGTATGATGTCATTTTCGGGTGGCTGAGATGAGCATTCTCCCGAT 660
Db 722 GTTAAGGCCCTTTTGGANGCAATTTTCGGGTGGC----GAGATCGCCAATTTTCCCGA 667
QY 661 AACGAGACCGGCACACCTGCCATATCGTGGTGCATCATCGCGCAGCTTTCATCCCGAT 720
Db 666 TAAGGAGACCGGCACAC-TGGCCATACGGTGGTGCATCA-GCGCGAGCTTCA-CCCCGAT 610
QY 721 ATGCACACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTCGACCTGGCCAG 780
Db 609 ATGCACACCGGNTAAAGTTTCACGGGAGACTTTAACGACAGCAGACGTCGACCTGGCCAG 550
QY 781 GGGGATCAGATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAACAG 840
Db 549 GGGGATCAGATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAACAG 490
QY 841 ACGATAACGGCTCTCTCTTTATAGTGTAACCTTAAACTGATTTACACGATCCCTGCT 900

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Db 489 ACGATAACGGCTCTCTCTTTATAGTGTAACCTTAAACTGCAATTTACACGATCCCTGT 430
QY 901 TCTGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCT 960
Db 429 TCTGTCAGC-AAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCT 371
QY 961 GATTTTCGCTTTTCAGCGTTTCGGACGACGACGACGCGGTTCATCTGCAATGGTGTGTC 1020
Db 370 GATTTTCGCTTTTCAGCGTTTCGGACGACGACGACGCGGTTCATCTGCAATGGTGTGTC 311
QY 1021 TTACGACCGGAGATATGACATCATATATGCTTGGAGCACTGATAGCTGTGCTGTC 1080
Db 310 TTACGACCGGAGATATGACATC--ATATGCTTGGAGCACTGATAG-TGTCCTGTC 254
QY 1081 AACTGTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGTGACATACTTCGGGTA 1137
Db 253 AACTGTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGTGACATACTTCGGGTA 197

RESULT 8
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LOCUS CB395230 487 bp mRNA linear EST 15-MAY-2003
DEFINITION OSUR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 487)
AUTHORS Reboul, J., Vaglio, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C. M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J. R., Hartley, J. L., Brasch, M. A., Vandenhaute, J., Boulton, S., Endress, G. A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P. P., Ptacek, J., Snyder, M., Huang, R., Chance, M. R., Lee, H., Doucette-Stamm, L., Hill, D. E. and Vidal, M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
POLY(A)=No.
FEATURES
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    /strain="N2"
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    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
ORIGIN
Query Match 7.6%; Score 357; DB 14; Length 487;
Best Local Similarity 93.6%; Pred. No. 5.2e-51;
Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
JOURNAL Published Only in DataBase (1998)
TITLE Homo sapiens genomic DNA, chromosome 21q
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
JOURNAL Direct Submission
Submitted (07-SEP-1998) Mashira Hattori, Kitasato University,
Department of Science, JSR Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
FEATURES             Location/Qualifiers
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Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;

QY 580 TTATATCCCCAGAAATCAGGTTAATGGCGTTTGTGATGTCATTTTCGGGTTGGCTGAG 639
Db  |||||
QY 723 TTATATATCCCCGAGCATCAGNTAANGCGTTTTCGAGGCCATTTTCGGCGTGGCTGAG 664
Db  |||||
QY 640 ATCAGCCACTTCTTCCCGGATACGGAGACGGGCACACTGGCCATATCGGTGCTCATCAT 699
Db  |||||
QY 663 ATCAGCNVNTTTCGCCGAATANGAGACGGACATGCGCATATCNGTGTTCATCAT 604
Db  |||||
QY 700 GCGCCAGCTTTCATCCCGGATATGACACCGGTTAAAGTTCACGGAG-ACCTTATCTG 758
Db  |||||
QY 603 GCGCCAGCTTTCATCCCGAATA-GCACCAAGGGGTAANGTTCACGGAGAACTTTATCTG 545
Db  |||||
QY 759 ACAGCAGCTGCACTGGCC-AGGGGATCACCATCGTCCGCGCGGCGTGTCAATAATA 817
Db  |||||
QY 544 ACAGCAGCTGCACTGGCCCAAGGGGATCACCATCCGTNGCCCGCGCGTGTCAATAATA 486
Db  |||||
QY 818 TCACTCTGTATATCCACAAACAGACGTAACGGCTCTCTCTTTTATAGGTGTAACCTTA 877
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QY 485 TCACTCTGTATATCCACAAACAGACGTAACGGCTCTCTCTTTTATAGGTGT-AACTTAA 427
Db  |||||
QY 878 AACTGCAATTTACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTCATTTCAATAAACCG 937
Db  |||||
QY 426 AACTGCAATTTACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTCATTTCAATAAACCG 367
Db  |||||
QY 938 GCGCACTCAGCCATCCCTTCTGTATTTTCGGCTTTCAGGTTCCGCGACGACGACG 997
Db  |||||
QY 366 GCGCACTCAGCCATCCCTTCTGTATTTTCGGCTTTCAGGTTTCGCGACGACGACG 307
Db  |||||
QY 998 GGCTTTCATCTGCAATGTTGTGCTTACGACACCGGAGATATGACATCATATATGCTCTG 1057
Db  |||||
QY 306 GGCTTTCATCTGCAATGTTGTGCTTACGACACCGGAGATATGACATC--ATATGCTTG 249
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QY 1058 AGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAAATAGCTGCTTCATAGCACACCTC 1117
Db  |||||
QY 248 AGCAACTGATA-NTGTGCTGTCAACTGTCACTGTAAATAGCTGCTTCATAGCACACCTC 190
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QY 1118 TTTTGTGACATCTTCGGGTA 1137

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Db 189 TTTTGTGACATCTTCGGGTA 170
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CB997937 522 bp mRNA linear EST 01-MAY-2003
AGENCOURT 13094516 NIH_MGC 148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
CB997937.1 GI:30292457
EST.
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDM391 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.
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                        /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
                        all-XhoI; Site_2: BamH; Library is oligo-dT primed and
                        directionally cloned using primer
                        5'-TTTTTTTTTTTTTTT-3', size-selected for average insert
                        size 2.3 kb and normalized to ROT 5. This is a primary
                        library enriched for full-length clones and constructed
                        using the Cap-trapper method (Carninci, in preparation).
                        Library constructed by M. Brownstein (NIH/NHGRI, in preparation).
                        National Institutes of Health). Note: this is a NIH_MGC
                        Library."

ORIGIN
Query Match      8.6%; Score 404; DB 14; Length 522;
Best Local Similarity 96.2%; Pred. No. 4.8e-59;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 546 CTGCACAGCTGGCTGTGTATATAAGGAGCGCTGACATTTATATATCCCAAGAACATCAGGTTAA 605
Db 23 CTGCACAGCTGGCTGTGTATATAAGGAGCGCTGACATTTATATATCCCAACACATCATGTAA 82
QY 606 TGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGG 665
Db 83 TGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGG 142
QY 666 AGACCGGACACTGGCCATATCGTGGTTCATGCGCCAGCTTTCATCCCGATATGCA 725
Db 143 AGACCGGACACTGGCCATATCGTGGTTCATGCGCCAGCTTTCATCCCGATATGCA 202
QY 726 CCACCGGGTAAAGTTTCAACGGAGCTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGA 785
Db 203 CCACCGGGTAAAGTTTCAACGGAGCTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGA 262

```

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM387 row: c column: 24
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 High quality sequence stop: 251.

FEATURES

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 /note="Organ: Placenta; Vector: pBluescriptR; Site: 1:
 all-XhoI; Site 2: BamH; Oligo-dT primed using primer
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 insert size 2.3 kb and normalized to R0.5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

ORIGIN

Query Match 9.3%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 1e-64;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

QY 546 CTGCAGACTGGCTGTGTTAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAA 605
 DB 23 CTGCAGACTGGCTGTGTTAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAA 82

QY 606 TGGCGTTTTTGATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 665
 DB 83 TGGCGTTTTTGATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 142

QY 666 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGCCAGCTTTTCATCCCGATATGCA 725
 DB 143 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGTTCAGCTTTTCATCCCGATATGCA 202

QY 726 CACCGGGTAAAGTTACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGA 785
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QY 786 TCACCATCGTCCCGGGGCTGCAATATATACCTCTGTATATCCACAAACAGACGAT 845
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QY 846 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
 DB 323 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 382

QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 965
 DB 383 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 442

QY 966 TCCGTTTCCA-GGGTTCGGCAGCAGAGC-ACGGGTTTCATTC-TGCATGTTGTGCT 1021
 DB 443 TCCGTTTCCAAGGTTTCGGCAGCAGAGCAGCGGTTTCATTCCTGATGTTGTGCT 502

QY 1022 TACCAGACGG-AGATATTGACATCATATATGCGTT 1056
 DB 503 TACCAGACGGAGATATTGACATCATATATGCGCT 538

RESULT 4

AG000761/c
 LOCUS AG000761 723 bp DNA linear GSS 06-FEB-1999
 DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
 survey sequence.
 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA, chromosome 21q
 JOURNAL Published Only in Database (1997)
 REFERENCE 2 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
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ORIGIN

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 Best Local Similarity 98.1%; Pred. No. 2e-60;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 545 CTGCAGACTGGCTGTGTTAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAA 605
 DB 450 CTGCAGACTGGCTGTGTTAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAA 391

QY 606 TGGCGTTTTTGATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 665
 DB 390 TGGCGTTTTTGATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 331

QY 666 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGCCAGCTTTTCATCCCGATATGCA 725
 DB 330 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGCCAGCTTTTCATCCCGATATGCA 271

QY 726 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGA 785
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QY 786 TCACCATCGTCCCGGGGCTGCAATATATACCTCTGTATATCCACAAACAGACGAT 845
 DB 210 TCACCATCGTCCCGGGGCTGCAATATATACCTCTGTATATCCACAAACAGACGAT 151

QY 846 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
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QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 965
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QY 966 TCCG 969
 DB 30 TCAG 27

RESULT 5
 AG013450/c
 LOCUS AG013450 725 bp DNA linear GSS 14-APR-1999

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ORIGIN

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Best Local Similarity 98.9%; Pred. No. 1.3e-78;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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Db 34 TTTATATCCCGAGAACATCAGGTTAATGCGGTTTTGATGTCATTTTCGCGGTGGCTGA 93
QY 639 GATCAGCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCA 698
Db 94 GATCAGCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCA 153
QY 699 TCGCCAGGCTTTTCATCCCGGATATGCAACCGGGTAAAGTTTCACGGGAGACTTTATCTG 758
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Db 273 CACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTAA 332
QY 879 ACTGCATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTAATAACCGG 938
Db 333 ACTGCATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTAATAACCGG 392
QY 939 GCGACCTCAGCCATCCCTTCCGATTTTCGCTTCCAGGTTTCGCGACGACGACGCG 998
Db 393 GCGACCTCAGCCATCCCTTCCGATTTTCGCTTCCAGGTTTCGCGACGACGACGCG 452
QY 999 GCTTCATTTGCACTGGTTGCTTACAGACCGGAGATATGACATCATATATGCTTGA 1058
Db 453 GCTTCATTTGCACTGGTTGCTTACAGACCGGAGATATGACATCATATATGCTTGA 510
QY 1059 GCACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
Db 511 GCACTGATAGC-GTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
QY 1119 TTTTGACATCTTCGGGTA 1137
Db 570 TTTTGACATCTTCGGGTA 588

RESULT 2

AG000762/c 713 bp DNA linear GSS 06-FEB-1999
LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
DEFINITION survey sequence.

ACCESSION AG000762

VERSION AG000762.1 GI:2579570

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in Database (1997)

2 (bases 1 to 713)

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Direct Submission

Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp).

Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

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1. 713
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ORIGIN

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Best Local Similarity 94.2%; Pred. No. 6.7e-75;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

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QY 643 AGCCATCTTCTCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCACTGCG 702
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QY 703 CAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAG 762
Db 479 CAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAG 420
QY 763 CAGAGCTGCACTGGCCAGGGGATCACCATCCGTCGCGCGGCGGTCTCAATAATATCACT 822
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QY 943 CCTCAGCCATCCCTCTCTGATTTTCGCTTCCAGGTTTCGCGACGACGACGCGCTT 1002
Db 239 CCTCAGCCATCCCTCTCTGATTTTCGCTTCCAGGTTTCGCGACGACGACGCGCTT 180
QY 1003 CATTCGATAGTTGTGCTTACAGACCGGAGATATGACATCATATATGCTTGGACAA 1062
Db 179 CATTCGATAGTTGTGCTTACAGACCGGAGATATGACATC--ATATGCTTGGACAA 122
QY 1063 CTGATAGCTGCTGCTGCTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTT 1122
Db 121 CTGATANTGTGCTGCTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTT 62
QY 1123 GACATACCTTCGGGTA 1137
Db 61 GACATACCTTCGGGTA 47

RESULT 3

CD109790

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD109790 542 bp mRNA linear EST 15-MAY-2003
IMAGECOURT 13988518 NIH MGC 147 Homo sapiens cDNA clone
IMAGC:30346919 5', mRNA sequence.

CD109790

EST.

CD109790.1 GI:30753999

EST.

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

NIH-MGC http://imgc.ncbi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7262.5 Seconds

(without alignments)

19251.609 Million cell updates/sec

Title: US-10-055-001B-26_COPY_13000_17681

Perfect score: 4682

Sequence: 1 ttctatgttgagagacacg.....atagtgcacataatctgc 4682

Scoring table: IDENTITY NUC

Gapop 10-0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

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27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	518.4	11.1	698	29 AG012840
C 2	496.6	10.6	713	29 AG000762
3	437.2	9.3	542	14 CD109790
C 4	411.8	8.8	723	29 AG000761

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 5	408.4	8.7	725	29	AG013450
6	404	8.6	522	14	CB997937
C 7	398.4	8.5	722	29	AG000763
C 8	357	7.6	487	14	CB395230
9	347.4	7.4	487	14	CB395230
10	340.2	7.3	384	12	BI174407
C 11	325.4	7.0	384	12	BI174407
C 12	301.4	6.4	337	12	BJ555980
C 13	273.2	5.8	1068	14	CF469981
C 14	271.8	5.8	1037	14	CF469119
C 15	264.4	5.6	724	29	AG000791
C 16	262.4	5.6	816	14	CF469496
C 17	257.4	5.5	557	12	BG220129
C 18	255.8	5.5	656	14	CK291800
C 19	254	5.4	569	14	CF469084
C 20	252.4	5.4	819	14	CF469247
C 21	247.4	5.3	320	29	CG206516
C 22	246	5.3	329	28	BH739300
C 23	245.4	5.2	1041	14	CF468941
C 24	243.6	5.2	1035	14	CF470036
C 25	242.8	5.2	1017	14	CF470004
C 26	239.2	5.1	659	14	CK287298
C 27	235.6	5.0	859	14	CF468865
C 28	234.8	5.0	506	14	CF468964
C 29	234.8	5.0	657	14	CF468948
C 30	229	4.9	628	14	CF469215
C 31	227.2	4.9	968	14	CF469474
C 32	220	4.7	583	14	CB403882
C 33	220	4.7	583	14	CB403882
C 34	215.2	4.6	393	14	CB403984
C 35	215.2	4.6	393	14	CB403984
C 36	215.2	4.6	1020	14	CF469337
C 37	214.6	4.6	1017	14	CF468787
C 38	214.2	4.6	1042	14	CF468958
C 39	213.8	4.6	945	14	CF468807
C 40	213.2	4.6	509	14	CF468864
C 41	213.2	4.6	716	29	AG000792
C 42	204.6	4.4	398	14	CF974207
C 43	203.4	4.3	1013	14	CF469353
C 44	203.2	4.3	973	14	CF469399
C 45	200.4	4.3	586	14	CF470068

ALIGNMENTS

RESULT 1	AG012840	Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.	698 bp	DNA linear	GSS 08-FEB-1999
LOCUS	AG012840				
DEFINITION	AG012840				
ACCESSION	AG012840.1	GI:3435047			
VERSION	AG012840				
KEYWORDS	GSS.				
SOURCE	GSS.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.				
JOURNAL	Homo sapiens genomic DNA, chromosome 21q				
REFERENCE	Published Only in Database (1998)				
AUTHORS	2 (bases 1 to 698)				
TITLE	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.				
JOURNAL	Direct Submission				
	Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)				
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QY	2528	TGTATATAATATCAATATATTAAATTAGATTTTTGCATAAAAAACAGACTACATATAACTG	2587
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Db	14350	TAAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGTTATTAGTGACCTGTA	14291
QY	2648	GTGACTTAAGTTGGCAGCATCAACCGACGCACTTTGCGCGGAATAAATACCTGTGACGGA	2707
Db	14290	GTGCACTTAAGTTGGCAGCATCAACCGACGCACTTTGCGCGGAATAAATACCTGTGACGGA	14231
QY	2708	AGATCACTTTCGCGAGAATAATAATCTCGTGTCCCTGTTGATACCGGGAAGCCCTGGGC	2767
Db	14230	AGATCACTTTCGCGAGAATAATAATCTCGTGTCCCTGTTGATACCGGGAAGCCCTGGGC	14171
QY	2768	CAACTTTTTCGCGAAAATGAGACGTTGATCGGATTTCACAACTCTTATPACTTTTTCTCTTAC	2827
Db	14170	CAACTTTTTCGCGAAAATGAGACGTTGATCGG---CACTACCGAAGTATGTCAAAAAGA	14115
QY	2828	AAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATCTTACTAAACGTGATAAGTTTC	2887
Db	14114	GGTGTGCTATGAAGCAGCGTATTTACAGTGACAGTTTGACAGCGACAGCTATCAGTTGCTCA	14055
QY	2888	TGTAATTTCTACTGTATCGACCTGCAGACTCG-----CTGTGTATAAGGAGCGCTG	2938
Db	14054	AGGCATATATGATGTCAATATCTCCGCTCTGTGTAGCAACACCATGCAAGTGAAGCCCG	13995
QY	2939	ACATTTATATTCGCCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGCGGTGGC	2998
Db	13994	TCGCTCTCGGTGCC---GAAACGCTGAAAGCGGAAAAATCAGGAAGGATGGCTGAGGTGCG	13938
QY	2999	TGAGATCAGCACTTCTTCCCCGATAACGAGACCGGCACACTGCCCATATCGGTGGTCA	3058
Db	13937	CCGGTTATTGAAATGAAACGGCTCTTTTGTCTACGAGAACAGGG-----ACTGGTGAAA	13884
QY	3059	TCATGCGCCAGCTTTTCATCCCGATATGCACCACCGGGTAAAGTTTCACGGAGACTTTAT	3118
Db	13883	TGCAGTTTAAGGTTTACACTATAAAGAGAGAGCGGTATTACGCTGTGTTGTGGATGTAC	13824
QY	3119	CTGACAGCAGAGTGTCAGCTGGCCAGGGGGATCACCATCGTCGCCCGCGCGGTGTCAATAA	3178
Db	13823	AGAGTGATATATTGACAGCCCGCGGCGAGGATGGTGATCCCCCTGGCCAGTCGACGTC	13764
QY	3179	TATCACTCTGTACATCCACAACACAGACGATAACGGCTCTCTCTTTTATAGTGTAAACCT	3238
Db	13763	TGCTGTCAAGTAAAGTCTCCGTGAACCTTTACCCGGTGGTGATATCGGGGATGAAGCT	13704
QY	3239	TAAACTGCATTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAAAGCCCGTTCATTTCA	3292
Db	13703	GGCGCATGATGACCAACCGATATGGCCAGTGTGCCGTCTCCGTATTCCGGGAAGAAGTGG	13644
QY	3293	ATAAACCGGGGACCTCAGCCATCCCTTCCTGATTTTCGGCTTTCACGCGTTC---GGCA	3349
Db	13643	CTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAAACCTGATTTCTGGGGAA	13584
QY	3350	CGCAGACGACGGCTTCATTTCTCATG---TTGTGCTTACCAGACCCGAGATATTGACA	3406
Db	13583	TATTAATGTACAGGCTCCCTTATACACAGCCAGTCTGCAGTGCATACAGTAGAATTACA	13524
QY	3407	TCATATATGCGCTTGAGCAACTGATAGCTGTGCGTGTCAACTGTCACTGTAATACGCTGCT	3466
Db	13523	GAAACTTTATCACGTTTAGTAAGTAAGAGGCTGAAAATCCAGATGAAGCGAACGACTT	13464
QY	3467	TCATAGCACACCTCTTTTTCACATACCTCTGTCTCTGTAGTGAGATGATTTTCAGACTAT	3526
Db	13463	GTAAGAGAAAGTATAAGAGTTGTGAAATGTTCTTGATGCAAGTGAATTTTCAGACTAT	13404

Db 16464 |||||CTCAAAACGGAATCGTGGTATCCAGCTACTCGCTATTGTCTCAATGCGGTATTAATCA 16405
QY 321 TAAAAAGAAATAAGAAAAGAGGTGGAGCTCTCTTTTGTGTGACAAAATAAAAAATC 380
Db 16404 TAAAAAGAAATAAGAAAAGAGGTGGAGCTCTCTTTTGTGTGACAAAATAAAAAATC 16345
QY 381 TACCTATTTCATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCAATCAAGAACAAATTC 440
Db 16344 TACCTATTTCATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCAATCAAGAACAAAGT 16285
QY 441 ACAACTCTTATCTCTCTTACAAAGTGGTGGCTTCACTGGATTTTCAGCCCTCTAT 500
Db 16284 ATGTCAAAAGAGGTGTGCTATGAA---GCAGCTATTACAGTGACAGTTGACAGCGACA 16228
QY 501 ACTTACTAAACGCGATAAGTCTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCATATATGATGTCAATACTCCGGTCTGGTAAGCACACCAT 16168
QY 561 GTATAGGAGGCTGTGACATTTATATTCGCCAGAACATCAGTTTAATGGGCTTTTGTGATG 620
Db 16167 GCAGAAATGAAGCCCGTCTGCTGCTGCC---GAACGCTGGAAGCGAAAAATCAGGAAG 16111
QY 621 CATTTTCGGGTGGCTGAGATCAGCACCTTCTCCCGATTAACGGAGACCGCACACTGG 680
Db 16110 GATGGCTGAGTCCCGGTTTATTGAATGAACGGCTCTTTTGTGACGAGAACAGGG- 16052
QY 681 CCATATCGGTGGTCTCATCATCGCGCAGCTTTTCATCCCGATATGACACCGCGGTAAAGTT 740
Db 16051 ----ACTGTGAAATGCAGTTTAAGTTTACACCTATATAAGAGAGAGCGGTTATCGTC 15997
QY 741 CACGGAGACTTTATCTGACAGCAGAGTGTCACTGGCAGGGGGATCACCATCCGTGCGC 800
Db 15996 TGTGTGGATGATACAGAGTATTTATGACACCGCCGGCGACGGATGGTATCCCC 15937
QY 801 CGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATACGCTCTCTCTTT 860
Db 15936 TGCCAGTGACGCTGCTGTGTGATTAAGTCTCCCGTGAACCTTTACCGGTGGTGATA 15877
QY 861 TAPAGTGTAAACCTTAAACTGCATTTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAA 914
Db 15876 TCGGGGATGAAGCTGGCGCATGATGACACCGATATGGCCAGTGTGCGGCTCTCCGTTA 15817
QY 915 GACCGTTTCAATTAACCGGGGACCTCAGCATCCCTTCTGTGATTTTCCGGCTTC 974
Db 15816 TCGGGGAAGAAGTGGCTGTGATCTCAGCCACCGGAAATGACATCAAAAAGCCATTAAAC 15757
QY 975 CAGCGTTC---GGCAGCGACACGCGGCTTCAATCTGCAATGGTTGTGCTTACGACCG 1031
Db 15756 TGATGTTCTGGGAATATAAATGTCAAGCTCCCTTATACACAG-----CCAGTCTG 15706
QY 1032 GAGATATTGACATCATATATGCTTGAGCAACTGTAGTGTGCGTGTCAACTGTCACTG 1091
Db 15705 CAGGTGATACAGTAGAAATACAGAAACCTTTATCACGTTAGTAAGTATAGAGGCTGAA 15646
QY 1092 TAATACGCTCTTCATAGACACACTCTTTTGTACATCTTCGGGTAGTG-----CCGATCA 1147
Db 15645 AATCCAGATGAGCGGACGACTTGTGAAGAAAGTATAGAGTTGTGAAATCCGATCA 15586
QY 1148 ACCTCTCATTTTCCGCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACCAAGGA 1207
Db 15585 ACCTCTCATTTTCCGCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACCAAGGA 15526
QY 1208 TTTATTTATTCGGAAGTGAATCTTCGTCACAGGTATTTATTTTCGGCGCAAGTGGCTG 1267
Db 15525 TTTATTTATTCGGAAGTGAATCTTCGTCACAGGTATTTATTTTCGGCGCAAGTGGCTG 15466
QY 1268 GGTGATGCTCCCACTAGTCGACTACAGTCACTAATACCACTAAGTAGTTGATCAT 1327
Db 15465 GGTGATGCTCCCACTAGTCGACTACAGTCACTAATACCACTAAGTAGTTGATCAT 15406
QY 1328 AGTGACTGGATATGTTGTGTTTACAGTATATGATGTCTGTTTTTATGCAAAATCTAA 1387
|||||

Db 15405 AGTGACTGGATGTTGTGTTTTTACAGTANTATGATGCTGTTTTTATGCAAAATCTAA 15346
QY 1388 TTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTACGCTTCTCTGTACAAAGTG 1447
Db 15345 TTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTACGCTTCTCTGTACAAAGTG 15286
QY 1448 GTCTCAGGAATTCGGTACCCAGCTGGTGAAGGAAATAATTTATTTCTTTTTCTTTTT 1507
Db 15285 GTCTAGAGGATCCAAGCTTATCGAATTCGAACCCAGCTTCCCACTGTAATCA----- 15233
QY 1508 AGTATAAATAGTCTAAGTGATGTTAATTTAGTATGATATAATAATATAGTTGTTATAAT 1567
Db 15232 ---ATCCAAATGTAGATCAATGATAACAATGACATGATCTCATGTTACCTTGT 15176
QY 1568 GTGAAAAAATAATTATATAATAATTGTTTATCAATAACAACATAGTAATGTAATAAATA 1627
Db 15175 ATTCAATTCGACTAATTCATTTAATTAATAGTCAATCCATTTAGAAAGTTAATAAACTA 15116
QY 1628 TGACAAGTGATGTGAAGACGAAGAGATAAAGTTGAGAGTAAGTATATTTATTTTAAAT 1687
Db 15115 CAA-----GTATTATTTTGAATTAATAAGAAATGTTGATTTGAAATTAATACTATA 15066
QY 1688 GAATTTGATCGAACATGTAAGATGATATACTAGCATTAATAATTGTTTTTAATCAATAAG 1747
Db 15065 TAAATGATAGATCTTGGCTTTGTTATATAGCAITAGATTATGTTTT----- 15017
QY 1748 TAATTTAGTGGTTTGTGATGAATTAATAATCAATGATAAAATFACTATAGTAATAAATA 1807
Db 15016 ----- 15017
QY 1808 ATAAATAAATTAATAATAATTTTTTTATGATTAATAGTTTTATTAATAATAATCT 1867
Db 15016 ---GTACATAGATTTACTGTTTCTATTAGTTTGTAT----- 14984
QY 1868 ATACATTTACTAAATATTTTGTGTTTAAAGTTTAAATAATTTTGTGAGAAATCCAACT 1927
Db 14983 -----ATTAATTTGTTTACTTTAGTCTTGTATTAAATAATTGTTTATGTAATAATACAG 14929
QY 1928 TGCTTGTAATTTATCAATAAACAATAATTAATAAACAGCTAAAAGTAAACAATAATATPC 1987
Db 14928 CAGATGGGAATTTTCAACAAAATAATTTAATACTTTTAAACTAAAATAATTTAGTAATGT 14869
QY 1988 AAACCTAATAGAAACAGTAATCTAATGTAACAAAACATAATCTAANTGCTAATAACAAAG 2047
Db 14868 ATAGATAT----- 14861
QY 2048 CGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTAATAATTTCTAAA 2107
Db 14860 -----TTAATTAATAATAAATTAATTAATCAAAAAATAATTTATTTATTTATTA 14808
QY 2108 TAATACTTGTAGTTTATTAATCTCTAAATGGATGACTATTAATTAATTAATGAATTAGTCG 2167
Db 14807 TTTCTATTTTACTATAGTATTTTATCATTTG-----ATATTTAATTCATCAAAACAGCT 14754
QY 2168 AACATGAATAACAAGGTAACATGATAGATCATGTCATGCTGTTATCATTTGATCTTACAT 2227
Db 14753 AGAATTAATTAATGAATTAATAAACAATAATTAATGCTAGTATATCATCTTACATGTTGAT 14694
QY 2228 TTGGATTTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGGCTGCAGTTATC 2287
Db 14693 CAAATTCATTAAAAAT-----AATATACTTACTCTCACTTTTATCTTC 14650
QY 2288 ATCATCATCATAGACACAGGAAATAAAGTAATCAGATTAATCAGTTTAAAGCTAATTAAT 2347
Db 14649 TTCGCTTTACACATCACTTGTCTATTTTTTACATTTTACATTTACTATGTTCTTTATCTA 14590
QY 2348 TTGGCCCAATAACCAATCAATTAABAATAAGATCAGTTTAAAGAAAGATCAAGCTCBAAT 2407
Db 14589 ATATTATAAATTTATTTTTTTCACAAATTAACAATAATTAATTAATTAATCACTAATTA 14530
QY 2408 AATAAAAAAGAAAAGGGTCTCTCAACGAATAATGAAGGAGAAAAAATCTAGAAAAATTTAC 2467
Db 14529 ACATCACTTAATTTTATCTAATAAGAAAATAAATAATTTATTTCTTCCATTACCAAGC 14470
|||||

APPLICANT: LI, XIAO
APPLICANT: ESPPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 4627
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 23.5%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 6.7e-158;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAGTTTGTACAAAAAGCTGAAACGAGAACGTAAGTAAATGATATAAAATATCAATATATT 85
DB 90 GCCAATTTTGTACAAAAAGCTGATATCGAAAGCTAAAAATGATATAAAATATCAATATATT 149

QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAACACACACATATCCAGTC 145
DB 150 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAACACACACATATCCAGTC 209

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACCGACAGCCTTCCAAA 205
DB 210 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACCGACAGCCTTCCAAA 269

QY 206 TGTCTTCGGGTGATGCTGCGAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 265
DB 270 TGTCTTCGGGTGATGCTGCGAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 329

QY 266 ACGGAATGCTGTATCGACGCTACTGCTATTGTCCTCAATCGCTATTAAATCATATAAA 325
DB 330 ACGGAATGCTGTATCGACGCTACTGCTATTGTCCTCAATCGCTATTAAATCATATAAA 389

QY 326 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
DB 390 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 449

QY 386 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACAAATTCACAA 445
DB 450 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACAAATTCACAA 509

QY 446 TCTTATCTTTTCTTACAGTCTGTTGGCTTCTATCTGANTTTTCAGCCTCTATCTTAA 505
DB 510 TCTTATCTTTTCTTACAGTCTGTTGGCTTCTATCTGANTTTTCAGCCTCTATCTTAA 569

QY 506 CTAACAGTGAATAGTTTCTGTAATTTCTATGTAFCGACCTGCGAGCTGGCTGTATATA 565
DB 570 CTAACAGTGAATAGTTTCTGTAATTTCTATGTAFCGACCTGCGAGCTGGCTGTATATA 629

QY 566 AGGAGCCTGACATTTATATATCCCGAATCATCAGTTAATGGCGTTTGTGATGTCATTT 625
DB 630 AGGAGCCTGACATTTATATATCCCGAATCATCAGTTAATGGCGTTTGTGATGTCATTT 689

QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGACACCTGGCCATA 685
DB 690 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGACACCTGGCCATA 749

QY 686 TCGGTGGTCAATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCA 745
DB 750 TCGGTGGTCAATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCA 809

QY 746 GAGACTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATACCATCCGTCGCGCGGCG 805
DB 810 GAGACTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATACCATCCGTCGCGCGGCG 869

QY 806 GTGTCAATAATATCATCTGTATCATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 865
DB 870 GTGTCAATAATATCATCTGTATCATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 929

QY 866 GTGTAAACCTTAAACCTGCAATTTTCCAGTCCTGTTCTGTCAGCAAAAGACCGTTTCA 925
DB 930 GTGTAAACCTTAAACCTGCAATTTTCCAGTCCTGTTCTGTCAGCAAAAGACCGTTTCA 989

QY 926 TTCAATAAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 990 TTCAATAAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 1049

QY 986 ACGGACAGACGGGCTTCAATTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
DB 1050 ACGGACAGACGGGCTTCAATTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1109

QY 1046 ATATATGCTTGCAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1105
DB 1110 ATATATGCTTGCAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1169

QY 1106 ATAGCACACCTCTTTTGTGACATATCTTCGGGTA 1137
DB 1170 ATAGCACACCTCTTTTGTGACATATCTTCGGGTA 1201

RESULT 15
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 23.0%; Score 1074.8; DB 15; Length 17476;
Best Local Similarity 59.9%; Pred. No. 1.7e-153;
Matches 2349; Conservative 0; Mismatches 1302; Indels 273; Gaps 22;

QY 21 CTCGACAGCAAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 80
DB 16704 CTCGACAGCAAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 16645

QY 81 ATATTAAATAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 140
DB 16644 ATATTAAATAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 16585

QY 141 CAGTCACATATGAATCAACTACTTAGATGTTAGTACCTGTAGTCGACGAGCCTTCCAAATGCTT 200
DB 16584 CAGTCACATATGAATCAACTACTTAGATGTTAGTACCTGTAGTCGACGAGCCTTCCAAATGCTT 16525

QY 201 CCAATGTTCTTCGGGTGATGCTGCCAATCTTAGTCGACCGCAGCAGCTTCCAAATGCTTCT 260
DB 16524 CCAATGTTCTTCGGGTGATGCTGCCAATCTTAGTCGACCGCAGCAGCTTCCAAATGCTTCT 16465

QY 261 CTCAAACGGAATGCTGCTATCCAGCCTTACTCGCTATTGTCCTCAATGCGGTATTAAATCA 320

QY	746	GAGACTTTATCTGACAGACGTGCACTGGCCAGGGGGGATCAACATCCCGTCGCCCGGGC	805
Db	1659	GAGACTTTATCTGACAGACGTGCACTGGCCAGGGGGGATCAACATCCCGTCGCCCGGGC	1718
QY	806	GTGTCAAATAATATCACTCTGTACATCCACAAACAGAGATAACGGCTCTCTCTTTTATAG	865
Db	1719	GTGTCAAATAATATCACTCTGTACATCCACAAACAGAGATAACGGCTCTCTCTTTTATAG	1778
QY	866	GTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCA	925
Db	1779	GTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCA	1838
QY	926	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGC	985
Db	1839	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGC	1898
QY	986	ACGAGACGACGGGCTTCATTCCTCATGTTGTGCTTTACGAGCCGAGATATTGACATC	1045
Db	1899	ACGAGACGACGGGCTTCATTCCTCATGTTGTGCTTTACGAGCCGAGATATTGACATC	1958
QY	1046	ATATATGCTTGAGCAACTGATAGCTGCGCTGTCAACTGTCACTGTAATAACGCTGCTTC	1105
Db	1959	ATATATGCTTGAGCAACTGATAGCTGCGCTGTCAACTGTCACTGTAATAACGCTGCTTC	2018
QY	1106	ATAGCACACCTCTTTTGTGACATATTCGGGTA	1137
Db	2019	ATAGCACACCTCTTTTGTGACATATTCGGGTA	2050

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RESULT 13
US-101-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10151.690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-101-151-690-63

```

Qy	206	TGTTCTTCGGGTGATGCTGCGAACTTAGTCGACCGCAGCGCTTCCAAATGTTCTTCTCAA	265
Db	270	TGTTCTTCGGGTGATGCTGCGAACTTAGTCGACCGCAGCGCTTCCAAATGTTCTTCTCAA	329
Qy	266	ACGGATTCGTCGTATCCAGCGCTACTCGCTATTTCTCTCAATGCGGATTTAAATCATAAAA	325
Db	330	ACGGATTCGTCGTATCCAGCGCTACTCGCTATTTCTCTCAATGCGGATTTAAATCATAAAA	389
Qy	326	AGAAAATAAGAAAAAGAGGTCCGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT	385
Db	390	AGAAAATAAGAAAAAGAGGTCCGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT	449
Qy	386	ATTCTATATAGCTAGTGTCTAGTCTCTGAAAAATCATCTGCAACAAGCAATTTACAAC	445
Db	450	ATTCTATATAGCTAGTGTCTAGTCTCTGAAAAATCATCTGCAACAAGCAATTTACAAC	509
Qy	446	TCCTTATATCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGATTTTCAGCGCTCTATACTTA	505
Db	510	TCCTTATATCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGATTTTCAGCGCTCTATACTTA	569
Qy	506	CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATA	565
Db	570	CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATA	629
Qy	566	AGGAGCGCTGACATTTATATATCCCGAGAACATCAGGTTAAATGGGTTTTTGTATGTCAATTT	625
Db	630	AGGAGCGCTGACATTTATATATCCCGAGAACATCAGGTTAAATGGGTTTTTGTATGTCAATTT	689
Qy	626	TCGCGGTGGCTGAGATCAGGCACCTTCTTCCCGATAACCGAGACCGGCACACTGGCCATA	685
Db	690	TCGCGGTGGCTGAGATCAGGCACCTTCTTCCCGATAACCGAGACCGGCACACTGGCCATA	749
Qy	686	TCGGTGGTCAATCATGCGCCACGCTTTATCCCGATATGCAACCGCGGTAAAGTTCAACGG	745
Db	750	TCGGTGGTCAATCATGCGCCACGCTTTATCCCGATATGCAACCGCGGTAAAGTTCAACGG	809
Qy	746	GAGACTTTATCTACGACGACAGCTGCACTGGCCAGGGGATCAGCATCCGTCGCCCGGGC	805
Db	810	GAGACTTTATCTACGACGACAGCTGCACTGGCCAGGGGATCAGCATCCGTCGCCCGGGC	869
Qy	806	GTGTCAATAATATCAGTCTCTACATCCAAAAAGACGATAACGGCTCTCTCTTTTATATAG	865
Db	870	GTGTCAATAATATCAGTCTCTACATCCAAAAAGACGATAACGGCTCTCTCTTTTATATAG	929
Qy	866	GTGTAAACCTTAACTGCAATTCACGAGTCCCTGTCTCTGTCAGCAAAAGAGCGGTTTCAT	925
Db	930	GTGTAAACCTTAACTGCAATTCACGAGTCCCTGTCTCTGTCAGCAAAAGAGCGGTTTCAT	989
Qy	926	TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCAGAGGTTCCGC	985
Db	990	TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCAGAGGTTCCGC	1049
Qy	986	ACGACAGCAGCGGCTTCATTCTTCGATGGTGTGTGCTTACCAGACCGGAGATATTGACATC	1045
Db	1050	ACGACAGCAGCGGCTTCATTCTTCGATGGTGTGTGCTTACCAGACCGGAGATATTGACATC	1109
Qy	1046	ATATATGCCCTTGAGCAACTGATAGTGTGCGCTGTCAACTGTCTACTGTAAACGCTGCTTC	1105
Db	1110	ATATATGCCCTTGAGCAACTGATAGTGTGCGCTGTCAACTGTCTACTGTAAACGCTGCTTC	1169
Qy	1106	ATAGCACACCTCTTTTGTGACATACCTTCGGGTA	1137
Db	1170	ATAGCACACCTCTTTTGTGACATACCTTCGGGTA	1201

RESULT 14
US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHRO, DAVID

Db 5363 ACTATGATCACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 5304
QY 206 TGTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 265
Db 5303 TGTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 5244
QY 266 ACCGAATCGTGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAATATCAFAAA 325
Db 5243 ACCGAATCGTGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAATATCAFAAA 5184
QY 326 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 5183 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 5124
QY 386 ATTCATATACGCTAGTGTCTATAGTCTCGAAATCATCTGCATCAAGAAACAATTTCAAC 445
Db 5123 ATTCATATACGCTAGTGTCTATAGTCTCGAAATCATCTGCATCAAGAAACAATTTCAAC 5064
QY 446 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGCCTCTATACCTA 505
Db 5063 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGCCTCTATACCTA 5004
QY 506 CTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACTGCAGCTGGCTGTCTATA 565
Db 5003 CTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACTGCAGCTGGCTGTCTATA 4944
QY 566 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 625
Db 4943 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 4884
QY 626 TCCGCTGTGCTGATGATCAGCCTCTTCCCGATACCGGACCGGACACTGGCCATA 585
Db 4883 TCCGCTGTGCTGATGATCAGCCTCTTCCCGATACCGGACCGGACACTGGCCATA 4824
QY 686 TCCGCTGTGCTGATGATCAGCCTCTTCCCGATACCGGACCGGACACTGGCCATA 745
Db 4823 TCCGCTGTGCTGATGATCAGCCTCTTCCCGATACCGGACCGGACACTGGCCATA 4764
QY 746 GAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATACCAATCCGTCGCGCGGC 805
Db 4763 GAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATACCAATCCGTCGCGCGGC 4704
QY 806 GTGTCAATATATCACTCTGTATCATCCACAAACAGACGATACGCTCTCTTTTATAG 865
Db 4703 GTGTCAATATATCACTCTGTATCATCCACAAACAGACGATACGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAAACCTGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 925
Db 4643 GTGTAAACCTTAAACCTGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 4584
QY 926 TTCAATACACCGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTTCGGC 985
Db 4583 TTCAATACACCGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTTCGGC 4524
QY 986 ACCGAGACGACGGCTTCATTTCTGATGTTGTGCTTACGACCGGAGATATGACATC 1045
Db 4523 ACCGAGACGACGGCTTCATTTCTGATGTTGTGCTTACGACCGGAGATATGACATC 4464
QY 1046 ATATATGCTTGTAGCAACTGTAGTGTGCTGTCTCACTGTATTAAGCTGCTTC 1105
Db 4463 ATATATGCTTGTAGCAACTGTAGTGTGCTGTCTCACTGTATTAAGCTGCTTC 4404
QY 1106 ATAGCACACCTCTTTTGTACATCTTCGGGTA 1137
Db 4403 ATAGCACACCTCTTTTGTACATCTTCGGGTA 4372

RESULT 12

US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID M
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62
Query Match 23.5%; Score 1102.4; DB 15; Length 4428;
Best Local Similarity 99.5%; Pred. No. 6.e-158;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 26 GACAAAGTTGTACAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAATATATT 85
Db 939 GCCAATTTGTACAAAAGCTGATATCGAAACGTAAATATGATATAAATATCAATATATT 998
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGTC 145
Db 999 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGTC 1058
QY 146 ACTATGATCACTACTTAGATGGTATTAGTCACTGTAGTGCACCGACAGCCTTCCAAA 205
Db 1059 ACTATGATCACTACTTAGATGGTATTAGTCACTGTAGTGCACCGACAGCCTTCCAAA 1118
QY 206 TGTCTCTCGGTGTAGTGTGCCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 265
Db 1119 TGTCTCTCGGTGTAGTGTGCCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 1178
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAA 325
Db 1179 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAA 1238
QY 326 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 1239 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 1298
QY 386 ATTCATATACGCTAGTGTATAGTCTGAAAATCATCTGCATCAAGAAACAATTTCAAC 445
Db 1299 ATTCATATACGCTAGTGTATAGTCTGAAAATCATCTGCATCAAGAAACAATTTCAAC 1358
QY 446 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGGAATTTTCAGCCTCTATACCT 505
Db 1359 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGGAATTTTCAGCCTCTATACCTA 1418
QY 506 CTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTCTATA 565
Db 1419 CTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTCTATA 1478
QY 566 AGGAGCCTGACATTTATTTCCCGAACAATCATAGGTTAATGCGCTTTTGTGATGTCATTT 625
Db 1479 AGGAGCCTGACATTTATTTCCCGAACAATCATAGGTTAATGCGCTTTTGTGATGTCATTT 1538
QY 626 TCCGCTGTGCTGATGATCAGCCTCTTCTTCCCGATACCGGACCGGACACTGGCCATA 685
Db 1539 TCCGCTGTGCTGATGATCAGCCTCTTCTTCCCGATACCGGACCGGACACTGGCCATA 1598
QY 686 TCCGCTGTGCTGATGATCAGCCTCTTCTTCCCGATACCGGACCGGACACTGGCCATA 745
Db 1599 TCCGCTGTGCTGATGATCAGCCTCTTCTTCCCGATACCGGACCGGACACTGGCCATA 1658

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/ OTHER INFORMATION: attP1 recombination site
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (959)..(1264)
/ OTHER INFORMATION: ccdB gene
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1606)..(2265)
/ OTHER INFORMATION: Cam(r) gene
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2513)..(2744)
/ OTHER INFORMATION: attP2 recombination site
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2868)..(3677)
/ OTHER INFORMATION: Kan(r) gene
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (3794)..(4537)
/ OTHER INFORMATION: pUC oriV / RK2 oriT
US-10-357-268-1

Query Match      23.7%; Score 1108.8; DB 16; Length 4892;
Best Local Similarity 99.8%; Pred. No. 7.3e-159;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTGTACAAAAGAGCTGAACGAGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 102 GCCAACTTTGTACAAAAGAGCTGAACGAGAGAAACGTAATAATGATATAAATATCAATATAT 161

QY 86 AAATTAGATTTTCATATAAAGAGAGCTACATATATCTGTAATAACACATATCCAGTC 145
DB 162 AAATTAGATTTTCATATAAAGAGAGCTACATATATCTGTAATAACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTATGATGGTATTAGTAGACCTGTAGTCAGCGAGAGCCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTATGATGGTATTAGTAGACCTGTAGTCAGCGAGAGCCCTTCCAAA 281

QY 206 TGTCTTCGGGTGATGCTGCACAACTAGTAGCGAGAGAGCCCTTCCAAAAGTTCTTCTCAA 265
DB 282 TGTCTTCGGGTGATGCTGCACAACTAGTAGCGAGAGAGCCCTTCCAAAAGTTCTTCTCAA 341

QY 266 ACGGAATCGTCGATCCAGCTACTCGCTATTCCTGCTCAATGCGGTATTAATCATATAA 325
DB 342 ACGGAATCGTCGATCCAGCTACTCGCTATTCCTGCTCAATGCGGTATTAATCATATAA 401

QY 326 AGAAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGACAAAAATAAAAAACATCTACCT 385
DB 402 AGAAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGACAAAAATAAAAAACATCTACCT 461

QY 386 ATTATATAGCGTAGTGTCTATGCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCT 445
DB 462 ATTATATAGCGTAGTGTCTATGCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCT 521

QY 446 TCTTATATCTTCTCTTACAAAGTCGTTTCGGCTTCATCTGATTTTCAGGCTCTATATCTTA 505
DB 522 TCTTATATCTTCTCTTACAAAGTCGTTTCGGCTTCATCTGATTTTCAGGCTCTATATCTTA 581

QY 506 CTAAACGCTGATAAAGTTTCTGTAATTTCTATCTGATCTGACCTGACAGCTGGCTGTGTATA 565
DB 582 CTAAACGCTGATAAAGTTTCTGTAATTTCTATCTGATCTGACCTGACAGCTGGCTGTGTATA 641

QY 566 AGGAGGCTGACATTTATATATCCCGAGAACATCAGGTTAATGCGGTTTGTGATGTCATT 625
DB 642 AGGAGGCTGACATTTATATATCCCGAGAACATCAGGTTAATGCGGTTTGTGATGTCATT 701

QY 626 TCGCGGTGGCTGAGATCAGCACTTCTTCCCGATACAGAGACCGGACACTGGCCATA 685
DB 702 TCGCGGTGGCTGAGATCAGCACTTCTTCCCGATACAGAGACCGGACACTGGCCATA 761

QY 686 TCGGTGCTCATATGCGCCAGCTTTTCATCCCGATATGCAACCGGCTAAAGTTCCACGG 745
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DB 762 TCGGTGCTCATCATCGCCAGCTTTTCATCCCCGATATGCACACCGGGTAAAGTTCCACGG 821
QY 746 GAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCCGGGC 805
DB 822 GAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCCGGGC 881
QY 806 GTGTCAATAATATCTCTGTACATCCCAAAACAGACAGATACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATCTCTGTACATCCCAAAACAGACAGATACGGCTCTCTCTTTTATAG 941
QY 866 GTGTAAACCTTAAACCTGCAATTTTCCAGTCCCTGTTTCTGTCAGCAAAAGAGCCGTTTCA 925
DB 942 GTGTAAACCTTAAACCTGCAATTTTCCAGTCCCTGTTTCTGTCAGCAAAAGAGCCGTTTCA 1001
QY 926 TTCAATAAAACCGGGGAGCCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 1002 TTCAATAAAACCGGGGAGCCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 1061
QY 986 ACGCAGACGACGGGCTTCAATCTGATGGTTGTGTTTACAGACCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGACGGGCTTCAATCTGATGGTTGTGTTTACAGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTGTAGCAAACTGATAGCTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1105
DB 1122 ATATATGCTTGTAGCAAACTGATAGCTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTGTGACATATCTCCGGTA 1137
DB 1182 ATAGCACACCTCTTTTGTGACATATCTCCGGTA 1213

RESULT 11
US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match      23.7%; Score 1108.8; DB 15; Length 5584;
Best Local Similarity 99.8%; Pred. No. 7.7e-159;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTGTACAAAAGAGCTGAACGAGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 5483 GCCAACTTTGTACAAAAGAGCTGAACGAGAGAAACGTAATAATGATATAAATATCAATATAT 5424

QY 86 AAATTAGATTTTGCATATAAAGAGAGCTACATATATCTGTAATAACACACATATCCAGTC 145
DB 5423 AAATTAGATTTTGCATATAAAGAGAGCTACATATATCTGTAATAACACACATATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTATGATGGTATTAGTACCTGTAGTCAGCGGCTTCCAAA 205
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (29)..(260)
/ OTHER INFORMATION: attP1
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (656)..(961)
/ OTHER INFORMATION: ccdB
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1099)..(1184)
/ OTHER INFORMATION: ccdA
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1303)..(1962)
/ OTHER INFORMATION: Cmr
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2210)..(2442)
/ OTHER INFORMATION: attP2
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2565)..(3374)
/ OTHER INFORMATION: Kmr
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (3495)..(4134)
/ OTHER INFORMATION: ori
/
US-10-151-690-21

Query Match      23.7%; Score 1108.8; DB 15; Length 4470;
Best Local Similarity 99.8%; Pred. No. 7e-159;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTCAACGAGAAAGCTAAATATGATATAATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAAAGAGAAAGCTAAATATGATATAATCAATATATT 161

QY 86 AAATAGATTTTGCATAAAAAAGAGACTACATATACTGTAAACACACATATCCAGTC 145
DB 162 AAATAGATTTTGCATAAAAAAGAGACTACATATACTGTAAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTAGATGGTATTAGTACCTGTAGTCAGCAGAGCCCTCCAAA 205
DB 222 ACTATGAATCAACTACTAGATGGTATTAGTACCTGTAGTCAGCAGAGCCCTCCAAA 281

QY 206 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265
DB 282 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 341

QY 266 ACGGAATCGTCGATCCAGCCTACTCGCTATTGCTCTCAATGCGGATTAAATCATATAA 325
DB 342 ACGGAATCGTCGATCCAGCCTACTCGCTATTGCTCTCAATGCGGATTAAATCATATAA 401

QY 326 AGAAATAGAAAGAGAGGTGCGAGCCTCTTTTGTGACAAATATAAAGATCTACCT 385
DB 402 AGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGACAAATATAAAGATCTACCT 461

QY 386 ATTATATATAGCTAGTGTATAGTCTGAAATCACTGATCAAGAAATTTTCAAC 445
DB 462 ATTATATAGCTAGTGTATAGTCTGAAATCACTGATCAAGAAATTTTCAAC 521

QY 446 TCTTATATCTTTCTCTTACAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATCTTA 505
DB 522 TCTTATATCTTTCTCTTACAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATCTTA 581

QY 506 CTAAGAGTGATAAGTTTCGTAATTTCTACTGATCGACCTGACAGCTGCTGTATA 565
DB 582 CTAAGAGTGATAAGTTTCGTAATTTCTACTGATCGACCTGACAGCTGCTGTATA 641

QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGATGTCATTT 625
DB 642 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGATGTCATTT 701
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QY 626 TCGCGTGGCTGAGATCAGCCTTTCTTCCCGATAACGAGACCGGCACACTGGCCATA 685
DB 702 TCGCGTGGCTGAGATCAGCCTTTCTTCCCGATAACGAGACCGGCACACTGGCCATA 761

QY 686 TCGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGACCAACCGGGTAAAGTTACGG 745
DB 762 TCGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGACCAACCGGGTAAAGTTACGG 821

QY 746 GAGACTTTTATCTGACAGCAGAGTGTCACCTGGCCAGGGGATCACCATTCGTCGCCGGC 805
DB 822 GAGACTTTTATCTGACAGCAGAGTGTCACCTGGCCAGGGGATCACCATTCGTCGCCGGC 881

QY 806 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 941

QY 866 GTGTAACCTTAAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCA 925
DB 942 GTGTAACCTTAAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCA 1001

QY 926 TTCAATAAAACCGGGGAGCCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGG 985
DB 1002 TTCAATAAAACCGGGGAGCCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGG 1061

QY 986 ACGCAGACGACGGGCTTCAATTTCTGATGTTGTGCTTACAGACCGAGATATGACATC 1045
DB 1062 ACGCAGACGACGGGCTTCAATTTCTGATGTTGTGCTTACAGACCGAGATATGACATC 1121

QY 1046 ATATATGCTTGGAGCACTGATAGTGTGCTGTGTCAGTGTCACTGTATATAGCTGCTTC 1105
DB 1122 ATATATGCTTGGAGCACTGATAGTGTGCTGTGTCAGTGTCACTGTATATAGCTGCTTC 1181

QY 1106 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1213
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RESULT 10
US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US20030219902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; FILE REFERENCE: WSP-1-20291
; CURRENT APPLICATION NUMBER: US/10/357,268
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4892
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (73)..(100)
; OTHER INFORMATION: T2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(563)
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Db 14856 ACTCTCAACTTTTATCTCTCTGCTTATACATCACTTGTGCATATTTTTTTTACATTA 14797
Qy 2234 TGATTTACAGTTGGGAGCTGGTTCGAATCGATAAGCTTGGCTGCAGTTTATCATATC 2293
Db 14796 TGTGCTTTATGTAACAATATATTTTATAAATTTATTTTTCACAAATATAACACATATAT 14737
Qy 2294 ATCATAGACACACGAAATAAAGTAATCAGATTATCAGTTAAAGCTATGTAATATTTGGC 2353
Db 14736 ATTATTAATCACTAATTAACATCACTTAATTTTATATACTAAAGGAAAGAAAT 14677
Qy 2354 CATACCAATCAATTAATAAATAAGATGTTTAAAGAAAGATCAAGCTCAAAAAATAA 2413
Db 14676 AATTATTTCTTACCAAGCTGGGTACCGAATTCCTCGAG---GAGCTGCAGCTGGATG 14621
Qy 2414 AAAGGAAAGGGCTCTTAACCAAGAAATGAAGGAGAAATACTAGAAATTTACCTGCACA 2473
Db 14620 GCAATAATGATTTTATTTTGACTGATAGTACCTGTTGCTGTTGCAACAAATTTGATAAGCA 14561
Qy 2474 AGCTTGGATCTCTAGACCACTTTTGTACAAGAAAGCTGAAACGAGAAAGCTAAATGATAT 2533
Db 14560 ATGCTTTCTTATAATGCCAATCTTTGTACAAGAAAGCTGAAACGAGAAACGTTAAATGATAT 14501
Qy 2534 AATATCAATATTAATAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAAC 2593
Db 14500 AATATCAATATTAATAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAAC 14441
Qy 2594 ACAATATCCAGTCACTATGAATCAACTTACATTTAGTGTATTTAGTACCTGTAGTCGAC 2653
Db 14440 ACAATATCCAGTCACTATGAATCAACTTACATTTAGTGTATTTAGTACCTGTAGTCGAC 14381
Qy 2654 TAAGTTGGCAGATCAACCGACGCACTTTGCGCCGAATAAATCACTGTGACGGAAGATCA 2713
Db 14380 TAAGTTGGCAGATCAACCGACGCACTTTGCGCCGAATAAATCACTGTGACGGAAGATCA 14321
Qy 2714 CTTCCGAGATAAATAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2773
Db 14320 CTTCCGAGATAAATAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14261
Qy 2774 TTGGCGAAATGAGAGCTGATCGGATTTCAAACTCTTATATCTTCTTCTTCAAGTCG 2833
Db 14260 TTGGCGAAATGAGAGCTGATCGG---CACTACCGGAAGTATGTCAAAAAGAGGTGTG 14205
Qy 2834 TTCCGCTTCATCTGATTTTTCAGCTCTATATCTTAACTGATGATAAGTTTCTGTAT 2893
Db 14204 CTATGAAGCAGCGTATTTACAGTGACAGTTTGACAGCGACAGCTATCAGTTGCTCAAGGCAT 14145
Qy 2894 TTCTACTGTATCGACTCGAGCTGG-----CTGTGTATTAAGGGAGCTGCATTT 2944
Db 14144 ATATGATGTCAATATCTCCGCTGTGTAAAGACCAACATGCAAGATGAAGCCGCTGCT 14085
Qy 2945 ATATTTCCCGAACAATCAGGTTAAATGGCGTTTGTATGTCAATTTTCGCGTGGCTGAGAT 3004
Db 14084 GCGTGC---GAACGCTGGAAGCGGAAATCAGGAAGGATGGCTGAGTGCCTGCGCGTT 14028
Qy 3005 CAGCCTACTTCTCCCGATAACGGAACCGGACACTGGCCATATCGGTGGTGCATCATGC 3064
Db 14027 TATTGAATGAACGGCTCTTTTCTGACGAGAACAGGG-----ACTGGTGAATGCACT 13974
Qy 3065 GCCAGCTTTTCATCCCGATATGACCAACCGGTTAAAGTTTCACGGGAGACTTTATCTGACA 3124
Db 13973 TTAAGGTTTACACTATAAAGAGAGAGCGCTTATCTGTGTTGGAGTACAGAGTG 13914
Qy 3125 GCAGAGTGCACCTGGCCAGGGGATCACCATCCGTCGCCCGGCGGTGTCAATAATATCAC 3184
Db 13913 ATATTATTGACACGCCCGGCGAGGATGTTGATCCCTGCGCAGTGCACGCTCTGCT 13854
Qy 3185 TCTGTACATCCAAACAGAGATACGGCTCTCTCTTTTATAGGTGTAAACCTTAACT 3244
Db 13853 CAGATAAAGTCTCCCGTGACTTTTACCCGGTGTGATATTCGGGGATGAAGCTGGCGCA 13794
Qy 3245 GCATTTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCAATTAAC 3298

Db 13793 TGATGACCACCGATATGAGCCAGTGTCCGGTCTCCGTTATCGGGGAAAGATGGCTGATC 13734
Qy 3299 CGGCGACCTTCAGCATCCCTTCTGATTTTCCGCTTTCAGAGCGTTC---GGCACGAGCA 3355
Db 13733 TCAGCCACCGGAAATGACATCAAAAACGCCATTAACTGATGTTCTGGGATATAAA 13674
Qy 3356 CGACGGCTTCACTCTCATGG---TTGTGCTTACCAGACCGGAGATATTGACATCATAT 3412
Db 13673 TGTCAAGCTCCCTTATACACAGCCAGTCTGCGAGTCGATACAGTAGAAAATTACAGAACT 13614
Qy 3413 ATGCTTTGAGCACTGATAGCTGCTGCTGCTCACTGTCACTGTAAATACGCTGCTTCATAG 3472
Db 13613 TTATCACGTTTAGTAAGTATAGAGCTGAAAATCCAGATGAAGCCGACGACTTGTAGA 13554
Qy 3473 CACACCTCTTTTGCACATCTCTCTGTTCTTGATCGAGATGATTTTTCAGGACTATGACACT 3532
Db 13553 GAAAGATATAGAGTGTGTGAATTTGTTCTTGATCGAGATGATTTTCAGGACTATGACACT 13494
Qy 3533 AGCTATATGAATAGTAGATGTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCT 3592
Db 13493 AGCTATATGAATAGTAGATGTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCT 13434
Qy 3593 TTTTCTTATTTCTTTTATGATTTTAAATACGCTTGAAGCAATTTGGAAGCTGTAAGTGGCTGGAT 3652
Db 13433 TTTTCTTATTTCTTTTATGATTTTAAACGCTTGAAGCAATTTGGAAGCTGTAAGTGGCTGGAT 13374
Qy 3653 ACAGCATTCGCTTTTGAAGAACAATTTGGAAGCTGTCGCTGCACTAAAGTTGGCAGCAT 3712
Db 13373 ACAGCATTCGCTTTTGAAGAACAATTTGGAAGCTGTCGCTGCACTAAAGTTGGCAGCAT 13314
Qy 3713 CACCGAAGAACATTTGGAAGCTGTCGCTGCACTAGCTCACTAATACCATCTAAGTA 3772
Db 13313 CACCGAAGAACATTTGGAAGCTGTCGCTGCACTAGCTCACTAATACCATCTAAGTA 13254
Qy 3773 GTTGATTCATAGTCACTGATGTTGTTTGTATTTTACAGTATTATGTAGTCTGTTTTTATG 3832
Db 13253 GTTGATTCATAGTCACTGATGTTGTTTGTATTTTACAGTATTATGTAGTCTGTTTTTATG 13194
Qy 3833 CAAATCTAAATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3892
Db 13193 CAAATCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13134
Qy 3893 GTACAACTTGTG 3905
Db 13133 GTACAACTTGTG 13121

RESULT 9

US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT FILING DATE: 2002-05-21
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; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201

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; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
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; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match      68.3%; Score 3199.6; DB 15; Length 18691;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 4460; Conservative 0; Mismatches 84; Indels 1140; Gaps 7;

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DB 13601 CTAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCTGACCTGACAGCTGGCTGTGATA 13660

QY 566 AGGAGAGCTGACATTTATATTTCCCGACAGACATCAGGTTAATGGGTTTTTGTATGTCATTT 625
DB 13661 AGGAGAGCTGACATTTATATTTCCCGACAGACATCAGGTTAATGGGTTTTTGTATGTCATTT 13720

QY 626 TCGCGGTGGGTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 685
DB 13721 TCGCGGTGGGTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 13780

686 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCAACGG 745
13781 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCAACGG 13840

746 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 805
13841 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 13900

806 GTGTCAATAATATCACTCTGTATACCAAAACAGACGATACGGCTCTCTCTTTATAG 865
13901 GTGTCAATAATATCACTCTGTATACCAAAACAGACGATACGGCTCTCTCTTTATAG 13960

866 GTGTAAACCTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTCAAT 925
13961 GTGTAAACCTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTCAAT 14020

926 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCGATTTTCGGTTTCCAGCGTTCCGC 985
14021 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCGATTTTCGGTTTCCAGCGTTCCGC 14080

986 AGCAGACGACGGCTTTCATTTCTGATGTTGCTTACGACGCGAGATATTGACATC 1045
14081 AGCAGACGACGGCTTTCATTTCTGATGTTGCTTACGACGCGAGATATTGACATC 14140

1046 ATATATGCTTTCAGCAACTGATAGCTGTGCTGTCTCAACTGTCTCACTGTAATACGCTCTTC 1105
14141 ATATATGCTTTCAGCAACTGATAGCTGTGCTGTCTCAACTGTCTCACTGTAATACGCTCTTC 14200

1106 ATAGCAGACTCTTTTTCATATCTGCGGTAGTGCAGTCAACGCTCTCATTTTCGCCAA 1165
14201 ATAGCAGACTCTTTTTCATATCTGCGGTAGTGCAGTCAACGCTCTCATTTTCGCCAA 14260

1166 AAGTTCGCCCGAGGCTTCCCGGTATCAACAGGAGACACAGGATTTATTTATTTCTCGAAG 1225
14261 AAGTTCGCCCGAGGCTTCCCGGTATCAACAGGAGACACAGGATTTATTTATTTCTCGAAG 14320

1226 TGATCTTCGCTCAGAGTATTTTATTCGGCGCAAGTGCCTCGGGTGATCTGCAACTTA 1285
14321 TGATCTTCGCTCAGAGTATTTTATTCGGCGCAAGTGCCTCGGGTGATCTGCAACTTA 14380

1286 GTCGACTCAGGTCATATACATCTAAGTAGTGTGATTCATAGTACCTGGATATGTTGT 1345
14381 GTCGACTCAGGTCATATACATCTAAGTAGTGTGATTCATAGTACCTGGATATGTTGT 14440

1346 GTTTTACAGTATTATGTAGTCTGTTTATGCAAAATCTAATTTAATATATATGATATTT 1405
14441 GTTTTACAGTATTATGTAGTCTGTTTATGCAAAATCTAATTTAATATATATGATATTT 14500

1406 ATATCATTTTACGTTTCTCGTTCAGCTTTCTTTGTAACAAAGTGG- 1448
14501 ATATCATTTTACGTTTCTCGTTCAGCTTTCTTTGTAACAAAGTGGCAATTAAGAAAGCAT 14560

1449 ----- 1448
14561 TGCTTATCAATTTGTTGCAACGAAACAGTGCATATCAGTCAAAATAAATATATTTTGC 14620

1449 -----TCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATTTATTT 1493
14621 CATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATAATTTATTT 14679

1494 TCTTTTTCCTTTTATGATAAATAATAGTTAAGTGTGTTAATTAGTATGATATATAATAATA 1553
14680 TCTTTTTCCTTTTATGATAAATAATAGTTAAGTGTGTTAATTAGTATGATATATAATAATA 14739

1554 TAGTCTGTATATAATGTGAAAAAATAATTTATATAATATTTGTTTACATAAACAACATAGT 1613
14740 TAGTCTGTATATAATGTGAAAAAATAATTTATATAATATTTGTTTACATAAACAACATAGT 14799

1614 AATGTAAAAAATAATGACAAAGTGTGTAAGACGAAAGAGATAAAGTTGAGAGTAAGT 1673
14800 AATGTAAAAAATAATGACAAAGTGTGTAAGACGAAAGAGATAAAGTTGAGAGTAAGT 14859
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QY 3526 TGACATAGCGTATATGAATAGTAGATGTTTTATTTTGTACACAAAAAGAGGCTCG 3585
Db |
QY 16609 TGACATAGCGTATATGAATAGTAGATGTTTTATTTTGTACACAAAAAGAGGCTCG 16668
Db |
QY 3586 CACCTCTTTTCTTATTTCTTTTATGATTAATAGCGCATTCAGACAAATAGCGAGTAG 3645
Db |
QY 16669 CACCTCTTTTCTTATTTCTTTTATGATTAATAGCGCATTCAGACAAATAGCGAGTAG 16728
Db |
QY 3646 GCTGGATACGACGATTCCTGTTTGGAGAAGAACATTTGGAAAGCTGTCCGTCGACTAAGTTG 3705
Db |
QY 16729 GCTGGATACGACGATTCCTGTTTGGAGAAGAACATTTGGAAAGCTGTCCGTCGACTAAGTTG 16788
Db |
QY 3706 GAGCATACCCGAGAAACAAATTTGGAAAGCTGTCCGTCGACTACAGTCACTAATACCAT 3765
Db |
QY 16789 GAGCATACCCGAGAAACAAATTTGGAAAGCTGTCCGTCGACTACAGTCACTAATACCAT 16848
Db |
QY 3766 CTAAGTAGTTGATTCATAGTAGTACGATGATGTTGTTTTTACAGTATTATGATGCTGTT 3825
Db |
QY 16849 CTAAGTAGTTGATTCATAGTAGTACGATGATGTTGTTTTTACAGTATTATGATGCTGTT 16908
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QY 3826 TTTTATGCAAAATCTAATTAATATATGATTAATTTATATCATTTTACGTTTCTCGTTTCA 3885
Db |
QY 16909 TTTTATGCAAAATCTAATTAATATATGATTAATTTATATCATTTTACGTTTCTCGTTTCA 16968
Db |
QY 3886 CTTTTTGTACAAACTG----- 3903
Db |
QY 16969 CTTTTTGTACAAAGTTGGCAATTATAAAAAAGCATTGCTCATCAATTTGTTGCAACGAAC 17028
Db |
QY 3904 -----TCATAG 3908
Db |
QY 17029 AGTCACTATCAGTCAAAATATAATCATTTATTTGGGCGCCGAGATCCATGCTAGCTCTAG 17088
Db |
QY 3909 AGTCCTGCTTTAATGAGATATGCGAGACGCCATATGATCGCATGATATTTGCTTTTCAATTC 3968
Db |
QY 17089 AGTCCTGCTTTAATGAGATATGCGAGACGCCATATGATCGCATGATATTTGCTTTTCAATTC 17148
Db |
QY 3969 TGTGTGACGCTGTGAAAAAAGCTGAGCATGTGTAGTCTAGATCCTTACCGCGGTTTCG 4028
Db |
QY 17149 TGTGTGACGCTGTGAAAAAAGCTGAGCATGTGTAGTCTAGATCCTTACCGCGGTTTCG 17208
Db |
QY 4029 GTTCATCTTAATGAATATATACCCGTTACTATCGTATTTTATGATTAATATTTCTCCGT 4088
Db |
QY 17209 GTTCATCTTAATGAATATATACCCGTTACTATCGTATTTTATGATTAATATTTCTCCGT 17268
Db |
QY 4089 TCAATTTACTGATGTACCCCTACTACTTATATGATGATCAATATTAATAATGAAAAACAATATAT 4148
Db |
QY 17269 TCAATTTACTGATGTACCCCTACTACTTATATGATGATCAATATTAATAATGAAAAACAATATAT 17328
Db |
QY 4149 TGTGCTGATAGTTTATAGCGACATCTATGATAGAGCGCCACATTAACAACAATTCGG 4208
Db |
QY 17329 TGTGCTGATAGTTTATAGCGACATCTATGATAGAGCGCCACATTAACAACAATTCGG 17388
Db |
QY 4209 TTTTATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTTAAAGACT 4268
Db |
QY 17389 TTTTATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTTAAAGACT 17448
Db |
QY 4269 GATTACATAAATCTTATTTCAAAATTTCAAAAGCCCGGAGGCTAGTATCTACGACACACC 4328
Db |
QY 17449 GATTACATAAATCTTATTTCAAAATTTCAAAAGCCCGGAGGCTAGTATCTACGACACACC 17508
Db |
QY 4329 GAGCGCGGAACCTAATAAGCTTCACTGAGGGAACCTCCGTTCCCGCGCGCGGATGGG 4388
Db |
QY 17509 GAGCGCGGAACCTAATAAGCTTCACTGAGGGAACCTCCGTTCCCGCGCGCGGATGGG 17568
Db |
QY 4389 TGAGATTCCTTTGAAGTTGAGTATGGCCGCTCTACCGAAAGTTACGGGCACCATTC 4448
Db |
QY 17569 TGAGATTCCTTTGAAGTTGAGTATGGCCGCTCTACCGAAAGTTACGGGCACCATTC 17628
Db |
QY 4449 AACCGGCTCCAGCAGCGCGCGGCTTAACCGATCTGCTGCCCGGAGAAATTAATGACGAT 4508
Db |
QY 17629 AACCGGCTCCAGCAGCGCGCGGCTTAACCGATCTGCTGCCCGGAGAAATTAATGACGAT 17688
Db |

QY 4509 TTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACCTTGAACCTGACGACAAAT 4568
Db |
QY 17689 TTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACCTTGAACCTGACGACAAAT 17748
Db |
QY 4569 CTTTGGCGGGTCCAGGGCGAAATTTTGCACAACATGTGAGGCTCAGAGACCTGCGAG 4628
Db |
QY 17749 CTTTGGCGGGTCCAGGGCGAAATTTTGCACAACATGTGAGGCTCAGAGACCTGCGAG 17808
Db |
QY 4629 GCATGCAAGCTAGCTTACTAGTAGTGATGATATTTCTATAGTGTACCTAAATCTGC 4682
Db |
QY 17809 GCATGCAAGCTAGCTTACTAGTAGTGATGATATTTCTATAGTGTACCTAAATCTGC 17862
Db |

RESULT 6

US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmuth, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17830)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)

QY 4381 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGCTCGCTCTACCGAAAGTTACGGG 4440
Db 17157 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGCTCGCTCTACCGAAAGTTACGGG 17216
QY 4441 CACCAATCAACCGGTCACGACGGCGGCGGCTTAACCGACTTGTGCGCCCGAGAAATTAT 4500
Db 17217 CACCAATCAACCGGTCACGACGGCGGCGGCTTAACCGACTTGTGCGCCCGAGAAATTAT 17276
QY 4501 GCAGCAATTTTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACTTCGACAGTGA 4560
Db 17277 GCAGCAATTTTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACTTCGACAGTGA 17336
QY 4561 CGCAAAATCGTTGGCGGGTCCAGGGCGAAATTTTGGCAAAATGTCGAGGCTCAGCAGG 4620
Db 17337 CGCAAAATCGTTGGCGGGTCCAGGGCGAAATTTTGGCAAAATGTCGAGGCTCAGCAGG 17396
QY 4621 ACCTGCAGGCGATGCAAGTACTGCTTACTAGTGATGATATTTCTATAGTGTCAACCTTAATCT 4680
Db 17397 ACCTGCAGGCGATGCAAGTACTGCTTACTAGTGATGATATTTCTATAGTGTCAACCTTAATCT 17456
QY 4681 GC 4682
Db 17457 GC 17458

RESULT 5

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 87.1%; Score 4077.2; DB 15; Length 17862;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 447; Conservative 0; Mismatches 68; Indels 309; Gaps 5;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 85
Db 13121 GCCAATTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 13180
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAACACACATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAACACACATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGATATAGTACACCTGTAGTGCAGCGAGCGCTTCCCAA 205
Db 13241 ACTATGAATCAACTACTTAGATGATATAGTACACCTGTAGTGCAGCGAGCGCTTCCCAA 13300
QY 206 TGTCTCTCGGCTGATGCTGCCAACTTAGTGCAGCGAGCGCTTCCAAATGTTCTCTCAA 265
Db 13301 TGTCTCTCGGCTGATGCTGCCAACTTAGTGCAGCGAGCGCTTCCAAATGTTCTCTCAA 13360
QY 266 ACGGAATCGTGTATCCAGCGCTACTCGCTATTGTCTCAATGCGGATTAATCAATAA 325
Db 13361 ACGGAATCGTGTATCCAGCGCTACTCGCTATTGTCTCAATGCGGATTAATCAATAA 13420

QY 326 AGAAATAAGAAAAAGAGTGGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
Db 13421 AGAAATAAGAAAAAGAGTGGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13480
QY 386 ATTCAATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAAACAATTTCAAC 445
Db 13481 ATTCAATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAAACAATTTCAAC 13540
QY 446 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCATCTGGATTTTTCAGGCTCTATATTA 505
Db 13541 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCATCTGGATTTTTCAGGCTCTATATTA 13600
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTTCTAGTGTATCGACCTGCAGACTGGCTGTGTATA 565
Db 13601 CTAAACGCTGATAAAGTTTCTGTAAATTTTCTAGTGTATCGACCTGCAGACTGGCTGTGTATA 13660
QY 566 AGGAGCCTGACATTTATATTCCCGAGAACATCAGGTTAATGGCGTTTGTGATCATTT 625
Db 13661 AGGAGCCTGACATTTATATTCCCGAGAACATCAGGTTAATGGCGTTTGTGATCATTT 13720
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTCCCGATAACGAGACCGGCACACTGGCCATA 685
Db 13721 TCGCGGTGGCTGAGATCAGCCACTTCTCCCGATAACGAGACCGGCACACTGGCCATA 13780
QY 686 TCGGTGCTCATATGCGCCAGCTTTTATCCCGATATGACCAACCGGGTAAAGTTCAACG 745
Db 13781 TCGGTGCTCATATGCGCCAGCTTTTATCCCGATATGACCAACCGGGTAAAGTTCAACG 13840
QY 746 GAGACTTTATCTGACAGCAGAGCTGACGTCGGCCAGGGGATCACATCCGTCGCGCGGC 805
Db 13841 GAGACTTTATCTGACAGCAGAGCTGACGTCGGCCAGGGGATCACATCCGTCGCGCGGC 13900
QY 806 GTGTCAATTAATATCACTCTGTATACATCCACAAACAGACAGATAACGGCTCTCTTTTATAG 865
Db 13901 GTGTCAATTAATATCACTCTGTATACATCCACAAACAGACAGATAACGGCTCTCTTTTATAG 13960
QY 866 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTCTCGTCAGCAAAAAGAGCGTTTAT 925
Db 13961 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTCTCGTCAGCAAAAAGAGCGTTTAT 14020
QY 926 TTCAATAAACCGGGCGACCTGACGCTCCCTCTCTGATTTTCCGCTTCCAGGTTCCGC 985
Db 14021 TTCAATAAACCGGGCGACCTGACGCTCCCTCTCTGATTTTCCGCTTCCAGGTTCCGC 14080
QY 986 ACGCAGACGACGGCTTCAATCTGTGATGTTGTCTTACAGACCGGAGATTTGACATC 1045
Db 14081 ACGCAGACGACGGCTTCAATCTGTGATGTTGTCTTACAGACCGGAGATTTGACATC 14140
QY 1046 ATATATGCTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 1105
Db 14141 ATATATGCTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 14200
QY 1106 ATAGCACACCTCTTTTTCACATACCTTCCGCTAGTGCAGTCAACGCTCTCATTTTCGCA 1165
Db 14201 ATAGCACACCTCTTTTTCACATACCTTCCGCTAGTGCAGTCAACGCTCTCATTTTCGCA 14260
QY 1166 AAGTTGGCCAGGCTTCCCGGTATCAACAGAGGACACAGAGTTTATTTATCTCGAAG 1225
Db 14261 AAGTTGGCCAGGCTTCCCGGTATCAACAGAGGACACAGAGTTTATTTATCTCGAAG 14320
QY 1226 TGATCTTCCGTCACAGGTTATTTTTCGGGCAAAAGTGGTGGGTGATGCTGCCAACTTA 1285
Db 14321 TGATCTTCCGTCACAGGTTATTTTTCGGGCAAAAGTGGTGGGTGATGCTGCCAACTTA 14380
QY 1286 GTCGACTACAGTCACTAATACCTAAGTAGTTGATTCATAGTACGTGATATGTTGT 1345
Db 14381 GTCGACTACAGTCACTAATACCTAAGTAGTTGATTCATAGTACGTGATATGTTGT 14440
QY 1346 GTTTTACAGTATATAGTGTCTGTTTTTATGCAAAAATCTAATTTAATATATGATATTT 1405
Db 14441 GTTTTACAGTATATAGTGTCTGTTTTTATGCAAAAATCTAATTTAATATATGATATTT 14500
QY 1406 ATATCATTTTACGTTTCTCGTTACAGCTTCTTTGTACAAAGTGG----- 1448

Db	15156	TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATGTTGTTATCATTCAT	15215
Qy	2221	CTTACATTTGGATTGATTACAGTTGGGAAGCTGGGTTGCAGAAATCGATAAGCTTGGCGTGC	2280
Db	15216	CTTACATTTGGATTGATTACAGTTACTTACCT	15247
Qy	2281	AGTTATCATCATCATCATAGACACAGAAATAAAGTAATCAGATTATCAGTTTAAAGCTTAT	2340
Db	15248	-----	15247
Qy	2341	GTAATATTTGGCCATAACCAATCAATTAAATAATAGATCAGTTTAAAGAAGATCAAAG	2400
Db	15248	-----	15247
Qy	2401	CTCAAAAAATAAAAGAGAGAAAAGGGTCCTAACCAAGAAAAATGAAGGAGAAAAA	2460
Db	15248	-----	15247
Qy	2461	ATTTACCTGCACAAGCTTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAAACGAGAAA	2520
Db	15248	-----	15296
Qy	2521	CGTAAATGATATAAATATCAATATATTAATTAATTTAGATTTTGCATAAAAA	2580
Db	15297	CGTAAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAA	15356
Qy	2581	AATACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACCTTAGATTGTTAGTG	2640
Db	15357	AATACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACCTTAGATTGTTAGTG	15416
Qy	2641	ACCTGTAGTCGATAAGTTGGCAGCATACCCGACGCACTTTTGCGCCGAATAAATACCTG	2700
Db	15417	ACCTGTAGTCGATAAGTTGGCAGCATACCCGACGCACTTTTGCGCCGAATAAATACCTG	15476
Qy	2701	TGACGGAGATCACTTCGCAGATAAATAAATCCTGGTGTCCTGTTGATACCGGGAAC	2760
Db	15477	TGACGGAGATCACTTCGCAGATAAATAAATCCTGGTGTCCTGTTGATACCGGGAAC	15536
Qy	2761	CCTGGGCCAACTTTTGGCGAAAATGAGCGTTGATCGGAATTTCACAACTCTTTATACTTTT	2820
Db	15537	CCTGGGCCAACTTTTGGCGAAAATGAGCGTTGATCGGAATTTCACAACTCTTTATACTTTT	15596
Qy	2821	CTCTTACAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACCTTAAACGTTGATA	2880
Db	15597	CTCTTACAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACCTTAAACGTTGATA	15656
Qy	2881	AAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATTAAGGAGCCTGAC	2940
Db	15657	AAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATTAAGGAGCCTGAC	15716
Qy	2941	ATTTATATTTCCCGAGAACATCAGGTTAAATGGCGTTTATTTGATGTCAATTTTCGGTGGCTG	3000
Db	15717	ATTTATATTTCCCGAGAACATCAGGTTAAATGGCGTTTATTTGATGTCAATTTTCGGTGGCTG	15776
Qy	3001	AGATCAGCACTTCTTCCCGGATAACGAGACAACCGCACTGGCCGATATCGGTGGTCAATC	3060
Db	15777	AGATCAGCACTTCTTCCCGGATAACGAGACAACCGCACTGGCCGATATCGGTGGTCAATC	15836
Qy	3061	ATCGCCGAGTTTCAATCCCGATATGCACACCGGGTAAAGTTTACGGGAGACTTTATCT	3120
Db	15837	ATCGCCGAGTTTCAATCCCGGATATGCACACCGGGTAAAGTTTACGGGAGACTTTATCT	15896
Qy	3121	GACAGCAGAGCTGCACCTGGCCAGGGGATACACATCCGTCGCCCGGGCGTGTCAATAATA	3180
Db	15897	GACAGCAGAGCTGCACCTGGCCAGGGGATACACATCCGTCGCCCGGGCGTGTCAATAATA	15956
Qy	3181	TCATCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTA	3240
Db	15957	TCATCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTA	16016
Qy	3241	AACTGCATTTCAACAGTCCCTGTTCTCCGTACGAAAAAGAGCGGTTCAATTAACACCG	3300

DB	16017	AACTGCATTTCCACAGTCCCTGTCTCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCG	16076
QY	3301	GGCGACCTCAGCGCATCCCTTCCTGATTTTCGCTTTCCAGCGTTCCGACGCGGACGACGACG	3360
DB	16077	GGCGACCTCAGCGCATCCCTTCCTGATTTTCGCTTTCCAGCGTTCCGACGCGGACGACGACG	16136
QY	3361	GGCTTCATTTCTGCAATGGTTGTGCTTACCAGACGGAGATATTGCATCATATATGCTCTTG	3420
DB	16137	GGCTTCATTTCTGCAATGGTTGTGCTTACCAGACGGAGATATTGCATCATATATGCTCTTG	16196
QY	3421	AGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTGTAATAGCTGCTTCAATAGCACACCTC	3480
DB	16197	AGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTGTAATAGCTGCTTCAATAGCACACCTC	16256
QY	3481	TTTTTGCATACATCTTCGTTCTTCATGCGAGATGTTTTCAGGACTATGACACTAGCGGTATA	3540
DB	16257	TTTTTGCATACATCTTCGTTCTTCATGCGAGATGTTTTCAGGACTATGACACTAGCGGTATA	16316
QY	3541	TGAATAGGTAGATGTTTTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCTTTTTCTTTA	3600
DB	16317	TGAATAGGTAGATGTTTTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCTTTTTCTTTA	16376
QY	3601	TTTTCTTTTTATGATTTAATACGCATGTAGGACAAATAGCGAGTAGGCTGGATACGACGAT	3660
DB	16377	TTTTCTTTTTATGATTTAATACGCATGTAGGACAAATAGCGAGTAGGCTGGATACGACGAT	16436
QY	3661	TCCGTTTTGAGAGAACATTTTGAAGGCTGTGCGTCGACTAAGTTGCGACGATCACCCGAA	3720
DB	16437	TCCGTTTTGAGAGAACATTTTGAAGGCTGTGCGTCGACTAAGTTGCGACGATCACCCGAA	16496
QY	3721	GAACATTTGGAAGGCTGTGCGTCGACTACAGGTCACATAATCACTCAAGTAGTTGATTC	3780
DB	16497	GAACATTTGGAAGGCTGTGCGTCGACTACAGGTCACATAATCACTCAAGTAGTTGATTC	16556
QY	3781	ATAGTGACTGGATATGTTGTGTTTTACAGTATTTATGTAGTCGTGTTTTTATGCAAAATCT	3840
DB	16557	ATAGTGACTGGATATGTTGTGTTTTACAGTATTTATGTAGTCGTGTTTTTATGCAAAATCT	16616
QY	3841	AAATTAATATATGATATTTATATCAATTTTACGTTTCTCGTTCAGCTTTTGTGTAACAAC	3900
DB	16617	AAATTAATATATGATATTTATATCAATTTTACGTTTCTCGTTCAGCTTTTGTGTAACAAC	16676
QY	3901	TTGTTAGAGTCTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTGCT	3960
DB	16677	TTGTTAGAGTCTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTGCT	16736
QY	3961	TTCAATCTGTTGTCGACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACGCG	4020
DB	16737	TTCAATCTGTTGTCGACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACGCG	16796
QY	4021	CGGTTTCGGTTCAATCTAATGAATATATCAACCGTTTACTATGCTATTTTATGAATAATA	4080
DB	16797	CGGTTTCGGTTCAATCTAATGAATATATCAACCGTTTACTATGCTATTTTATGAATAATA	16856
QY	4081	TTCTCCGTTCAATTTACTGTTTACCCCTACTTATATGTACAAATATTAATAATGAAAA	4140
DB	16857	TTCTCCGTTCAATTTACTGTTTACCCCTACTTATATGTACAAATATTAATAATGAAAA	16916
QY	4141	CAATATATTTGTCGTAATAGTTTATAGGCACTATGATAGAGCGGCACTAATACAAA	4200
DB	16917	CAATATATTTGTCGTAATAGTTTATAGGCACTATGATAGAGCGGCACTAATACAAA	16976
QY	4201	CAATTCGGTTTTATTAATACAAATCCAAATTTTAAAAAAGCGGACGACCGTCAACCT	4260
DB	16977	CAATTCGGTTTTATTAATACAAATCCAAATTTTAAAAAAGCGGACGACCGTCAACCT	17036
QY	4261	AAAAGACTGATTACATAAAATCTTATTCAAATTTCAAAAAGCGCCAGGGCTAGTATCTAC	4320
DB	17037	AAAAGACTGATTACATAAAATCTTATTCAAATTTCAAAAAGCGCCAGGGCTAGTATCTAC	17096
QY	4321	GACACCGGAGCGGAACTAATAAGCTTCACTGAAAGGAACTCCGGTTCCCGCGCGCG	4380
DB	17097	GACACCGGAGCGGAACTAATAAGCTTCACTGAAAGGAACTCCGGTTCCCGCGCGCG	17156

QY 1 TTTTCATTGGAGAGGACACGCTCGAGCAAGTTTGTACAAAAAGCTGAACGAGAAACGT 60
Db TTTTCATTGGAGAGGACACGCTCGAGCAAGTTTGTACAAAAAGCTGAACGAGAAACGT 13059
QY 61 AAAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db AAAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13060
QY 121 ACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 180
Db ACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 13179
QY 181 TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCCGGGTGATGCTGCCAACTTAGTCGACCG 240
Db TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCCGGGTGATGCTGCCAACTTAGTCGACCG 13239
QY 241 ACAGCCTTCCAAATGTTCTTCCAAATGTTCTTCCAAATGTTCTTCCAAATGTTCTTCCAA 300
Db ACAGCCTTCCAAATGTTCTTCCAAATGTTCTTCCAAATGTTCTTCCAAATGTTCTTCCAA 13240
QY 301 CTCATGCGGTATTAATCATAAAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTGTG 360
Db CTCATGCGGTATTAATCATAAAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTGTG 13300
QY 361 TGTGCAAAATAAACAATCTACTATCATATACGCTAGTGTCAATGATCTCTGAAAAATCA 420
Db TGTGCAAAATAAACAATCTACTATCATATACGCTAGTGTCAATGATCTCTGAAAAATCA 13360
QY 421 TCTGCAATCAAGAACAAATTCACAACTCTTATCTTTCTTTCAAGAGTGGTTCGGCTTCA 480
Db TCTGCAATCAAGAACAAATTCACAACTCTTATCTTTCTTTCAAGAGTGGTTCGGCTTCA 13420
QY 481 TCTGGATTTTACGCTCTATCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 540
Db TCTGGATTTTACGCTCTATCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 13480
QY 541 TCGACTCGAGACTGGCTGTATATAGGAGGCTGACATTAATATPCCCGAACAATCAG 600
Db TCGACTCGAGACTGGCTGTATATAGGAGGCTGACATTAATATPCCCGAACAATCAG 13540
QY 601 GTTAATGGCGTTTTCATGCTCAATTTTCGGGTGGCTGAGATCAGCACTCTTCCCGAT 660
Db GTTAATGGCGTTTTCATGCTCAATTTTCGGGTGGCTGAGATCAGCACTCTTCCCGAT 13600
QY 661 AACGGAGACCGGCACACTGGCCATATCGGTGTGTCATCATGCGCCAGCTTTCATCCCGAT 720
Db AACGGAGACCGGCACACTGGCCATATCGGTGTGTCATCATGCGCCAGCTTTCATCCCGAT 13660
QY 721 ATGCAACCGCGGTAAAGTTTCAGGAGACTTTATCTGACAGACGTCGACTGGCCAG 780
Db ATGCAACCGCGGTAAAGTTTCAGGAGACTTTATCTGACAGACGTCGACTGGCCAG 13720
QY 781 GGGGATCACCATCCGTCGGCCGGGTGTCAATATATCACTCTGTCATATCCCAACAG 840
Db GGGGATCACCATCCGTCGGCCGGGTGTCAATATATCACTCTGTCATATCCCAACAG 13780
QY 841 AGATAAGCGCTCTCTCTTTTATAGGTGTAACCTTAAACCTGATTTACCAAGTCCCTGT 900
Db AGATAAGCGCTCTCTCTTTTATAGGTGTAACCTTAAACCTGATTTACCAAGTCCCTGT 13840
QY 901 TCTCGTCAGCAAAAGACCGCTTCAATTAATAAACCGGGGACCTCAGCCATCCCTTCT 960
Db TCTCGTCAGCAAAAGACCGCTTCAATTAATAAACCGGGGACCTCAGCCATCCCTTCT 13900
QY 961 GATTTTCCGCTTTCAGGCTTCGGACGACGAGCGGCTTCAATTCGATGGTGTGTC 1020
Db GATTTTCCGCTTTCAGGCTTCGGACGACGAGCGGCTTCAATTCGATGGTGTGTC 13960
QY 1021 TTACGAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTC 1080
Db TTACGAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTC 14020
QY 14020 TTACGAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTC 14079

QY 1081 AACTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTTCACATCTCTGGGTAGTG 1140
Db AACTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTTCACATCTCTGGGTAGTG 14139
QY 1141 CCGATCAACGCTCTCAATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC 1200
Db CCGATCAACGCTCTCAATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC 14199
QY 1201 ACCAGATTTATTTATCTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAG 1260
Db ACCAGATTTATTTATCTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAG 14259
QY 1261 TCGCTCGGCTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATAACCACTTAAGTAGTT 1320
Db TCGCTCGGCTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATAACCACTTAAGTAGTT 14319
QY 1321 GATTCATAGTGAATGATGTTGTTTACAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1380
Db GATTCATAGTGAATGATGTTGTTTACAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 14379
QY 1381 AATCTAAATTTAATATATGATATTTATATCAATTTTACGTTCTCGTTCAGCTTCTTGT 1440
Db AATCTAAATTTAATATATGATATTTATATCAATTTTACGTTCTCGTTCAGCTTCTTGT 14439
QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATATTTTCTTTTT 1500
Db CAAAGTGTCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATATTTTCTTTTT 14495
QY 1501 TCGTTTTAGTATATAATAGTTAAGTGAATTAAGTATTAAGTATTAAGTATTAAGTATTA 1560
Db TCGTTTTAGTATATAATAGTTAAGTGAATTAAGTATTAAGTATTAAGTATTAAGTATTA 14555
QY 1561 TATAATGTGAAAAAATAATTTATATAATATTTATATAATTTTACATAAACAACATAGTATA 1620
Db TATAATGTGAAAAAATAATTTATATAATTTATATAATTTTACATAAACAACATAGTATA 14615
QY 1621 AAAAAATATGCAAGTGTGTGAAGCAAGAAAGATAAAGTTGAGAGTAAGTATATATAT 1680
Db AAAAAATATGCAAGTGTGTGAAGCAAGAAAGATAAAGTTGAGAGTAAGTATATATAT 14675
QY 1681 TTTTAAATGAATTTGATGCAACATGTAAGATATATAGCAATTAATTTGTTTAAATC 1740
Db TTTTAAATGAATTTGATGCAACATGTAAGATATATAGCAATTAATTTGTTTAAATC 14735
QY 1741 ATAAATAGTAAATTTCTAGCTGTTTGAATTAATAATCAATGATAAATACATATAGTAAA 1800
Db ATAAATAGTAAATTTCTAGCTGTTTGAATTAATAATCAATGATAAATACATATAGTAAA 14795
QY 1801 AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860
Db AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 14796
QY 1861 AATATCTATACATTTACTTAATATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT 1920
Db AATATCTATACATTTACTTAATATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT 14855
QY 1921 TCCAAATCTGTTGTAATTTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1980
Db TCCAAATCTGTTGTAATTTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 14915
QY 1981 TAAATCAAACTAATAGAAAAGTAAATCTAATGTAAACAAAACATAATCTAATGCTAATAT 2040
Db TAAATCAAACTAATAGAAAAGTAAATCTAATGTAAACAAAACATAATCTAATGCTAATAT 15035
QY 2041 AACAAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACAACTTATTAATAT 2100
Db AACAAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACAACTTATTAATAT 15095
QY 2101 TTTTAAATTAATCTGTTGTTTATTAATCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2160
Db TTTTAAATTAATCTGTTGTTTATTAATCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 15155
QY 2161 TTAGTCGAACGAATAAACAAAGGTAAACATGATAGATCATCTGTTGTTTATCATTTAT 2220

QY	781	GGGGATCACCATCGGTGCGCCGGGGGTGCAATAATACATCTCTGTACATCCACAAAACAG	840
Db	13780	GGGGATCACCATCGGTGCGCCGGGGGTGCAATAATACATCTCTGTACATCCACAAAACAG	13839
QY	841	ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACACAGTCCCTGT	900
Db	13840	ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACACAGTCCCTGT	13899
QY	901	TCTCGTCAGCAAAAGAGCCGTTCAITTTCAATAAACGGGCGACCTCAGCCATCCCTTCCT	960
Db	13900	TCTCGTCAGCAAAAGAGCCGTTCAITTTCAATAAACGGGCGACCTCAGCCATCCCTTCCT	13959
QY	961	GATTTTCGGCTTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCACTTCGCAATGGTTGTC	1020
Db	13960	GATTTTCGGCTTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCACTTCGCAATGGTTGTC	14019
QY	1021	TTACCAGACGGAGATATTGACATCATATATGCTTGAGCAACTGATAGTCTCGCTGTC	1080
Db	14020	TTACCAGACGGAGATATTGACATCATATATGCTTGAGCAACTGATAGTCTCGCTGTC	14079
QY	1081	AACTGTCACTGTAAATAGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTAGTG	1140
Db	14080	AACTGTCACTGTAAATAGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTAGTG	14139
QY	1141	CCGATCAACGTCATNTTTCGCCAAAAGTTGGCCGAGGCTTCCCGGTATCAACAGGAC	1200
Db	14140	CCGATCAACGTCATNTTTCGCCAAAAGTTGGCCGAGGCTTCCCGGTATCAACAGGAC	14199
QY	1201	ACCAGGATTTATTTATCTCCGAAGTGATCTTCGGTCACAGGTATTTATTCGGCGCAAG	1260
Db	14200	ACCAGGATTTATTTATCTCCGAAGTGATCTTCGGTCACAGGTATTTATTCGGCGCAAG	14259
QY	1261	TGCGTCGGGTGATGCTGCCAACTTAGTTCGACTACAGGTCACTAAATCCATCTAAGTAGTT	1320
Db	14260	TGCGTCGGGTGATGCTGCCAACTTAGTTCGACTACAGGTCACTAAATCCATCTAAGTAGTT	14319
QY	1321	GATTCATAGTGACTGGATATGTTGCTGTTTACAGTATTATGTAGTCTGTTTTTATGCAA	1380
Db	14320	GATTCATAGTGACTGGATATGTTGCTGTTTACAGTATTATGTAGTCTGTTTTTATGCAA	14379
QY	1381	AATCTAATTTAAATATTTGATATTTATATCATTTTACGTTTTCTCGTTCAGCTTCTTGTA	1440
Db	14380	AATCTAATTTAAATATTTGATATTTATATCATTTTACGTTTTCTCGTTCAGCTTCTTGTA	14439
QY	1441	CAAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGCTAAGGAAATAATATTTCTTTT	1500
Db	14440	CAAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGCTAAGGAAATAATATTTCTTTT	14499
QY	1501	TCCTTTTAGTATAAATAGTTAAGTGATGTTAATTTAGTATGATTAATATATAGTTGT	1560
Db	14500	TCCTTTTAGTATAAATAGTTAAGTGATGTTAATTTAGTATGATTAATATATAGTTGT	14559
QY	1561	TATAATTTGTCAAAAAATAATTTATAATATTTGTTTACATAAACAACATAGTAATGTA	1620
Db	14560	TATAATTTGTCAAAAAATAATTTATAATATTTGTTTACATAAACAACATAGTAATGTA	14619
QY	1621	AAAAATGACAAAGTGATGTGAAGACGAAGAGATAAAAGTTGAGAGTAAGTATATTAT	1680
Db	14620	AAAAATGACAAAGTGATGTGAAGACGAAGAGATAAAAGTTGAGAGTAAGTATATTAT	14679
QY	1681	TTTTTAATGAATTTGATCGAACATGTAAGATGATATCTAGCATTAATTTGTTTTAATC	1740
Db	14680	TTTTTAATGAATTTGATCGAACATGTAAGATGATATCTAGCATTAATTTGTTTTAATC	14739
QY	1741	ATAATAGTAATCTAGCTGGTTTGATGAATTAATAATCAATGATAAATCTATAGTAAA	1800
Db	14740	ATAATAGTAATCTAGCTGGTTTGATGAATTAATAATCAATGATAAATCTATAGTAAA	14799
QY	1801	AATAAGAAATAAATAAATAAATAATTTTTTATGATTAAGTTATTTATATAATTA	1860
Db	14800	AATAAGAAATAAATAAATAAATAATTTTTTATGATTAAGTTATTTATATAATTA	14859

QY	1861	AATATCTATACCAATTA	CTAAATAATTTAGT	TTAAAAAGTTAA	TAAATATTTTGTTAGAAAT	1920
DB	14860	AATATCTATACCAATTA	CTAAATAATTTAGT	TTAAAAAGTTAA	TAAATATTTTGTTAGAAAT	14919
QY	1921	TCCAAATCTGCTGTAA	TTTATCAATAAA	CAABAATATTTAAAT	TAAACAGCTTAAAGTTACAAA	1980
DB	14920	TCCAAATCTGCTGTAA	TTTATCAATAAA	CAABAATATTTAAAT	TAAACAGCTTAAAGTTACAAA	14979
QY	1981	TAAATCAAACTAATAG	AAAAACAGTAATCT	AAATGTAA	CAAAAAACATAATCTAAATGCTTAATAT	2040
DB	14980	TAAATCAAACTAATAG	AAAAACAGTAATCT	AAATGTAA	CAAAAAACATAATCTAAATGCTTAATAT	15039
QY	2041	AACAAAGGCAAGATCT	ATCATCTTTATATAG	TATATTTTCAAT	CAACATCTCTATTAAT	2100
DB	15040	AACAAAGGCAAGATCT	ATCATCTTTATATAG	TATATTTTCAAT	CAACATCTCTATTAAT	15099
QY	2101	TTCTAAATAATACCT	GTGTAGTTTTATTA	ACTTCTAAATGGA	TTCACATTTAAATGAAGAA	2160
DB	15100	TTCTAAATAATACCT	GTGTAGTTTTATTA	ACTTCTAAATGGA	TTCACATTTAAATGAAGAA	15159
QY	2161	TTAGTCCAAACATGA	ATAAAAAACAGGTAA	CATGATAGATCAT	GTGCTGTATTCATTTGAT	2220
DB	15160	TTAGTCCAAACATGA	ATAAAAAACAGGTAA	CATGATAGATCAT	GTGCTGTATTCATTTGAT	15219
QY	2221	CTTACATTTGGATGAT	TACAGTTGGAAAGCT	GGGTTTGGAAAT	TCGATAAGCTTTGCGCTGC	2280
DB	15220	CTTACATTTGGATGAT	TACAGTTGGAAAGCT	GGGTTTGGAAAT	TCGATAAGCTTTGCGCTGC	15266
QY	2281	AGTTATCATCATCAT	CATAGACACACGA	AAATAAGTAATCA	CAGTTATCAGTTTAAAGCTTAT	2340
DB	15267	AGTTATCATCATCAT	CATAGACACACGA	AAATAAGTAATCA	CAGTTATCAGTTTAAAGCTTAT	15266
QY	2341	GTAATATTGGCCATA	AAACCAATCAAT	TAAAAAATAGATCA	GTTTAAAGAAAGATCAAAG	2400
DB	15267	GTAATATTGGCCATA	AAACCAATCAAT	TAAAAAATAGATCA	GTTTAAAGAAAGATCAAAG	15266
QY	2401	CTCAAAAAATAAAAG	AGAAAAAGGTCCT	TAACCAAGAAAAAT	TCAAGGAGAAAAAATAGAA	2460
DB	15267	CTCAAAAAATAAAAG	AGAAAAAGGTCCT	TAACCAAGAAAAAT	TCAAGGAGAAAAAATAGAA	15266
QY	2461	ATTTACCTGCACAG	CTTGGATCCTCTAG	ACCACCTTTGTAC	AGAAAGCTGAAACGAGAAA	2520
DB	15267	ATTTACCTGCACAG	CTTGGATCCTCTAG	ACCACCTTTGTAC	AGAAAGCTGAAACGAGAAA	15314
QY	2521	CGTAAAAATGATAA	ATAATCAATATATA	TTAGATTTTGAT	ATAAAAAACAAGACTTACAT	2580
DB	15315	CGTAAAAATGATAA	ATAATCAATATATA	TTAGATTTTGAT	ATAAAAAACAAGACTTACAT	15374
QY	2581	AATACTGTAAAAACA	ACATATCCAGTCAT	ATGAATCAACTACT	TAGATGGTATTAGTG	2640
DB	15375	AATACTGTAAAAACA	ACATATCCAGTCAT	ATGAATCAACTACT	TAGATGGTATTAGTG	15434
QY	2641	ACCTGTAGTCGACT	TAAGTTGGAGCAT	CACCGAGCCACT	TTGCGCGGAAATAAATACCTG	2700
DB	15435	ACCTGTAGTCGACT	TAAGTTGGAGCAT	CACCGAGCCACT	TTGCGCGGAAATAAATACCTG	15494
QY	2701	TGACGGAAGATCA	CTTTCGCAGATAA	ATAATAAATCCT	GTGTCTGTATACGGGAAGC	2760
DB	15495	TGACGGAAGATCA	CTTTCGCAGATAA	ATAATAAATCCT	GTGTCTGTATACGGGAAGC	15554
QY	2761	CTTGGGCCAACTTT	TGGCGAAAAATG	AGACGTGTATCG	GATTTTCACACTCTTTATATCTTTT	2820
DB	15955	CTTGGGCCAACTTT	TGGCGAAAAATG	AGACGTGTATCG	GATTTTCACACTCTTTATATCTTTT	15614
QY	2821	CTCTTCAAGTCGTT	CGGCTTCTATCT	GGAATTTTCAGCTT	CTATATCTTAAACGTGATA	2880
DB	15615	CTCTTCAAGTCGTT	CGGCTTCTATCT	GGAATTTTCAGCTT	CTATATCTTAAACGTGATA	15674
QY	2881	AAGTTTCTGTAAAT	TTCTACTGTATCC	ACCTGCAGACTG	CTGTGTATTAAGGGAGCCTGAC	2940
DB	15675	AAGTTTCTGTAAAT	TTCTACTGTATCC	ACCTGCAGACTG	CTGTGTATTAAGGGAGCCTGAC	15734
QY	2941	ATTTATATTTCCCA	GAAACATCAGGTT	TAAATGGCGTTT	TTTGTATTCATTTTTCGGGTGGCTG	3000

Qy	1561	TATAATTTGTCGAAAAATAAATTTATAAATAATTTGTTTACATAAAACAACATAGTAATGTAA	1620
Db	14560	TATAAATTTGTCGAAAAATAAATTTATAAATAATTTGTTTACATAAAACAACATAGTAATGTAA	14619
Qy	1621	AAAAATATGACAAAGTCGATGTTGAAGCGAGAGAGATAAAGTTGAGAGTAAGTATATTAT	1680
Db	14620	AAAAATATGACAAAGTCGATGTTGAAGCGAGAGAGATAAAGTTGAGAGTAAGTATATTAT	14679
Qy	1681	TTTTTAATGAAATTTGATCGCAACATGTAAAGTATATACTATAGCAATTAATATTTGTTTAAATC	1740
Db	14680	TTTTTAATGAAATTTGATCGCAACATGTAAAGTATATACTATAGCAATTAATATTTGTTTAAATC	14739
Qy	1741	ATTAATAGTAATTTCTAGCTGGTTTGATGAAATTAATAATCAATGATAAATACTATAGTAAA	1800
Db	14740	ATTAATAGTAATTTCTAGCTGGTTTGATGAAATTAATAATCAATGATAAATACTATAGTAAA	14799
Qy	1801	AATAAGAAATAAATAAATAAATAATATTTTATGATTAATAGTTATGTTATATAAATTA	1860
Db	14800	AATAAGAAATAAATAAATAAATAATATTTTATGATTAATAGTTATGTTATATAAATTA	14859
Qy	1861	AAATCTATACCAATTACTTAATAATTTTTAGTTTTAAAAGTTTAATAAATTTTTCTAGAAAT	1920
Db	14860	AAATCTATACCAATTACTTAATAATTTTTAGTTTTAAAAGTTTAATAAATTTTTCTAGAAAT	14919
Qy	1921	TCCAATCTGCTGTGAATTTATCAATAAACAATAATTAATAATCAAGCTAAAGTAACAAA	1980
Db	14920	TCCAATCTGCTGTGAATTTATCAATAAACAATAATTAATAATCAAGCTAAAGTAACAAA	14979
Qy	1981	TAATATCAAACTAATAGAACAGTAATCTAAATGTAACAAAAATTAATCTAATGCTAAATAT	2040
Db	14980	TAATATCAAACTAATAGAACAGTAATCTAAATGTAACAAAAATTAATCTAATGCTAAATAT	15039
Qy	2041	ARCAAAAGCGCAAGATCTATCAATTTATATAGTATTTTTCATCAACATCTCTTATTAAT	2100
Db	15040	ARCAAAAGCGCAAGATCTATCAATTTATATAGTATTTTTCATCAACATCTCTTATTAAT	15099
Qy	2101	TTCTAAATAATATCTGTGATTTTATTAACCTCTTAATGGAATGCACTATTAATAATGAA	2160
Db	15100	TTCTAAATAATATCTGTGATTTTATTAACCTCTTAATGGAATGCACTATTAATAATGAA	15159
Qy	2161	TTAGTCGAAACATCAATAAACAAGTAACATGATAGATCAATGTCATGTTGTTATCATTCAT	2220
Db	15160	TTAGTCGAAACATCAATAAACAAGTAACATGATAGATCAATGTCATGTTGTTATCATTCAT	15219
Qy	2221	CTTTACATTTTGGATTTGATTTACAGTTTGGGAAGCTGGGTTTGGAAATTCGATTAAGCTTGGCGTGC	2280
Db	15220	CTTTACATTTTGGATTTGATTTACAGTTTGGGAAGCTGGGTTTGGAAATTCGATTAAGCTTGGCGTGC	15266
Qy	2281	AGTTATCATCATCATATAGACACACAGAAATAAAGTAATCAGATTATCAGTTAAAGCTPAT	2340
Db	15267	AGTTATCATCATCATATAGACACACAGAAATAAAGTAATCAGATTATCAGTTAAAGCTPAT	15266
Qy	2341	GTAATAATTTGGCGCATAAACCAATCAATTAATAAATAAGATCAGTTTAAAGAAAGATCAAG	2400
Db	15267	GTAATAATTTGGCGCATAAACCAATCAATTAATAAATAAGATCAGTTTAAAGAAAGATCAAG	15266
Qy	2401	CTCAAAAAATAAAGAGAGAAAGGGTCTCTAAACCAAGAAATGAAGGAGAGAAAAAACAAGAA	2460
Db	15267	CTCAAAAAATAAAGAGAGAAAGGGTCTCTAAACCAAGAAATGAAGGAGAGAAAAAACAAGAA	15266
Qy	2461	ATTTTACCTGCACAGCTTGGATCTCTAGACCACTTTGTACAGAAAGCTGAACGAGAAA	2520
Db	15267	ATTTTACCTGCACAGCTTGGATCTCTAGACCACTTTGTACAGAAAGCTGAACGAGAAA	15314
Qy	2521	CGTAAATGATATATAATATCAATATTAATAATTTAGATTTTGATTAATAAACAAGACTACAT	2580
Db	15315	CGTAAATGATATATAATATCAATATTAATAATTTAGATTTTGATTAATAAACAAGACTACAT	15374
Qy	2581	AATACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACCTTACATTTAGATGTTTACTGTG	2640
Db	15375	AATACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACCTTACATTTAGATGTTTACTGTG	15434
Qy	2641	ACTGTAGTCGACTAAGTTGGCGACATCAACCGACGCACTTTTGGCGCCGAAATAAATACCTGTG	2700

Db	15435		ACCTGTAGTCGACTAAAGTTGGCAGCATCACCCGACGCACTTTGGCGCGGAATAAATACCTG	15494
Qy	2701		TGACGGAGAGTACACTTCGCGAGATAAATAAATCCTGGTGTCCCTGTCTGATACACGGGAAGC	2760
Db	15495		TGACGGAGAGTACACTTCGCGAGATAAATAAATCCTGGTGTCCCTGTCTGATACACGGGAAGC	15554
Qy	2761		CCTGGGCCAACTTTTGGCGAAATGAGCGTTGATCGGANTTCAACACTCTTATACATTTT	2820
Db	15555		CCTGGGCCAACTTTTGGCGAAATGAGCGTTGATCGGANTTCAACACTCTTATACATTTT	15614
Qy	2821		CTCTTACAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATA	2880
Db	15615		CTCTTACAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATA	15674
Qy	2881		AAGTTTTCTGAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATTAAGGGAGCCTGAC	2940
Db	15675		AAGTTTTCTGAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATTAAGGGAGCCTGAC	15734
Qy	2941		ATTTATATTCCCCAGAAATCATCAGGTAAATGGCGTTTTTGTCTCATTTTCGGCGTGGCTG	3000
Db	15735		ATTTATATTCCCCAGAAATCATCAGGTAAATGGCGTTTTTGTCTCATTTTCGGCGTGGCTG	15794
Qy	3001		AGATCAAGCCACTTCTTTCCTCCGATAAACGGAGAACCGACACACTGGCCATATCGGTGGTCAATC	3060
Db	15795		AGATCAAGCCACTTCTTTCCTCCGATAAACGGAGAACCGACACACTGGCCATATCGGTGGTCAATC	15854
Qy	3061		ATCGGCCAGCTTTCATCCCGGATATGCACCACCGGGTAAAGTTTACGGGAGACTTTATCT	3120
Db	15855		ATCGGCCAGCTTTCATCCCGGATATGCACCACCGGGTAAAGTTTACGGGAGACTTTATCT	15914
Qy	3121		GACAGCAGACGTGCACCTGCCAGGGGGATCACCATCGCTCGCCCGGGCGTGTCAATAATA	3180
Db	15915		GACAGCAGACGTGCACCTGCCAGGGGGATCACCATCGCTCGCCCGGGCGTGTCAATAATA	15974
Qy	3181		TCACTCTGTACATCCAAACACAGACGATAACGGCTCTCTCTTTTATAGTGTATAACCTTA	3240
Db	15975		TCACTCTGTACATCCAAACACAGACGATAACGGCTCTCTCTTTTATAGTGTATAACCTTA	16034
Qy	3241		AACGTCAATTCACCAAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTCATAAACCG	3300
Db	16035		AACGTCAATTCACCAAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTCATAAACCG	16094
Qy	3301		GGGCACTCAGCCATCCCTTCCTGATTTTCGCTTCCAGCGTTCGGCACCGACGACGACG	3360
Db	16095		GGGCACTCAGCCATCCCTTCCTGATTTTCGCTTCCAGCGTTCGGCACCGACGACGACG	16154
Qy	3361		GGCTTCATTCTGCATGGTTGTGCTTTACCAGACCGGAGATATTGACATCATATATGCGCTTG	3420
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Qy	3421		AGCAACTGATAGCTGCGCTGTCAACTGTCACTGTAAATACGGTGTCTATAGCACACCTC	3480
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Db	16395		TTTCTTTTTATGATTTAATACCGGCAATGAGGACATAAGCGAGTAGGTAGGTGGATACGACAT	16454
Qy	3661		TCGGTTTGAGAGAACATTTGAAAGGCTGTCGGTTCGACTAAGTTGGCAGCATCACCCGAA	3720
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QY 4681 GC 4682
Db 17680 GC 17681

RESULT 2
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 91.0%; Score 4262; DB 15; Length 17476;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 205; Gaps 1;

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QY 361 TGTGACAAAATAAAGAAATCACTATTATCATATACGCTAGTGTGATAGTCTCGTGAATAATCA 420
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Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 588172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
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19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4262	91.0	17476	15	US-10-055-001A-24
3	4262	91.0	17476	15	US-10-055-001A-25
4	4200	89.7	17458	15	US-10-055-001A-25
5	4077.2	87.1	17862	15	US-10-055-001A-23
6	3199.6	68.3	18691	15	US-10-055-001A-13
7	1208.4	25.8	17681	15	US-10-055-001A-26
8	1174.2	25.1	17862	15	US-10-055-001A-23
9	1108.8	23.7	4470	15	US-10-151-690-21
10	1108.8	23.7	4892	16	US-10-357-268-1
11	1108.8	23.7	5584	15	US-10-151-690-61
12	1102.4	23.5	4428	15	US-10-151-690-62
13	1102.4	23.5	4627	15	US-10-151-690-63
14	1102.4	23.5	4627	15	US-10-151-690-64

c	15	1074.8	23.0	17476	15	US-10-055-001A-24
c	16	1074.8	23.0	17476	15	US-10-385-546-7
c	17	1072.8	22.9	17458	15	US-10-055-001A-25
c	18	780	16.7	786	15	US-10-385-521-9
c	19	737	15.7	3002	15	US-10-353-454-57
c	20	736	15.7	2116	12	US-10-644-335-3
c	21	735.6	15.7	2873	15	US-10-356-088-55
c	22	735.6	15.7	2873	15	US-10-353-454-38
c	23	735	15.7	3034	15	US-10-356-088-48
c	24	735	15.7	3034	15	US-10-353-454-31
c	25	713	15.2	4947	9	US-09-118-276-21
c	26	710.2	15.2	7599	15	US-10-027-880-5
c	27	703	15.0	2867	15	US-10-176-884-9
c	28	703	15.0	2867	15	US-10-177-478-20
c	29	617.6	13.2	18691	15	US-10-055-001A-13
c	30	597	12.8	1846	15	US-10-023-208-63
c	31	597	12.8	5558	15	US-10-241-596-137
c	32	597	12.8	6464	15	US-10-151-690-20
c	33	597	12.8	7278	17	US-10-097-034A-37
c	34	597	12.8	9249	16	US-10-389-120-2
c	35	597	12.8	10463	16	US-10-389-120-1
c	36	597	12.8	12789	13	US-10-666-778-9
c	37	593.8	12.7	11180	9	US-09-887-576-581
c	38	478.8	10.2	528	15	US-10-162-214-4
c	39	406.8	8.7	4470	15	US-10-151-690-21
c	40	406.8	8.7	4892	16	US-10-357-268-1
c	41	406.8	8.7	5584	15	US-10-151-690-61
c	42	400.4	8.6	4428	15	US-10-151-690-62
c	43	400.4	8.6	4627	15	US-10-151-690-63
c	44	400.4	8.6	4627	15	US-10-151-690-64
c	45	323.4	6.9	2877	13	US-09-861-925-11

ALIGNMENTS

RESULT 1
US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

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Best Local Similarity	100.0%			
Matches 4682	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	TTTCTATTGGAGGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACAGAAACCT	60	
DB	13000	TTTCTATTGGAGGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACAGAAACCT	13059	
QY	61	AAATGATATAAATATCAATATATTAATAGATTTTGCATAAAAACAGACTACATAAT	120	
DB	13060	AAATGATATAAATATCAATATATTAATAGATTTTGCATAAAAACAGACTACATAAT	13119	
QY	121	ACTGTAACACACATATCCAGTCACTATGATCACTACTAGATGTTAGTGACC	180	

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..378
OTHER INFORMATION:
US-08-379-614-3

Query Match 6.9%; Score 323.2; DB 2; Length 416;
Best Local Similarity 99.1%; Pred. No. 4.5e-60;
Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	559	GTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGAT	618
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QY	619	GTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTCCCGGATAACGGAGACCGGCACACT	678
Db	342	GTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTCCCGGATAACGGAGACCGGCACACT	283
QY	679	GGCCATATCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGCCACCGGGTAAAG	738
Db	282	GGCCATATCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGCCACCGGGTAAAG	223
QY	739	TTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGGATCACCATCGGTGG	798
Db	222	TTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGGATCACCATCGGTGG	163
QY	799	CCCGGGCGGTGCAATAATATCACTCTGTATCCCAAAACAGACGATAACGGCTCTCTCT	858
Db	162	CCCGGGCGGTGCAATAATATCACTCTGTATCCCAAAACAGACGATAACGGCTCTCTCT	103
QY	859	TTTATAGGTGTAACCTTAACTGCATT	886
Db	102	TTTATAGGTGTAACCTTAACTGCATT	75

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Job time : 204.187 secs

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
; US-08-379-614-2

Query Match          7.0%; Score 325.4; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 1.5e-60;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGA 617
DB 403 TGTGTATAACGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGA 344
QY 618 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 677
DB 343 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 284
QY 678 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 737
DB 283 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 224
QY 738 GTTCACGGGAGACTTTATCTGACAGCAGACGTCGACCGGCGGATCACCATCCGTC 797
DB 223 GTTCACGGGAGACTTTATCTGACAGCAGCTGTCATCGCCAGGGGATCACCATCCGTC 164
QY 798 GCCCGGGCGTGTCAATAATATACCTCTGTACATCCACAAAACAGACGATAACGGCTCTCTC 857
DB 163 GCCCGGGCGTGTCAATAATATACCTCTGTACATCCACAAAACAGACGATAACGGCTCTCTC 104
QY 858 TTTTATAGGTGTAAACCTTAAACTGCA 884
DB 103 TTTTATAGGTGTAAACCTTAAACTGCA 77

RESULT 15
US-08-379-614-3/c
; Sequence 3, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
; US-08-379-614-2

Query Match          7.0%; Score 325.4; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 1.5e-60;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGA 617
DB 403 TGTGTATAACGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGA 344
QY 618 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 677
DB 343 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 284
QY 678 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 737
DB 283 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 224
QY 738 GTTCACGGGAGACTTTATCTGACAGCAGCTGTCATCGCCAGGGGATCACCATCCGTC 797
DB 223 GTTCACGGGAGACTTTATCTGACAGCAGCTGTCATCGCCAGGGGATCACCATCCGTC 164
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DB 163 GCCCGGGCGTGTCAATAATATACCTCTGTACATCCACAAAACAGACGATAACGGCTCTCTC 104
QY 858 TTTTATAGGTGTAAACCTTAAACTGCA 884
DB 103 TTTTATAGGTGTAAACCTTAAACTGCA 77

RESULT 14
US-09-225-152A-2/c
; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMA10.001CPI

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Db 7170 TGTGACGTTGTAAACAACTGAGCATGTGTAGCTCAGATCCTTACCGCGCGTTTCGGTT 7229
QY 4032 CATTCCTAATGAATATATACACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCA 4091
Db 7230 CATTCCTAATGAATATATACACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCA 7289
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QY 4212 TATTATTACAAATCCAAATTTTAAACAAAGCGGACACCGGTCACACCTTAAAGACTGAT 4271
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Db 7650 CCGGTCCAGCAGCGCGCGGCTTACCG 7677

RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF INVENTIONS: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.1%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-111;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 14274 CATTCCTAATGAATATATACACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCA 14215
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Db 14214 ATTACTGATGTACCTACTACTATATGTACAAATTTAAATGAAACAAATATTTGT 14155
QY 4152 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGGCACAAATACAAACAAATTCGGTT 4211
Db 14154 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGGCACAAATACAAACAAATTCGGTT 14095
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Db 14094 TATTATTACAAATCCAAATTTTAAACAAAGCGGACAGACCGGTCACACCTTAAAGACTGAT 14035
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Db 13974 CGCGCAACTTAATAACGTTCACTGAAGGGAACCTCCGGTTCGCCGCGCGCATGGTGA 13915
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Db 13854 CCGGTCCAGCAGCGCGCGGCTTACCG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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RESULT 10
5428147-1/c
;PATENT NO. 5428147
;APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
;TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
;NUMBER OF SEQUENCES: 17
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/91,538
;FILING DATE: 13-JUL-1993
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 869,216
;FILING DATE: 13-APR-1992
;APPLICATION NUMBER: 869,216
;FILING DATE: 13-APR-1992
;APPLICATION NUMBER: 440,432
;FILING DATE: 21-NOV-1989
;APPLICATION NUMBER: 553,786
;FILING DATE: 19-NOV-1983
;APPLICATION NUMBER: 741,034
;FILING DATE: 06-AUG-1991
;APPLICATION NUMBER: 144,775
;FILING DATE: 20-JAN-1988
;APPLICATION NUMBER: 485,614
;FILING DATE: 15-APR-1983
;APPLICATION NUMBER: 713,624
;FILING DATE: 10-JUN-1991
;APPLICATION NUMBER: 260,574
;FILING DATE: 21-OCT-1988
;APPLICATION NUMBER: 848,733
;FILING DATE: 01-APR-1986
;APPLICATION NUMBER: 535,354
;FILING DATE: 26-SEP-1983
;SEQ ID NO:1
;LENGTH: 24595
5428147-1
Query Match 15.1%; Score 707; DB 6; Length 24595;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3913 CTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCGTTCAATTCGT 3972
DB 12541 CTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCGTTCAATTCGT 12482
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DB 12481 GTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTTACCGCGGTTTCGTTTC 12422
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DB 12421 ATTCTAATGAATATATACCCGTTACTATGCTATTTTATGATATATTCCTCGTTCAA 12362
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DB 12241 ATTATTACAAATCCAAATTTTAAATAAAGCGGAGAACCGGTCAACCTAAAGACTGATT 12182
QY 4273 ACATAAATCTTATTCAAATTTCAAAGGCCCGGAGGCTAGTATCTACGACACACCGAGC 4332
DB 12181 ACATAAATCTTATTCAAATTTCAAAGGCCCGGAGGCTAGTATCTACGACACACCGAGC 12122
QY 4333 GGGCACTAATAACGTTTCACTGAAGGAACTCCGGTTCCCGCGGCGGCGCATGGGTGAG 4392
DB 12121 GGGCACTAATAACGTTTCACTGAAGGAACTCCGGTTCCCGCGGCGGCGCATGGGTGAG 12062
QY 4393 ATTCTTGAAGTTGAGTATTGGCGGCTCTTACCGAAAGTTACGGGACCAATTCACCC 4452
Db 12061 ATTCTTGAAGTTGAGTATTGGCGGCTCTTACCGAAAGTTACGGGACCAATTCACCC 12002
QY 4453 CGGTCCAGCAGCGGCGGCGGTAACCGACTTGTGCCCCGAGAAATTATGCGAGCATTTT 4512
DB 12001 CGGTCCAGCAGCGGCGGCGGTAACCGACTTGTGCCCCGAGAAATTATGCGAGCATTTT 11942
QY 4513 TGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAAACCTTGACAGTGCAGCAAAATCGTT 4572
DB 11941 TGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAAACCTTGACAGTGCAGCAAAATCGTT 11882
QY 4573 GGGCGGCTCCAGGCGCAATTTTGCAGCAACATGTGAGGCTCAGCAG 4619
DB 11881 GGGCGGCTCCAGGCGCAATTTTGCAGCAACATGTGAGGCTCAGCAG 11835
RESULT 11
US-08-673-768-1
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence Y.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1
Query Match 12.1%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-111;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3912 CTTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCGTTCAATTCGT 3971
DB 7110 CTTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCGTTCAATTCGT 7169
QY 3972 TGTGCGAGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCTTACCGCGGTTTCGTT 4031
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OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-J1"

FEATURE:

NAME/KEY: -
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: -
LOCATION: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2

Query Match 15.2%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	3912	CCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTTGCTTTCAATTCTGT	3971
Db	3429	CCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTTGCTTTCAATTCTGT	3488
QY	3972	TGTGACGCTTGAAAAAACCCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	4031
Db	3489	TGTGACGCTTGAAAAAACCCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	3548
QY	4032	CACTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA	4091
Db	3549	CACTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA	3608
QY	4092	ATTACTGATGACCTACTACTATATGTACAATATTAATAATGAATAATATATTTCT	4151
Db	3609	ATTACTGATGACCTACTACTATATGTACAATATTAATAATGAATAATATATTTCT	3668
QY	4152	GCTGATAGTGTATAGGACATCTATGATAGCGCCCAATAAACAACAATTTGCGTTT	4211
Db	3669	GCTGATAGTGTATAGGACATCTATGATAGCGCCCAATAAACAACAATTTGCGTTT	3728
QY	4212	TATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	4271
Db	3729	TATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	3788
QY	4272	TACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	4331
Db	3789	TACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	3848
QY	4332	CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCTCCGCGCGCGCATGGTGA	4391
Db	3849	CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCTCCGCGCGCGCATGGTGA	3908
QY	4392	GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGGGCAACCATTTCAAC	4451
Db	3909	GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGGGCAACCATTTCAAC	3968
QY	4452	CCGGTCCAGCACCGCGCGCGGTAACCGACTTCTGCTCCCGGAGAAATATGACGATTTTT	4511
Db	3969	CCGGTCCAGCACCGCGCGCGGTAACCGACTTCTGCTCCCGGAGAAATATGACGATTTTT	4028
QY	4512	TTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGAGTCAAAACCTTGACAGTGCAGCAAAATCGT	4571
Db	4029	TTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGAGTCAAAACCTTGACAGTGCAGCAAAATCGT	4088
QY	4572	TGGCGGGGTCCAGGGCGAAATTTTGGGACAAACATGTGAGGCTCAGCAGGACCT	4624
Db	4089	TGGCGGGGTCCAGGGCGAAATTTTGGGACAAACATGTGAGGCTCAGCAGGACCT	4141

RESULT 9

US-09-577-424-3
Sequence 3, Application US/09577424
Patent No. 6525245
GENERAL INFORMATION:
APPLICANT: Rhoads, David M
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
TRANSDUCTION PATHWAYS IN HIGHER PLANTS
FILE REFERENCE: UNL2990
CURRENT APPLICATION NUMBER: US/09/577,424
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 14194
TYPE: DNA
ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 15.2%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 3.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	3912	CCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTTGCTTTCAATTCTGT	3971
Db	9830	CCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTTGCTTTCAATTCTGT	9889
QY	3972	TGTGACGCTTGAAAAAACCCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	4031
Db	9890	TGTGACGCTTGAAAAAACCCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	9949
QY	4032	CACTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA	4091
Db	9950	CACTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA	10009
QY	4092	ATTACTGATGACCTACTACTATATGTACAATATTAATAATGAATAATATATTTCT	4151
Db	10010	ATTACTGATGACCTACTACTATATGTACAATATTAATAATGAATAATATATTTCT	10069
QY	4152	GCTGATAGTGTATAGGACATCTATGATAGCGCCCAATAAACAACAATTTGCGTTT	4211
Db	10070	GCTGATAGTGTATAGGACATCTATGATAGCGCCCAATAAACAACAATTTGCGTTT	10129
QY	4212	TATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	4271
Db	10130	TATTTATCAAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	10189
QY	4272	TACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	4331
Db	10190	TACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGAT	10249
QY	4332	CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCTCCGCGCGCGCATGGTGA	4391
Db	10250	CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCTCCGCGCGCGCATGGTGA	10309
QY	4392	GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGGGCAACCATTTCAAC	4451
Db	10310	GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGGGCAACCATTTCAAC	10369
QY	4452	CCGGTCCAGCACCGCGCGCGGTAACCGACTTCTGCTCCCGGAGAAATATGACGATTTTT	4511
Db	10370	CCGGTCCAGCACCGCGCGCGGTAACCGACTTCTGCTCCCGGAGAAATATGACGATTTTT	10429
QY	4512	TTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGAGTCAAAACCTTGACAGTGCAGCAAAATCGT	4571
Db	10430	TTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGAGTCAAAACCTTGACAGTGCAGCAAAATCGT	10489
QY	4572	TGGCGGGGTCCAGGGCGAAATTTTGGGACAAACATGTGAGGCTCAGCAGGACCT	4624
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/ LOCATION: 3257..4315
/ OTHER INFORMATION: /label= 3'ocs
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA octopine synthase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 4316..6555
/ OTHER INFORMATION: /label= pUC18
/ OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-351-413-2

Query Match 15.2%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CCGCTCTTATGATATCGGAGCGCTATGATCGCATGATATTTGCTTCAATTCCTG 3971
Db |||||
QY 3429 CCGCTTATGATATCGGAGCGCTATGATCGCATGATATTTGCTTCAATTCCTG 3488
Db |||||
QY 3972 TGTGACGTTGTAAAAAAGCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4031
Db TGTGACGTTGTAAAAAAGCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3548
QY 4032 CATTCTAATGAATATATCACCGGTACTACTATGATATTTTATGAATATATTCCTCGTTCA 4091
Db |||||
QY 3549 CATTCTAATGAATATATCACCGGTACTACTATGATATTTTATGAATATATTCCTCGTTCA 3608
QY 4092 ATTACTGATTTGACCTTACTCTATATGTACAAATATTAATGAAACAAATATATTCCT 4151
Db |||||
QY 3609 ATTACTGATTTGACCTTACTCTATATGTACAAATATTAATGAAACAAATATATTCCT 3668
QY 4152 GCTGAATAGCTTTATAGGACATCTATGATAGAGCGGCTAGTATCTACGACACCGGAG 4211
Db |||||
QY 3669 GCTGAATAGCTTTATAGGACATCTATGATAGAGCGGCTAGTATCTACGACACCGGAG 3728
QY 4212 TATTATACAAATCCAAATTTTAAAAAGCGGAGACCGGCTCAAACTTAAAGACTGAT 4271
Db |||||
QY 3729 TATTATACAAATCCAAATTTTAAAAAGCGGAGACCGGCTCAAACTTAAAGACTGAT 3788
QY 4272 TACATAAATCTTATTCAAATTTTCAAAGGCGGCTAGTATCTACGACACCGGAG 4331
Db |||||
QY 3789 TACATAAATCTTATTCAAATTTTCAAAGGCGGCTAGTATCTACGACACCGGAG 3848
QY 4332 CGGCGAATTAATAGCTTACTGAAAGGAACTCGGTTCCCGCGGCGGCGATGCGTGA 4391
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QY 3849 CGGCGAATTAATAGCTTACTGAAAGGAACTCGGTTCCCGCGGCGGCGATGCGTGA 3908
QY 4392 GATTCTTGAAGTTGAGTATGCGGCTCGGCTCTACGAAAGTTACGGGCAACCATTCAC 4451
Db |||||
QY 3909 GATTCTTGAAGTTGAGTATGCGGCTCGGCTCTACGAAAGTTACGGGCAACCATTCAC 3968
QY 4452 CCGGTCGAGCACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGCAATTTT 4511
Db |||||
QY 3969 CCGGTCGAGCACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGCAATTTT 4028
QY 4512 TTGGTGTATGCGGCGGCGGTAACGAGTGTGAGGTCAAACCTTGACAGTACGACAAATCGT 4571
Db |||||
QY 4029 TTGGTGTATGCGGCGGCGGTAACGAGTGTGAGGTCAAACCTTGACAGTACGACAAATCGT 4088
QY 4572 TGGGCGGCTCCAGGCGGAAATTTTGGGACAAATGTCGAGGCTCAGCAGGACCT 4624
Db |||||
QY 4089 TGGGCGGCTCCAGGCGGAAATTTTGGGACAAATGTCGAGGCTCAGCAGGACCT 4141
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RESULT 8

US-09-025-583-2

; Sequence 2, Application US/09025583

; Patent No. 597433

; GENERAL INFORMATION:

; APPLICANT: Williams, Mark

; APPLICANT: Leemans, Jan

; TITLE OF INVENTION: Maintenance of male-sterile plants

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/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
/ STREET: 8110 Gatehouse Road, Suite 500 East
/ CITY: Falls Church
/ STATE: Virginia
/ COUNTRY: U.S.A.
/ ZIP: 2046
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025.583
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/351.413
/ FILING DATE:
/ APPLICATION NUMBER: US 07/899,072
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/970,849
/ FILING DATE: 03-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svensson, Leonard R.
/ REGISTRATION NUMBER: 30,330
/ REFERENCE/DOCKET NUMBER: 2121-102PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ TELEX: 248345
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6555 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: plasmid pVE144 (replicable in E.coli)
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..396
/ OTHER INFORMATION: /label= pUC18
/ OTHER INFORMATION: /note= "pUC18 derived sequence"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (397..751)
/ OTHER INFORMATION: /label= 3'nos
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA nopaline synthase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (752..1024)
/ OTHER INFORMATION: /label= barstar
/ OTHER INFORMATION: /note= "coding region of the barstar gene of
/ OTHER INFORMATION: Bacillus amyloliquefaciens"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (1025..1607)
/ OTHER INFORMATION: /label= TA29
/ OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
/ OTHER INFORMATION: Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1608..2440
/ OTHER INFORMATION: /label= 35S3
/ OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-084-889-1

Query Match 15.2%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CTTGCTTTTATGATGATGGAGACCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3971
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QY 3972 TGTGACGTTGTAATAAATCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTGCGTT 4031
DB 2333 TGTGACGTTGTAATAAATCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTGCGTT 2392
QY 4032 CATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGATATATTTCTCGTTCA 4091
DB 2393 CATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGATATATTTCTCGTTCA 2452
QY 4092 ATTTACTGATTTGACCTTACTTATATGATGATCAATATTTAAATGAAAAACAATATTCGT 4151
DB 2453 ATTTACTGATTTGACCTTACTTATATGATGATCAATATTTAAATGAAAAACAATATTCGT 2512
QY 4152 GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATAAACAACAATATTCGTTT 4211
DB 2513 GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATAAACAACAATATTCGTTT 2572
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QY 4272 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGCTAGTATCTAGCACACCCGAG 4331
DB 2633 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGCTAGTATCTAGCACACCCGAG 2692
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DB 2693 CGCGCAACTAATAACGTTTCACTGAAGGAACTCCCGTTCCCGCGCGCGCATGGTGA 2752
QY 4392 GATTCCTTGAAGTTGAGTATGCGCTTACCGAAGTTACGGGCAACCAATCAAC 4451
DB 2753 GATTCCTTGAAGTTGAGTATGCGCTTACCGAAGTTACGGGCAACCAATCAAC 2812
QY 4452 CCGGTCACGACCGCGCGCGGTAACCGACTTCTGCTCCCGGAGAAATATGACATTTT 4511
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QY 4512 TTGGTGTATGTGGGCGGCAATGAAGTGAGGTCAAACTTGACAGTGACGACAAATCGT 4571
DB 2873 TTGGTGTATGTGGGCGGCAATGAAGTGAGGTCAAACTTGACAGTGACGACAAATCGT 2932
QY 4572 TGGGCGGCTCCAGGCGGCAATTTTGGCAGCAACATGTGAGGCTCAGCAGGACCT 4624
DB 2933 TGGGCGGCTCCAGGCGGCAATTTTGGCAGCAACATGTGAGGCTCAGCAGGACCT 2985

RESULT 7

US-08-351-413-2
Sequence 2, Application US/08351413

Patent No. 5750867

GENERAL INFORMATION:

APPLICANT: Williams, Mark

APPLICANT: Leemans, Jan

TITLE OF INVENTION: Maintenance of male-sterile plants

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
FEATURE:
NAME/KEY: -
LOCATION: 1..396
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OTHER INFORMATION: /note= "pUC18 derived sequence"
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NAME/KEY: -
LOCATION: complement (397..751)
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OTHER INFORMATION: T-DNA nopaline synthase gene"
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NAME/KEY: -
LOCATION: complement (752..1024)
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NAME/KEY: -
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
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OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: -

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; OTHER INFORMATION: /label= NPT11
; OTHER INFORMATION: /note= "coding sequence of neomycine
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; NAME/KEY: -
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; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
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; FEATURE:
; NAME/KEY: -
; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; US-08-475-975-1

Query Match      15.2%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTTCAATTCGT 3971
DB 2273 CCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTTCAATTCGT 2332
QY 3972 TGTGCAGCTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 4031
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QY 4032 CATTCCTAATGAATATATCAACCGTCTACTCGTATTTTATGATGAATATATTCCTCGTTCA 4091
DB 2393 CATTCCTAATGAATATATCAACCGTCTACTCGTATTTTATGATGAATATATTCCTCGTTCA 2452
QY 4092 ATTTACTGATTTGACCTACTACTATATGATACAAATATTAATAATGAAACAAATATTTGT 4151
DB 2453 ATTTACTGATTTGACCTACTACTATATGATACAAATATTAATAATGAAACAAATATTTGT 2512
QY 4152 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGGCACATTAACAAACAAATTCGGTT 4211
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QY 4212 TATTATTACAAATCCCAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTAAAAAGACTGAT 4271
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QY 4272 TACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGCGCTAGTATCTACGACACACCGAG 4331
DB 2633 TACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGCGCTAGTATCTACGACACACCGAG 2692
QY 4332 CGGCGGCTAATAACGTTTCACTGAAGGGAATCCGGTTCCTCCCGCGCGCATGGGTGA 4391
DB 2693 CGGCGGCTAATAACGTTTCACTGAAGGGAATCCGGTTCCTCCCGCGCGCATGGGTGA 2752
QY 4392 GATTCTCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTAGCGGACCAATTCAC 4451
DB 2753 GATTCTCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTAGCGGACCAATTCAC 2812
QY 4452 CCGGTCAGCACGCGCGCGGTTAACCGACTTGTGTCGCCGAGAAATATGACGATTTT 4511
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QY 4512 TTGCTGTATGTGGGCCCCCAATTAAGTGCAGGTCAAAACCTTGACAGTGACGACAAATCGT 4571
DB 2873 TTGCTGTATGTGGGCCCCCAATTAAGTGCAGGTCAAAACCTTGACAGTGACGACAAATCGT 2932
QY 4572 TGGCGGGGTTCAGGGCGGAAATTTTGCAGACAAATGTCGAGGCTCAGCAGGACCT 4624
DB 2933 TGGCGGGGTTCAGGGCGGAAATTTTGCAGACAAATGTCGAGGCTCAGCAGGACCT 2985

RESULT 6
US-09-084-889-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Burns, Doane, Swecker & Mathis
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY: -
; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-J1"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1285..2100
; OTHER INFORMATION: /label= NPT11
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
; FEATURE:
; NAME/KEY: -
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OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
FEATURE:
NAME/KEY: -
LOCATION: 452..1284
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosaic virus isolate CabbB-J1"
FEATURE:
NAME/KEY: -
LOCATION: 1285..2100
OTHER INFORMATION: /label= NP111
OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase gene"
FEATURE:
NAME/KEY: -
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from the Agrobacterium T-DNA octopline synthase"
FEATURE:
NAME/KEY: -
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-478-015-1
Query Match 15.2%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3912 CTGCTTTAATGAGATATCGGAGAGCCCTATGATCGCATGATATTTGCTTCAATCTGT 3971
DB 2273 CTGCTTTAATGAGATATCGGAGAGCCCTATGATCGCATGATATTTGCTTCAATCTGT 2332
QY 3972 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTTACCGCGGTTTCGGTT 4031
DB 2333 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTTACCGCGGTTTCGGTT 2392
QY 4032 CATTCCTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATTTCCGGTTCA 4091
DB 2393 CATTCCTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATTTCCGGTTCA 2452
QY 4092 ATTACTGATTTGACCTACTATATGATACATATTAATGAATAATGAATAATATGTT 4151
DB 2453 ATTACTGATTTGACCTACTATATGATACATATTAATGAATAATGAATAATATGTT 2512
QY 4152 GCTGAATAGTTTATAGGACATCTATGATAGGCGCACAATAACAAACAATTCGGTT 4211
DB 2513 GCTGAATAGTTTATAGGACATCTATGATAGGCGCACAATAACAAACAATTCGGTT 2572
QY 4212 TATTATTACAAATCCAAATTTAAAAAAGCGGAGACCGGTCAACCTTAAAGACTGAT 4271
DB 2573 TATTATTACAAATCCAAATTTAAAAAAGCGGAGACCGGTCAACCTTAAAGACTGAT 2632
QY 4272 TACATAAATCTTATTCAAATTTCAAAGCCCGGAGGTAGTATCTAGCACACCGGAG 4331
DB 2633 TACATAAATCTTATTCAAATTTCAAAGCCCGGAGGTAGTATCTAGCACACCGGAG 2692
QY 4332 CGCGCAACTAATAACGTTCACTGAAGGGAACCTCCGTTCCCGCGGCGCATGGTGA 4391
DB 2693 CGCGCAACTAATAACGTTCACTGAAGGGAACCTCCGTTCCCGCGGCGCATGGTGA 2752
QY 4392 GATTCCTTGAAGTTGAGTATGCGCGTCTACCGAAAGTTACGGGACCACTTCAAC 4451
DB 2753 GATTCCTTGAAGTTGAGTATGCGCGTCTACCGAAAGTTACGGGACCACTTCAAC 2812
QY 4452 CGGTCACAGCGGCGGCGGTAAACGACTTGTCCCGGAGAAATATGACGACATTTT 4511
DB 2813 CGGTCACAGCGGCGGCGGTAAACGACTTGTCCCGGAGAAATATGACGACATTTT 2872
QY 4512 TTGGTGTATGTGGGCCCAAAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAATCGT 4571
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DB 2873 TTGGTGTATGTGGGCCCAAAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAATCGT 2932
QY 4572 TGGGCGGTTCCAGGCGCAATTTTGGCAACAACATGTCGAGGCTCAGCAGGACT 4624
DB 2933 TGGGCGGTTCCAGGCGCAATTTTGGCAACAACATGTCGAGGCTCAGCAGGACT 2985

RESULT 5
US-08-475-975-1
; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 9040332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 9140188.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crate-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY: -
; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosaic virus isolate CabbB-J1"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1285..2100
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TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
FEATURE:
NAME/KEY: -
LOCATION: 1..451 /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
FEATURE:
NAME/KEY: -
LOCATION: 452..1284 /label= 3583
OTHER INFORMATION: /note= "3583 promoter sequence derived from Cauliflower mosaic virus isolate CabBB-J1"
FEATURE:
NAME/KEY: -
LOCATION: 1285..2100 /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycinase gene"
FEATURE:
NAME/KEY: -
LOCATION: 2101..3160 /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from the Agrobacterium T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: 3161..5399 /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-064-121-1
Query Match 15.2%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2,7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3912 CCTGCTTTAATGAGATATCGGAGACGGCTATGATCGCATGATATTCCTTCAATCTGT 3971
DB 2273 CCTGCTTTAATGAGATATCGGAGACGGCTATGATCGCATGATATTCCTTCAATCTGT 2332
QY 3972 TGTGACGTTGTAAACAACTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4031
DB 2333 TGTGACGTTGTAAACAACTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 2392
QY 4032 CATCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATCTCCGTTCA 4091
DB 2393 CATCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATCTCCGTTCA 2452
QY 4092 ATTTACTGATGTACCTTACTTATGATATGATATTAATTAATCAACAAATATATGT 4151
DB 2453 ATTTACTGATGTACCTTACTTATGATATGATATTAATTAATCAACAAATATATGT 2512
QY 4152 GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCACAAATCAACAAATTCGGTT 4211
DB 2513 GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCACAAATCAACAAATTCGGTT 2572
QY 4212 TATTATTACAAATCCAAATTTTAAAAAGCGGCGAAGCGGTCAAACCTTAAGACTGAT 4271
DB 2573 TATTATTACAAATCCAAATTTTAAAAAGCGGCGAAGCGGTCAAACCTTAAGACTGAT 2632
QY 4272 TACATTAATCTTATCAAAATTTTCAAAAGCGCCGCTAGTCTACGACACACCGAG 4331
DB 2633 TACATAAATCTTATCAAAATTTTCAAAAGCGCCGCTAGTCTACGACACACCGAG 2692
QY 4332 CGCGGAACCTAATCACTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGTGA 4391
DB 2693 CGCGGAACCTAATCACTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGTGA 2752

QY 4392 GATTCCTTGAAGTTGAGTATTTGGCGCTTACCGAAAGTTACGGGACCAATTCAC 4451
DB 2753 GATTCCTTGAAGTTGAGTATTTGGCGCTTACCGAAAGTTACGGGACCAATTCAC 2812
QY 4452 CCGTCCAGCACGCGCGCGGTAACCGACTTGTGCTCCCGGAGAAATATGACGATTTT 4511
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RESULT 4

US-08-478-015-1
; Sequence 1, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,015
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451

RESULT 3
US-08-064-121-1
; Sequence 1, Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.

ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,121
 FILING DATE: 24-MAY-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 90403332.1
 FILING DATE: 23-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 91401888.2
 FILING DATE: 08-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Crane-Feury, Sharon E
 REGISTRATION NUMBER: 36,113
 REFERENCE/DOCKET NUMBER: 010830-043
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5399 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double

ORGANISM: plasmid DNA designated as pPS0212
FEATURE: CDS
NAME/KEY: 1..1785
LOCATION: 1..1785
OTHER INFORMATION: /note= "Coding region of a truncated modified bt2 (cryIAb) gene, also designated as the cryIAb6 gene."
OTHER INFORMATION: cryIAb6 gene."
FEATURE: misc feature
NAME/KEY: 1793..2026
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene 7."
OTHER INFORMATION: T-DNA gene 7."
FEATURE: misc feature
NAME/KEY: 2922..3581
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of chloramphenicol acetyl transferase gene."
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
FEATURE: misc feature
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LOCATION: 3582..4407
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FEATURE: misc feature
NAME/KEY: 5600..6457
LOCATION: 5600..6457
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OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter derived from Agrobacterium T-DNA (with modified leader with respect to sequence of pJD884 of SEQ ID NO. 22."
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23
Query Match 15.6%; Score 728.8; DB 2; Length 7566;
Best Local Similarity 99.7%; Pred. No. 2.7e-146;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3903 GTCTAGAGTCCTGCTTAATGAGATATGCGAGACGCTATGATCGCATGATATTGCTTT 3962
DB 3692 GTCTAGAGTCCTGCTTAATGAGATATGCGAGACGCTATGATCGCATGATATTGCTTT 3751
QY 3963 CAATTCGTTGTGACGCTGTAACAAACCTGAGCATGTGAGCTCAGATCCTTACCGCG 4022
DB 3752 CAATTCGTTGTGACGCTGTAACAAACCTGAGCATGTGAGCTCAGATCCTTACCGCG 3811
QY 4023 GTTTCGGTCAATTAATGATATATACCGCTTACTATCGTATTTTATGATATATT 4082
DB 3812 GTTTCGGTCAATTAATGATATATACCGCTTACTATCGTATTTTATGATATATT 3871
QY 4083 CTCGGTCAATTTACTGATGTCCTTACTTATATGATGATATTAATAAGAAACA 4142
DB 3872 CTCGGTCAATTTACTGATGTCCTTACTTATATGATGATATTAATAAGAAACA 3931
QY 4143 ATATATTGTGCTGAATAGTTTATAGGACATCTATGATAGAGCCGACAAATCAACA 4202
DB 3932 ATATATTGTGCTGAATAGTTTATAGGACATCTATGATAGAGCCGACAAATCAACA 3991
QY 4203 ATTTCGTTTATTATTACAAATCAATTTTAAAAAGCGGACGAGCGGTCAACCTAA 4262
DB 3992 ATTTCGTTTATTATTACAAATCAATTTTAAAAAGCGGACGAGCGGTCAACCTAA 4051
QY 4263 AAGACTGATTACATAAATCTTATTCAAAATTTCAAAAGCCCGGCTAGTATCTACGA 4322

DB 4052 AAGACTGATTACATAAATCTTATTCAAAATTTCAAAAGCCCGGCTAGTATCTACGA 4111
QY 4323 CACACCGAGCGGCGAAGCTTAATTAACGTTTCACTGAAGGGAATCCCGTTCCCGCGCGCG 4382
DB 4112 CACACCGAGCGGCGAAGCTTAATTAACGTTTCACTGAAGGGAATCCCGTTCCCGCGCGCG 4171
QY 4393 CATGGTGAGATTCTTGAAGTTGAGTATGCGCGCTCGCTTACCGAAGGTTACGGGCA 4442
DB 4172 CATGGTGAGATTCTTGAAGTTGAGTATGCGCGCTCGCTTACCGAAGGTTACGGGCA 4231
QY 4443 CCATTCAACCGGTCACACGCGCGGCTTAACCGGCTTTCCTGCCCGGAGAAATTATGC 4502
DB 4232 CCATTCAACCGGTCACACGCGCGGCTTAACCGGCTTTCCTGCCCGGAGAAATTATGC 4291
QY 4503 AGCATTTTTTTGGTGTATGTGGGCCCCCAATTAAGTGCAGGTCAAACTTGCAGTACG 4562
DB 4292 AGCATTTTTTTGGTGTATGTGGGCCCCCAATTAAGTGCAGGTCAAACTTGCAGTACG 4351
QY 4563 ACAAAATCGTTGGGCGGCTCCAGGCGGAATTTTGGACAAATGTCGAGGCTCAGCAGGAC 4622
DB 4352 ACAAAATCGTTGGGCGGCTCCAGGCGGAATTTTGGACAAATGTCGAGGCTCAGCAGGAC 4411
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DB 4412 CTGCAGGAAATTC 4423
RESULT 2
US-08-232-016-22
; Sequence 22, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETABERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN RARSSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7639 base pairs
; TYPE: nucleic acid

Job time : 1122.53 secs

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Db	13994	TCGCTCTCGTGGCC---GAAAGCTGGAAAGCGGAAATCAGGAAGGATGGCTGAGGTGCG	13958
Qy	2999	TGAGATCAGCCACTCTTCTCCCGATAAACGAGACCGGCACATCTGGCCATATCGGTGGTCA	3058
Db	13937	CCGGTTATTGAATGAAACGGCTCTTTTCTGACGAGAAACAGGG-----ACTGGTGAAA	13884
Qy	3059	TCATGCGCCAGCTTTTCATCTCCCGATATGCACACCGGGTAAAGTTTCACGGAGACTTTAT	3118
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Qy	3119	CTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTGCCCGGGCGTGTCAATAA	3178
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Qy	3179	TATCACTCTGTACATCCACAAACAGACGATAAACGGCTCTCTTTTATAGGTGTAACCT	3238
Db	13763	TGCTGTCCAGATAAAGTCTCCCGTGAACCTTTACCGGTGGTGATATCGGGATGAAGCT	13704
Qy	3239	TAAACTGCATTTCAAC-----AGTCCCTGTCTCGTACGAAAAGACCGGTTCAATTCA	3292
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Qy	3293	ATAAACCGGGCGACCTCAGCCATCCCTCTCGATTTCCGCTTTCCAGCGTTC---GGCA	3349
Db	13643	CTGATCTCASCACCCGGAAATGACATCAAAAACCCATTAACTGATGTTCTGGGAA	13584
Qy	3350	CGCAGACGAGGGCTTCATTTCTGCATGG---TTGTGCTTACAGACCCGGAGATATTGACA	3406
Db	13583	TATAAATGTCCAGCTCCCTTATACAGGCCAGTCTCGAGTGGATACAGTAGTAATAACA	13524
Qy	3407	TCATATATGCTTTGAGCACTGATAGCTGTCGCTGTCACTCTCACTGTATACGCTGCT	3466
Db	13523	GAACTTTATCAGTTTATGAGTATGAGGCTGAAAATCCAGATGAACCGAACGACTT	13464
Qy	3467	TCATAGCACACCTCTTTTGGACATCTCTGTTCTTGATGCGAGATGATTTTCAGGACTAT	3526
Db	13463	GTAAAGAAAAGTATAAGAGTTGTGAAATGTGTTCTTGATGCGAGATGATTTTCAGGACTAT	13404
Qy	3527	GACCTAGCGTATATCAATAGGTAGATGTTTTATTTTGTCTACACAAAAAGAGGCTGCG	3586
Db	13403	GACCTAGCGTATGAAATAGGTAGATGTTTTATTTTGTCTACAAAAAGAGGCTGCG	13344
Qy	3587	ACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTCAGGACCAATAGCCGATAGG	3646
Db	13343	ACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTCAGGACCAATAGCGATAGG	13284
Qy	3647	CTGGATACGACGATTCGGTTTGAGAGACATTTGGAAGCTGTGCGTGCATAGATTGG	3706
Db	13283	CTGGATACGACGATTCGGTTTGAGAGACATTTGGAAGGCTGTGCGTGCATAGATTGG	13224
Qy	3707	CAGCATCACCCGAAGAACATTTGGAAGGCTGTGCGTGCAGTACAGTCACTAAATACCATC	3766
Db	13223	CAGCATCACCCGAAGAACATTTGGAAGGCTGTGCGTGCAGTCACTAAATACCATC	13164
Qy	3767	TAGTAGTTGATTCATAGTGAATGAGATATGTTGTGTTTACAGTATATATAGTCTGTTT	3826
Db	13163	TAAGTAGTTGATTCATAGTGAATGAGTATGTTGTGTTTACAGTATATATAGTCTGTTT	13104
Qy	3827	TTTATGCAAAATCTAATTAATATATGATATTTATCATTTTACGTTTCTCGTTCAGC	3886
Db	13103	TTTATGCAAAATCTAATTAATATATGATATTTATCATTTTACGTTTCTCGTTCAGC	13044
Qy	3887	TTTTTTGTACAAACTGTCTAGAG	3910
Db	13043	TTTTTTGTACAAACTGTCTAGAG	13020

QY	741	CACGGGAGACTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGAGTACCAATCCGTCGCC	800
Db	15996	TGTTTGTGGATGTAACAGAGTGATATATTGACAGCCCGGCGACGGATGGTGAATCCGCC	15937
QY	801	CGGGCGTGTCAATAATATCACTCTGTATCATCCACAAACAGACAGTAAACGGCTCTCTCTTT	860
Db	15936	TGGCCAGTGCAAGTCTGCTGTGCATAAAGTCTCCGTGAACTTTACCCGGTGGTGCAATA	15877
QY	861	TATAGGTGTAAACCTTAAACGTGAATTTACCC-----AGTCCCTGTTCTCGTACAGCAAA	914
Db	15876	TCGGGGATGAAAGCTGGCGCATGTGATGACCAACCGATATGGCCAGTGTGCGGTCTCCGTTA	15817
QY	915	.GAGCCGTTTCATTTCAATAAAACCGGGCGACCTCAGGCATCCCTTCCTGATTTTCCGCTTTC	974
Db	15816	TCGGGGAAGAGTGGCTGATCTCAGCCACCGCGAANAATGACATCAAAAACGCCATTTAAC	15757
QY	975	CAGCGTTC---GGCACGCGACGACGCGGCTTCATTTCTGCATGGTTGTGCTTACCAGACG	1031
Db	15756	TGATGTTCTCGGGAATAATAATGTACGGCTCCCTTATACAG-----CCAGTCTG	15706
QY	1032	GAGATATTGACATCATATATGCCCTTGAGCAACATGATAGCTGTGCTGTCAACTGTCACTG	1091
Db	15705	CAGTCTGATACAGTAGAAAATTACAGAACTTTATCAGTTTGTAGTAAGTATAGAGGCTGAA	15646
QY	1092	TAATACTGCTGCTTCATAGCACACCTCTTTTGTGACATATCTCCGGTAGTG---CCGATCA	1147
Db	15645	AATCCAGATGAGCGGAACGACCTGTAGAGAAAAGTATAAGATTTGTGAAATCCGATCA	15586
QY	1148	ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACACAGA	1207
Db	15585	ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACACAGA	15526
QY	1208	TTTATTTATTTCTCGGAAGTGAATCTTCGGTCAAGGTATTTTTCGGCGCAAGTGGCTG	1267
Db	15525	TTTATTTATTTCTCGGAAGTGAATCTTCGGTCAAGGTATTTTTCGGCGCAAGTGGCTG	15466
QY	1268	GGTGATGCTGCCAACTTAGTCGACTACAGTCACTAATACCAATCAAGTAGTGTGATTCAT	1327
Db	15465	GGTGATGCTGCCAACTTAGTCGACTACAGTCACTAATACCAATCTAGTAGTGTGATTCAT	15406
QY	1328	AGTGACTGGATATGTTGTGTTTTACAGTATATGTAGTCTGTTTTTATGCAAAATCTAA	1387
Db	15405	AGTGACTGGATATGTTGTGTTTTACAGTATATGTAGTCTGTTTTTATGCAAAATCTAA	15346
QY	1388	TTTAAATATATGATATTTATCATTTTACGTTTCTCGTTTCAGCTTCTTGTAACAAAGTG	1447
Db	15345	TTTAAATATATGATATTTATCATTTTACGTTTCTCGTTTCAGCTTCTTGTAACAAAGTG	15286
QY	1448	GTCTCGAGGAATTCGGTACCCAGCTTGTGTAGGAAATAAATATTTTCTTTTTCCTTTT	1507
Db	15285	GTCTAGAGGATCCAAGCTTATCGATTTCCGAAACCCAGCTCCCAAGTGAATCA-----	15233
QY	1508	AGTATAAAATAGTTAAGTGAAGTTAATAGTAGTATTAATAATAATATAGTTGTTATAATT	1567
Db	15232	---ATCCAAATGTAAAGTCAAATGATAACAAATGATCATCTATCATGTTAGCTTGTTT	15176
QY	1568	GTGAAAAAATAATTTTATAAATAATTTGTTTACATAAAACAAATAGTAAATGAAAAATA	1627
Db	15175	ATTCAATGTCGACTAATTCATTTTAAATATGTCAATCCATTTAGAAGTTAATAAAGCTA	15116
QY	1628	TGCAAGTGTATGTTGAAGACGAAGAAGTAAAGTTGAGGTGAAGTATATATTTTAAAT	1687
Db	15115	CAA-----GTATTATTTAGAAATTAATAAGAAATGTTGATTTGAAAAATAACTATA	15066
QY	1688	GAATTTGATCGAACATGTAAGATGATATACTAGCAATTAATATTTGTTTTAATCATATAAG	1747
Db	15065	TAAAAATGATAGATCTTCGCGTTTGTATATAGCAATTAGATTATGTTTT-----	15017
QY	1748	TAATTTCTAGCTGGTTTGATGAATTAATATCAATGATAAAATACATATAGTAAAAATAGA	1807
Db	15016	-----	15017

QY	1808	ATAAATAAATTTAAATAATATTTTTTTTATAGTAATAATAGTTTATATATATAATTAATAATCT	1867
DB	15016	---GTTACATTTAGATTTACTGTGTTCTATTAGTTGAT---	14984
QY	1868	ATACCAATTAATAATATTTTTTAGTTTAAAAGTAAATAATTTTTGTTAGAAATTCGAATC	1927
DB	14993	-----ATTATTTGGTTACTTTAGCTTGTTTATTAATATTTTGGTTATTTAGTAATAATACAAG	14929
QY	1928	TGCTTGTAAATTTTCAATAAACAACAAATATTAAATAACACAGCTAAAGTAACAATAATATC	1987
DB	14928	CAGATTGGAAATTTCTACAAAATAATTTATTTAACTTTTAACTTAATAATATTTAGTTAATGGT	14869
QY	1988	AAACTAATAGAAACAGTAATCTAATGPAACAAACATAATCTAATGCTAATATAACAAAG	2047
DB	14868	ATAGATAT-----	14861
QY	2048	CGCAAGATCTATCATTTTATATAGTATTTTTCATCAACATTCATTAATTTCTTAAA	2107
DB	14860	-----TTAATATATAAATAAACTATTAATCATATAAAAAATATATTTTAAATTTATTTA	14808
QY	2108	TAATACTTGTAGTTTATTAACCTTCAATGGGATTCGACTATTAAATTAATGAATTAGTCG	2167
DB	14807	TTCCTATTTTACTATAGTATTTATCAATG-----ATAATTAATCATCAACACGCT	14754
QY	2168	AACATGAATAAACAAGTAAACATGATAGATCATGTCAATGTGTATCATTTGATCTTTACAT	2227
DB	14753	AGAAATCTATTATGATTTAAACAAATAATTAATGCTAGTATATCATCTTACATGTTTCGAT	14694
QY	2228	TTGGATTGATTTACAGTTGGGAAGCTGGGTTCGAAATCGATAGCTTGCCTCGAGTTATC	2287
DB	14693	CAAAATTCATTAATAAT-----AATATACTTACTCTCAACTTTTATCTCTC	14650
QY	2288	ATCATCATCATAGACACACGAAATAAAGTAATCAGATTTATCAGTTTAAAGCTATGTAATAT	2347
DB	14649	TTGCTCTTACACATCACTTCTGCAATTTTTTTTACATTACTATGTTGTTTATGTTAAACAAT	14590
QY	2348	TTGGCCCATTAACCAATCAATTAATAAATAGATCAGTTTAAAGAAAGATCAAAAGCTCAAAA	2407
DB	14589	ATATTTATAAATATTTTTTTTCAAAATATAACAATATATTAATATTAATCATACTAATTA	14530
QY	2408	AAATAAAAAAGAGAAAAGGGTCTTAACCAAGAAATGAAGGAGAAAATTAATTTTCCCTTACCAAGC	2467
DB	14529	ACATCACTTAATTTTATTTTATCTAAAGGAAAAGAAAATTAATTTTCCCTTACCAAGC	14470
QY	2468	TGCAACAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAACGAGAAAACGTAAAA	2527
DB	14469	TGGGGTA-CCGAATTTCTCGAGACCACTTTGTACAAGAAAGCTGAACGAGAAAACGTAAAA	14411
QY	2528	TGATATAAATATCAATATATTAATTTAGATTTTGGCATAAAAACAGACTACATATACTG	2587
DB	14410	TGATATAAATATCAATATATTAATTTAGATTTTGGCATAAAAACAGACTACATATACTG	14351
QY	2588	TAAAAACAAACATATCCAGTCACTATGAATCAACTACTAGTGGTATTTAGTGACCTGTA	2647
DB	14350	TAAAAACAAACATATCCAGTCACTATGAATCAACTACTAGTGGTATTTAGTGACCTGTA	14291
QY	2648	GTGACTTAAGTTGGCAGCATCACCCGACGCACTTTTGGCCGGAATAAATACCTGTGAACGGA	2707
DB	14290	GTGACTTAAGTTGGCAGCATCACCCGACGCACTTTTGGCCGGAATAAATACCTGTGAACGGA	14231
QY	2708	AGATCACTTCGCGAATAAATAATTCCTGTTGCTGCTTGTATACCGGGAAAGCCCTGGGC	2767
DB	14230	AGATCACTTCGCGAATAAATAATTCCTGTTGCTGCTTGTATACCGGGAAAGCCCTGGGC	14171
QY	2768	CAACTTTTGGCGAAATGAGAGCTTGATCGGATTTTCAAACTCTTATACCTTTCTCTTAC	2827
DB	14170	CAACTTTTGGCGAAATGAGAGCTTGATCGGATTTTCAAACTCTTATACCTTTCTCTTAC	14115
QY	2828	AAGTCGTTGGCTTTCATCTGGGATTTTTCAGCCCTCTATCTTACTAAAAGTGAATAAGTTTC	2887
DB	14114	GGTGTGCTATGAAGCAGCGCTATTACAGTGACAGTTTGACGCGCAGCATACAGTTGCTCA	14055
QY	2888	TGTAATTTCTACTGTATGCACTCGCAGACTG-----CTGTGATAGGAGAGCCTG	2938

Db 510 TCTTATACCTTTCTCTTACAGTCGTTGGCTTCATCTGGAATTTTCAGCCTCTATACATTA 569
QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA 565
Db 570 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA 629
QY 566 AGGAGCCTGACATTTATATATCCAGAAACATCAGGTTAATGGCGTTTGTGATGATTT 625
Db 630 AGGAGCCTGACATTTATATATCCAGAAACATCAGGTTAATGGCGTTTGTGATGATTT 689
QY 626 TCGCGTGGCTGAGATCAGCCACTTTTCCCGATACCGAGACCGGACACTGGCCATA 685
Db 690 TCGCGTGGCTGAGATCAGCCACTTTTCCCGATACCGAGACCGGACACTGGCCATA 749
QY 686 TCGTGGCTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAGG 745
Db 750 TCGTGGCTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAGG 809
QY 746 GAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCGCGGCG 805
Db 810 GAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCGCGGCG 869
QY 806 GTGTCAATAATATCACTCTGTATCATCCACAAACAGAGATACGGCTCTCTTTTATAG 865
Db 870 GTGTCAATAATATCACTCTGTATCATCCACAAACAGAGATACGGCTCTCTTTTATAG 929
QY 866 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTAT 925
Db 930 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTAT 989
QY 926 TTTCAATAAACCGGCGACCTGACCATCCCTTCTGTATTTCCGCTTTCCAGCGTTCCGC 985
Db 990 TTTCAATAAACCGGCGACCTGACCATCCCTTCTGTATTTCCGCTTTCCAGCGTTCCGC 1049
QY 986 AGCAGACGACGGGCTTTCATTTGCAATGTTGTGCTTACAGACCGGAGATATGACATC 1045
Db 1050 AGCAGACGACGGGCTTTCATTTGCAATGTTGTGCTTACAGACCGGAGATATGACATC 1109
QY 1046 ATATATGCTTTGAGCAACTGATAGCTGTGCTGTCACTGTCACTGTATATACGCTGCTTC 1105
Db 1110 ATATATGCTTTGAGCAACTGATAGCTGTGCTGTCACTGTCACTGTATATACGCTGCTTC 1169
QY 1106 ATAGCACACCTTTTGTGACATACCTTCGGGTA 1137
Db 1170 ATAGCACACCTTTTGTGACATACCTTCGGGTA 1201

RESULT 14

ABZ58770

ID ABZ58770 standard; DNA; 4627 BP.

XX AC ABZ58770;

XX DT 01-MAY-2003 (first entry)

XX DE Destination plasmid pDONR212(R) nucleotide sequence.

XX DE Nucleic acid insertion; recombination; nucleic acid selection;

XX DE Nucleic acid isolation; ds.

XX OS Synthetic.

XX PN WO200295055-A2.

XX PD 28-NOV-2002.

XX PF 21-MAY-2002; 2002WO-US015947.

XX PF 21-MAY-2001; 2001US-0291973P.

XX PR (INVI-) INVITROGEN CORP.

XX PA

XX XX

PI XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
DR WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.

XX PS Disclosure; Fig 29B-C; 273pp; English.

XX CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(R) nucleotide sequence

XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 23.5%; Score 1102.4; DB 7; Length 4627;

Best Local Similarity 99.5%; Pred. No. 2.2e-147;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAATATCAATATATT 85

Db 90 GCCAACTTTGTACAAAAAGCTGATTCGAAACGTAAATGATATAATATCAATATATT 149

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 145

Db 150 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 209

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACGACGAGCTTCCAAA 205

Db 210 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACGACGAGCTTCCAAA 269

QY 206 TGTTCCTCGGTGATGTGCCAACTTAGTTCGACGACGAGCTTCCAAATGTTCTTCTCAA 265

Db 270 TGTTCCTCGGTGATGTGCCAACTTAGTTCGACGACGAGCTTCCAAATGTTCTTCTCAA 329

QY 266 ACAGAACTCGTCTATCCAGCTTACTCGCTATTGTCCTCAATGCCGTATTAATCATATAA 325

Db 330 ACAGAACTCGTCTATCCAGCTTACTCGCTATTGTCCTCAATGCCGTATTAATCATATAA 389

QY 326 AGAAATAGAAAAAGAGGTGCGACCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385

Db 390 AGAAATAGAAAAAGAGGTGCGACCTCTTTTGTGTGACAAAAATAAAACATCTACCT 449

QY 386 ATTCATATACGCTAGTGTCTAGTTCCTGAAATCATCTGCAATCAAGACAAATTTCAAC 445

Db 450 ATTCATATACGCTAGTGTCTAGTTCCTGAAATCATCTGCAATCAAGACAAATTTCAAC 509

QY 446 TCTTATACCTTTTCTTACAGTCTGTCGGCTTCTATCTGGATTTTTCAGCCCTTATACCTTA 505

Db 510 TCTTATACCTTTTCTTACAGTCTGTCGGCTTCTATCTGGATTTTTCAGCCCTTATACCTTA 569

QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTGAGACTGGCTGTGATA 565

Db 570 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTGAGACTGGCTGTGATA 629

QY 566 AGGAGCCTGACATTTATATTTCCCGAAGACATCAGGTTAATGGCGTTTGTGATGCTATT 625

Db 630 AGGAGCCTGACATTTATATTTCCCGAAGACATCAGGTTAATGGCGTTTGTGATGCTATT 689

QY 626 TCGCGTGGCTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGACACTGGCCATA 685

Db 690 TCGCGTGGCTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGACACTGGCCATA 749

DB 1119 TGTCTCTGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 1178
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAMAA 325
DB 1179 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAMAA 1238
QY 326 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACATCTACCT 385
DB 1239 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACATCTACCT 1298
QY 386 ATTATATACGCTAGTGTATGCTGAAATCACTGTCATCCAGAAATTTTTCAGCCTCTATCTTA 445
DB 1299 ATTATATACGCTAGTGTATGCTGAAATCACTGTCATCCAGAAATTTTTCAGCCTCTATCTTA 1358
QY 446 TCTTATACCTTTCTCTTACAAGTCGTTGGCTTCTATCTGGAATTTTTCAGCCTCTATCTTA 505
DB 1359 TCTTATACCTTTCTCTTACAAGTCGTTGGCTTCTATCTGGAATTTTTCAGCCTCTATCTTA 1418
QY 506 CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGTGTATA 565
DB 1419 CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGTGTATA 1478
QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGTTTTTGTGATGTCATTT 625
DB 1479 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGTTTTTGTGATGTCATTT 1538
QY 626 TCGCGTGTCTGAGATCAGCCATCTTCTCCCGATAACGAGACCGGCACACTGCCCATTA 685
DB 1539 TCGCGTGTCTGAGATCAGCCATCTTCTCCCGATAACGAGACCGGCACACTGCCCATTA 1598
QY 686 TCGGTGTCTATCATCGCCAGCTTTCATCCCGATATGACACACCGGTAAAGTTTCAAG 745
DB 1599 TCGGTGTCTATCATCGCCAGCTTTCATCCCGATATGACACACCGGTAAAGTTTCAAG 1658
QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGACGGGGATCACCATCGTCCGCGGCG 805
DB 1659 GAGACTTTATCTGACAGCAGCTGCTGCTGCGACGGGGATCACCATCGTCCGCGGCG 1718
QY 806 GTGTCAATAATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTTTTATAG 865
DB 1719 GTGTCAATAATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTTTTATAG 1778
QY 866 GTGTAACCTTAACTGATTTTCAACAGTCCCTGTTCTGTCAGAAAAGACCGCTTAT 925
DB 1779 GTGTAACCTTAACTGATTTTCAACAGTCCCTGTTCTGTCAGAAAAGACCGCTTAT 1838
QY 926 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 1839 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 1898
QY 986 ACGCAGACGCGGCTTCTATCTGATGTTGTGCTTACCGAGACGGAGATTTGACATC 1045
DB 1899 ACGCAGACGCGGCTTCTATCTGATGTTGTGCTTACCGAGACGGAGATTTGACATC 1958
QY 1046 ATATATGCTTGTAGCACTGATGCTGCTGCTCAACTGTCACTGATTAACGCTGCTTC 1105
DB 1959 ATATATGCTTGTAGCACTGATGCTGCTGCTCAACTGTCACTGATTAACGCTGCTTC 2018
QY 1106 ATAGCACACCTTTTGTGACATCTTCGGGTA 1137
DB 2019 ATAGCACACCTTTTGTGACATCTTCGGGTA 2050

RESULT 13

ABZ58769

ID ABZ58769 standard; DNA; 4627 BP.

XX AC

ABZ58769;

XX AC

DT 01-MAY-2003 (first entry)

XX DE

Destination plasmid pDONR212(F) nucleotide sequence.

XX

Nucleic acid insertion; recombination; nucleic acid selection;
nucleic acid isolation; ds.

Synthetic.

WO200295055-A2.

28-NOV-2002.

21-MAY-2002; 2002WO-US015947.

21-MAY-2001; 2001US-0291973P.

(INVI-) INVITROGEN CORP.

Braach MA, Cheo D, Li X, Esposito D, Byrd DRN;

WPI; 2003-129436/12.

Inserting a population of nucleic acids into a second target molecule for
selecting and isolating nucleic acid molecules by mixing the second
population of nucleic acid with a second target nucleic acid.

Disclosure; Fig 28B-C; 273pp; English.

The invention relates to inserting a population of nucleic acids into a
second target molecule. The method involves (a) mixing a first population
of nucleic acid comprising one or more recombination sites with a target
nucleic acid; (b) causing some or all of the nucleic acid molecules of
the first population to recombine with the first target nucleic acid
molecules to form a second population; (c) mixing the second population
of nucleic acid with a second target nucleic acid; and (d) causing some
or all of the nucleic acid molecules of the second population to
recombine with some or all of the second target nucleic acid molecules to
form a third population of nucleic acid. The method is useful for
selecting and isolating nucleic acid molecules. The present sequence
represents the destination plasmid pDONR212(F) nucleotide sequence

Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match

Best Local Similarity 23.5%; Score 1102.4; DB 7; Length 4627;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGCTAAATGATATAATATCAATATATT 85

DB 90 GCCAATTTGTACAAAAAGCTGATTCGAACGTAATGATATAATATCAATATATT 149

QY 86 AAATTAGATTTTGCAAAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTC 145

DB 150 AAATTAGATTTTGCAAAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTC 209

QY 146 ACTATGATCACTACTTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 205

DB 210 ACTATGATCACTACTTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 269

QY 206 TGTCTCTGGGTGATGCTGCCAATCTAGTCGACGACAGCTTCCAAATGTTCTTCTCAA 265

DB 270 TGTCTCTGGGTGATGCTGCCAATCTAGTCGACGACAGCTTCCAAATGTTCTTCTCAA 329

QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAAA 325

DB 330 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAAA 389

QY 326 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACATCTACCT 385

DB 390 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACATCTACCT 449

QY 386 ATTATATACGCTAGTGTATGCTGAAATCACTGTCATCCAGAAATTTTTCAGAAC 445

DB 450 ATTATATACGCTAGTGTATGCTGAAATCACTGTCATCCAGAAATTTTTCAGAAC 509

QY 446 TCTTATACCTTTTCTTACAAAGTCGTTCCGCTTCACTCGGCTTTCAGCCTCTATCTTA 505

QY 26 GACAAGTTTGTACAAAAAAGCTGACGAGAAACGTAATAATGATATAATCAATATATT 85
Db |
5483 GCCAACTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 5424
QY 86 AATATTAGATTTTCATATAAAGACGACTACATATACTGTAAACACACATATCCAGTC 145
Db |
5423 AATATTAGATTTTCATATAAAGACGACTACATATACTGTAAACACACATATCCAGTC 5364
QY 146 ACTATGAATCAACTACTTATAGATGATTAATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 205
Db |
5363 ACTATGAATCAACTACTTATAGATGATTAATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 5304
QY 206 TGTCTTCGCGGTGATGCTGCCAATCTAGTCGACGAGAGCCCTCCAAAAGTTCTCTCAA 265
Db |
5303 TGTCTTCGCGGTGATGCTGCCAATCTAGTCGACGAGAGCCCTCCAAAAGTTCTCTCAA 5244
QY 266 ACCGAATCGTGTATCCAGGCTACTCGCTATTGTCTCAATGCGTATTAAATCATAAAA 325
Db |
5243 ACCGAATCGTGTATCCAGGCTACTCGCTATTGTCTCAATGCGTATTAAATCATAAAA 5184
QY 326 AGAAATAAGAAAAGAGGTGCGAGCCCTTTTTTGTGTGACAAAAATAAAAACTACCT 385
Db |
5183 AGAAATAAGAAAAGAGGTGCGAGCCCTTTTTTGTGTGACAAAAATAAAAACTACCT 5124
QY 386 ATTCAATATACGCTAGTGTCTAGTCTGCTGAAATCATCTGATCAAGACAAATTTTCAAC 445
Db |
5123 ATTCAATATACGCTAGTGTCTAGTCTGCTGAAATCATCTGATCAAGACAAATTTTCAAC 5064
QY 446 TCTTATATCTTTCTCTTACAAAGTCGTTTGGGCTTCATCTGGATTTTCAGGCTCTATATCTTA 505
Db |
5063 TCTTATATCTTTCTCTTACAAAGTCGTTTGGGCTTCATCTGGATTTTCAGGCTCTATATCTTA 5004
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCACTGGCTGTGTATA 565
Db |
5003 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCACTGGCTGTGTATA 4944
QY 566 AGGAGCCCTGACATTTATATATCCCGAGACATCAGGTTAATGCGGTTTGTGATGCTATT 625
Db |
4943 AGGAGCCCTGACATTTATATATCCCGAGACATCAGGTTAATGCGGTTTGTGATGCTATT 4884
QY 626 TCGCGTGGCTGAGATCAGCACTTCTTCCCGATTAACGAGACCGGACACTGGCCATA 685
Db |
4883 TCGCGTGGCTGAGATCAGCACTTCTTCCCGATTAACGAGACCGGACACTGGCCATA 4824
QY 686 TCGGTGGCTCATATGCGGAGCTTTTATCCCGATATGACACCGGGTAAAGTTCCAGG 745
Db |
4823 TCGGTGGCTCATATGCGGAGCTTTTATCCCGATATGACACCGGGTAAAGTTCCAGG 4764
QY 746 GAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGC 805
Db |
4763 GAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGC 4704
QY 806 GTGTCAATTAATATCACTGTGATCAATCAACAAACAGACGATAACGGCTCTCTTTTATAG 865
Db |
4703 GTGTCAATTAATATCACTGTGATCAATCAACAAACAGACGATAACGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTAT 925
Db |
4643 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTAT 4584
QY 926 TTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 985
Db |
4583 TTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 4524
QY 986 ACGCAGACGAGCGGCTTCACTTCGATGTTGTGCTTACAGACCGAGATATTGACATC 1045
Db |
4523 ACGCAGACGAGCGGCTTCACTTCGATGTTGTGCTTACAGACCGAGATATTGACATC 4464
QY 1046 ATATATGCTTGAACGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db |
4463 ATATATGCTTGAACGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4404

QY 1106 ATAGCACACCTCTCTTTTGACATACCTTCGGGTA 1137
Db |
4403 ATAGCACACCTCTCTTTTGACATACCTTCGGGTA 4372
RESULT 12
ABZ58768
ID ABZ58768 standard; DNA; 4428 BP.
XX ABZ58768;
AC ABZ58768;
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brach MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 27B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence
XX
SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 23.5%; Score 1102.4; DB 7; Length 4428;
Best Local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 85
Db |
939 GCCAACTTTGTACAAAAAAGCTGATTCGAAACGTAATAATGATATAATCAATATATT 998
QY 86 AATATTAGATTTTCATATAAAGACGACTACATATACTGTAAACACACATATCCAGTC 145
Db |
999 AATATTAGATTTTCATATAAAGACGACTACATATACTGTAAACACACATATCCAGTC 1058
QY 146 ACTATGAATCAACTACTTATAGATGATTAATAGTACCTGTAGTCGACGAGCCCTCCAAA 205
Db |
1059 ACTATGAATCAACTACTTATAGATGATTAATAGTACCTGTAGTCGACGAGCCCTCCAAA 1118
QY 206 TGTCTTCGCGGTGATGCTGCCAATCTAGTCGACGAGCCCTCCAAATGTTCTCTCAA 265
Db |

CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
Query Match 23.7%; Score 1108.8; DB 3; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAAGTTTGTACAAAAGCTGAACGAGAAAGCTAAATGATATATATATCAATATATT 85
DB 5483 GCCAACTTTGTACAAAAGCTGAACGAGAAAGCTAAATGATATATATATCAATATATT 5424
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTAAACACACATATCCAGTC 145
DB 5423 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTAAACACACATATCCAGTC 5364
QY 146 ACTATGAATCACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGACGCTTCCAAA 205
DB 5363 ACTATGAATCACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGACGCTTCCAAA 5304
QY 206 TGTTCCTCGGGTGATGTCGCAACTTAGTCGACCGACGACGCTTCCAAAAGTCTCTCAA 265
DB 5303 TGTTCCTCGGGTGATGTCGCAACTTAGTCGACCGACGACGCTTCCAAAAGTCTCTCAA 5244
QY 266 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
DB 5243 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 5184
QY 326 AGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAATAAAACATCTACT 385
DB 5183 AGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAATAAAACATCTACT 5124
QY 386 ATTCAATACGCTAGTGTATAGTCTGAAATCATCTGCAATCAAGAAACAAATTTCCAAAC 445
DB 5123 ATTCAATACGCTAGTGTATAGTCTGAAATCATCTGCAATCAAGAAACAAATTTCCAAAC 5064
QY 446 TCTTATATCTTCTTCAAGTCGTCGGCTTCACTGGATTTCAGCCTCTATACCTTA 505
DB 5063 TCTTATATCTTCTTCAAGTCGTCGGCTTCACTGGATTTCAGCCTCTATACCTTA 5004
QY 506 CTAAACGCTGATAAGCTTTCTGTAATTTCTACTGTATCGACCTGCGCTGTGTATA 565
DB 5003 CTAAACGCTGATAAGCTTTCTGTAATTTCTACTGTATCGACCTGCGCTGTGTATA 4944
QY 566 AGGAGCCTGCATTTATATATCCCGAGAACATCAGGTTAAATGGCGTTTGTGATGTCATT 625
DB 4943 AGGAGCCTGCATTTATATATCCCGAGAACATCAGGTTAAATGGCGTTTGTGATGTCATT 4884
QY 626 TCGCGGTGGCTAGATACGCACTTCTTCCCGATAACGAGAACCGGACACTGCGCCATA 685
DB 4883 TCGCGGTGGCTAGATACGCACTTCTTCCCGATAACGAGAACCGGACACTGCGCCATA 4824
QY 686 TCGGTGGCTCATCGCCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCAGG 745
DB 4823 TCGGTGGCTCATCGCCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCAGG 4764
QY 746 GAGACTTTATCTGACAGCAGCTGCTGCGCCAGGGGATCACCATCGTCGCGCCGGC 805
DB 4763 GAGACTTTATCTGACAGCAGCTGCTGCGCCAGGGGATCACCATCGTCGCGCCGGC 4704
QY 806 GTGTCAATATATATCTCTGTATCTCCCAAAACAGACGATACGGCTCTCTTTTATAG 865
DB 4703 GTGTCAATATATATCTCTGTATCTCCCAAAACAGACGATACGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 925

DB 4643 GTGTAAACCTTAAACTGCTATTTACCACTCCCTGTTTCGTGACAAAGAGCCGTTTCAT 4584
QY 926 TTCATAAACCGGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 4583 TTCATAAACCGGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 4524
QY 986 ACGCAGACGACGCGCTTCTCATGTTGTGCTTACCAAGACCGGAGATATTGACATC 1045
DB 4523 ACGCAGACGACGCGCTTCTCATGTTGTGCTTACCAAGACCGGAGATATTGACATC 4464
QY 1046 ATATATGCTTTGAGCAACTGATAGTGTGCTGCTCAACTGCACTGTAATACGCTGCTTC 1105
DB 4463 ATATATGCTTTGAGCAACTGATAGTGTGCTGCTCAACTGCACTGTAATACGCTGCTTC 4404
QY 1106 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
DB 4403 ATAGCACACCTCTTTTGGACATCTTCGGGTA 4372
RESULT 11
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 18B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
Query Match 23.7%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Query Match 23.7%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PT protein production.

PS Claim 41; Page 47-51; 52pp; English.

XX The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The method of the invention is useful for studying the biology of an organism, including array construction, reporter gene fusions, CC mutagenesis, protein production and characterisation. The present DNA CC sequence represents the plasmid vector pMK2010 of the invention.

XX SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;

Query Match 23.7%; Score 1108.8; DB 8; Length 4892;

Best Local Similarity 99.8%; Pred. No. 2.7e-148;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAAGTAAATGATATATAATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAAGTAAATGATATATAATCAATATATT 161

QY 86 AATATAGATTTGTCATATAAAGACAGACTACATATATCTTAAACACACATATCCAGTC 145
DB 162 AATATAGATTTGTCATATAAAGACAGACTACATATATCTTAAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTATAGATGGTATTAGTAGACCTGTAGTCGACGACAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTATAGATGGTATTAGTAGACCTGTAGTCGACGACAGCCTTCCAAA 281

QY 206 TGTTCCTCGGTGATGTCGCAACTTAGTCGACGACAGCCTTCCAAAATGTTCTTCTCAA 265
DB 282 TGTTCCTCGGTGATGTCGCAACTTAGTCGACGACAGCCTTCCAAAATGTTCTTCTCAA 341

QY 266 ACGGAATCGTGTATCGAGCTACTCGTATTCTCTCAATGCGGTATTAATCATATAAA 325
DB 342 ACGGAATCGTGTATCGAGCTACTCGTATTCTCTCAATGCGGTATTAATCATATAAA 401

QY 326 AGAAATAAGAAAAAGAGTGCAGACCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
DB 402 AGAAATAAGAAAAAGAGTGCAGACCTCTTTTGTGTGACAAAAATAAAACATCTACCT 461

QY 386 ATTATATACGCTAGTGTCTAGTCTGAAATCATCTGATCAAGAAACATTTTCAAC 445
DB 462 ATTATATACGCTAGTGTCTAGTCTGAAATCATCTGATCAAGAAACATTTTCAAC 521

QY 446 TCTTATACCTTTCTCTTACAAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505
DB 522 TCTTATACCTTTCTCTTACAAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 581

QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGTGTATTA 565
DB 582 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGTGTATTA 641

QY 566 AGGAGCCTGACATTTATATATCCCGACAAATCATGAGTTAATGGGTTTGTGATCTATTT 625
DB 642 AGGAGCCTGACATTTATATATCCCGACAAATCATGAGTTAATGGGTTTGTGATCTATTT 701

QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACTGGCCATA 685
DB 702 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACTGGCCATA 761

QY 686 TCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTACGG 745
DB 762 TCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTACGG 821

QY 746 GAGACTTTATCTGACAGACAGCTGCACTGCGCCAGGGGGATCACCATCCCTCGCCGGGC 805
DB 822 GAGACTTTATCTGACAGACAGCTGCACTGCGCCAGGGGGATCACCATCCCTCGCCGGGC 881

QY 806 GTGTCAATATATACCTCTGTACATCCACAAAGAGAGTAACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATATATACCTCTGTACATCCACAAAGAGAGTAACGGCTCTCTCTTTTATAG 941

QY 866 GTGTAAACCTTAAACTGCAATTTACAGTCCTCTGTCTCTGTCAGCAAAAGAGCCGTTTCAT 925
DB 942 GTGTAAACCTTAAACTGCAATTTACAGTCCTCTGTCTCTGTCAGCAAAAGAGCCGTTTCAT 1001
QY 926 TTCAATAAACCGGGGAGCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCAGCGTTCCGC 985
DB 1002 TTCAATAAACCGGGGAGCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCAGCGTTCCGC 1061
QY 986 ACGCAGACGAGCGGCTTCAATTTCTGATGTTGTCTTACCGACCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGAGCGGCTTCAATTTCTGATGTTGTCTTACCGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATACGTCGTTTC 1105
DB 1122 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATACGTCGTTTC 1181
QY 1106 ATAGCACACCTCTTTTTCACATATCTTCGGTA 1137
DB 1182 ATAGCACACCTCTTTTTCACATATCTTCGGTA 1213

RESULT 9

AAC5525

ID AAC5525 standard; DNA; 4939 BP.

XX AC AAC5525;

XX DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

XX KW mutant; recombinational cloning; entry vector; destination vector;

XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.

OS Synthetic.

XX PN WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US005432.

XX PR 02-MAR-1999; 99US-0122389P.

XX PR 23-MAR-1999; 99US-0126049P.

XX PR 28-MAY-1999; 99US-0136744P.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

PT recombinational cloning of polypeptides.

XX Example 10; Fig 53; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated

XX 21-MAY-2002; 2002WO-US015947.
PF
XX
XX 21-MAY-2001; 2001US-0291973P.
PR
XX
XX (INVI-) INVITROGEN CORP.
PA
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
PI
XX
XX WPI; 2003-129436/12.
DR
XX
XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
XX Disclosure; Fig 26B-C; 273pp; English.
PS
XX
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR201 nucleotide sequence
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
SQ
Query Match 23.7%; Score 1108.8; DB 7; Length 4470;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACACCTTTGTACAAAAGCTGAACGAGAGAAAGTAAATGATATATAATCAATATATT 85
DB 102 GCCAATCTTGTACAAAAGCTGAACGAGAGAAAGTAAATGATATATAATCAATATATT 161
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAAATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAAATATCCAGTC 221
QY 146 ACTATGAATCAACTCTTAGATGGTATTAGTACCTGTAGTCACGACGACGCTTCCAA 205
DB 222 ACTATGAATCAACTCTTAGATGGTATTAGTACCTGTAGTCACGACGACGCTTCCAA 281
QY 206 TGTCTCTGGGTGATGCTGCAACTTAGTCGACGACGACGCTTCCAAATGCTTCTCAA 265
DB 282 TGTCTCTGGGTGATGCTGCAACTTAGTCGACGACGACGCTTCCAAATGCTTCTCAA 341
QY 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGCTCTCAATGCGGTATTAAATCATAAA 325
DB 342 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGCTCTCAATGCGGTATTAAATCATAAA 401
QY 326 AGAAATAGAAAAGAGGTCGGAGCCTCTTTTGTGTGACAAAATAAACAATCTACCT 395
DB 402 AGAAATAGAAAAGAGGTCGGAGCCTCTTTTGTGTGACAAAATAAACAATCTACCT 461
QY 386 ATTCAATAGCCTAGTGTCTCATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCAAC 445
DB 462 ATTCAATAGCCTAGTGTCTCATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCAAC 521
QY 446 TCTTATATCTTCTCTTACAAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACCTTA 505
DB 522 TCTTATATCTTCTCTTACAAAGTCGTTCCGCTTCATCTGGATTTTCAGCCTCTATACCTTA 581
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTCGAGACTGCTGTGTATA 565
DB 582 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTCGAGACTGCTGTGTATA 641
QY 566 AGGAGGCTGACATTTTATATTTCCCGAGAACATCAGGTTAATGGGCTTTTGTATGTCATTT 625

DB 642 AGGAGGCTGACATTTTATATTTCCCGAGAACATCAGGTTAATGGGCTTTTGTATGTCATTT 701
QY 626 TCGCGTGGCTGAGATCAGCCACTTTTCCCGAATAACGAGAGACGCGACACCTGGCCATA 685
DB 702 TCGCGTGGCTGAGATCAGCCACTTTTCCCGAATAACGAGAGACGCGACACCTGGCCATA 761
QY 686 TCGGTGTGTCATGCGCGCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAGG 745
DB 762 TCGGTGTGTCATGCGCGCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAGG 821
QY 746 GAGACTTTTATCTGACAGCAGACGTCACCTGGCCAGGGGGATCACCATCCGTCGCCCGGCG 805
DB 822 GAGACTTTTATCTGACAGCAGACGTCACCTGGCCAGGGGGATCACCATCCGTCGCCCGGCG 881
QY 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTTATAG 941
QY 866 GTGTAAACCTTAAACTGCAATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAT 925
DB 942 GTGTAAACCTTAAACTGCAATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAT 1001
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGGTCGCG 985
DB 1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGGTCGCG 1061
QY 986 AGCAGAGACGCGGCTTTCATTTCTGATGTTGCTTACGAGCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGCGGCTTTCATTTCTGATGTTGCTTACGAGCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTGGACCACTGATAGCTGCTGCTGCTCAACTGTCACTGTAAATAGCTGCTTC 1105
DB 1122 ATATATGCTTGGACCACTGATAGCTGCTGCTGCTCAACTGTCACTGTAAATAGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1213
RESULT 8
ADA50329
ID ADA50329 standard; DNA; 4892 BP.
XX
AC ADA50329;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid vector pMK2010 DNA sequence.
XX
KW site-specific recombination; array construction; reporter gene fusion;
KW mutagenesis; protein production; protein characterisation;
KW plasmid pMK2010; ds.
XX
OS Synthetic.
XX
XX WO2003064623-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003176.
XX
PR 31-JAN-2002; 2002US-0354063P.
XX
XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
PA Kahn ML, House BL, Mortimer MW;
PI WPI; 2003-679497/64.
XX
XX Moving an insert nucleic acid between vectors using sire-specific
PT recombination in vivo, useful for studying the biology of the organism,
PT including array construction, reporter gene fusions, mutagenesis and

CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention

Q Sequence 17681 BP; 4596 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other; 0 N

Query Match 25.8%; Score 1208.4; DB 6; Length 17681;
Best Local Similarity 60.4%;
P: Pred. No. 2e-162;
Matches 2174; Conservative 1476; Indels 80;

Qy	21	CTCAGACAAGTTTGTACAAAAAGCTGAAACGAGAAACGTAAATATGATATAAATATCAAT	80
Db	16909	CTCTAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAAT	16850
Qy	81	ATATTAAATTTAGATTTTGTCAATAAAAAACAGACTACATATACTGTAAACACAAATATC	140
Db	16849	ATATTAAATTTAGATTTTGTCAATAAAAAACAGACTACATATACTGTAAACACAAATATC	16790
Qy	141	CAGTCACATATGAATCAACTTTPAGATGTATTTAGTGACCTGTATGACCGACAGCCTT	200
Db	16789	CAGTCACATATGAATCAACTTTPAGATGTATTTAGTGACCTGTATGACCGACAGCCTT	16730
Qy	201	CCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTT	260
Db	16729	CCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTT	16670
Qy	261	CTCAACCGGAATCGTGGTATCCAGCCTTACTCGCTATTGTCTCAATCGCTATTAAATCA	320
Db	16669	CTCAACCGGAATCGTGGTATCCAGCCTTACTCGCTATTGTCTCAATCGCTATTAAATCA	16610
Qy	321	TAAAAAGAAATATAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAAATAAAAATC	380
Db	16609	TAAAAAGAAATATAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAAATAAAAATC	16550
Qy	381	TACCTATTCAATACGCTAGTGTCAATAGTCTTGAAATCATCTGCATCGAGACAAATTTTC	440
Db	16549	TACCTATTCAATACGCTAGTGTCAATAGTCTTGAAATCATCTGCATCGAGACAAATTTTC	16490
Qy	441	ACAACTCTTATCTTTTTCTCTTCAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTAT	500
Db	16489	ATGTCAAAAAGAGGTGTGCTATGAA--GCAGGTAATTACAGTGACAGTTTGACGGACA	16433
Qy	501	ACTTACTTAAACGTCATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGT	560
Db	16432	GCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGGTCTGGTAAGCACAAACAT	16373
Qy	561	GTATAGGGAGCCTGACATTTATATTTCCCGAGAAACATCAGGTTAATGGCGTTTTGATGT	620
Db	16372	GCAGAAATGAAGCCCGTCGTCTGCGTGCC---GAAACGCTGGAACGGGAAAAATCAGAAAG	16316
Qy	621	CATTTTCGCGGTGGCTGAGATCAGCACACTTCTTCCCGATTAACGGAGACGGGACACTGG	680
Db	16315	GATGGCTGAGTTCGCCCGGTTTATTGMAATGAACGGCTCTTTTGTGACGAGAAACAGG-	16257
Qy	681	CCATATCGGTGGTCATCATCGCCAGCTTTTCATCCCGATATGCAACCACGGGTAAAGTT	740
Db	16256	-----ACTGGTGAATCGAGTTTAAAGGTTTACACCTATATAAGAGAGAGCGTTATCGTC	16202
Qy	741	CACGGGAGACTTTATCTGACAGCAGACGTCGACTGGCAGGGGGATCAACATCCGTCGCC	800
Db	16201	TGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGACGGATGGTGATCCCC	16142
Qy	801	CGGGCGTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAAACGGCTCTCTCTTT	860
Db	16141	TGGCCAGTGACGTCCTGCTGCAGATAAAGTCTCCCGTGHACTTTTACCGGTGGTGCTATA	16082
Qy	861	TATAGTGTATAACCTTTAACTGCAATTTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAA	914
Db	16081	TCGGGGATGAAGCTGCGGCATGATGACCAACCGATATGGCCAGTGTGCCGCTCCCGTTA	16022
Qy	915	GAGCCGTTTCATTTCAATAAAACCGGGGACCTCAGCCCATCCCTTCTCGATTTTCCGCTTTC	974
Db	16021	TCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGGAAATGATCAATCAAAAACGCCATTAAAC	15962

Db 15280 CGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACACGACGATTT 15339
Qy 1727 ----- 1726
Db 15340 CCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAACACCTGGGCTA 15399
Qy 1727 ----- 1726
Db 15400 TTTCCCTAAAGGGTTTATTGAGATATGTTTTCGTCTCAGCCAATCCCTGGGTGAGTTT 15459
Qy 1727 ----- 1726
Db 15460 CACCAGTTTTCATTAAACGTGGCAATATGACAACTTCTTCGCCCCCGTTTTCACCAT 15519
Qy 1727 ----- 1726
Db 15520 GGGGAAATATTATACGAAGGGGACAAGGTGCTGATGCCGTGGGATTCAAGTTTCATCA 15579
Qy 1727 ----- 1726
Db 15580 TGGCGTCTGTGATGCTTCCATGTCCGACAGATGCTTAATGAATTTACAACAGTACTGCGA 15639
Qy 1727 ----- 1726
Db 15640 TGAGTGGCAGGGCGGGCGGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGTA 15699
Qy 1727 ----- 1743
Db 15700 TCGGTATTGGCGCGTATTTTGGGTTAAGAATATATCTGATATGTGGGCCCAT 15759
Qy 1744 ATAGTAATCTAGCTGGTTTGATGAATTAATATCAATGATATAATCTATAGTAAAAAT 1803
Db 15760 ATAGTAATCTAGCTGGTTTGATGAATTAATATCAATGATATAATCTATAGTAAAAAT 15819
Qy 1804 AAGATTAATTAATTAATTAATTTTATGATTAATAGTTTATTAATTAATTAAT 1863
Db 15820 AAGATTAATTAATTAATTAATTTTATGATTAATAGTTTATTAATTAATTAAT 15879
Qy 1864 ATCTATACATTACTAAATATTTTATGTTTAAAGTTAATAATTTTGTAGAAATTC 1923
Db 15880 ATCTATACATTACTAAATATTTTATGTTTAAAGTTAATAATTTTGTAGAAATTC 15939
Qy 1924 AATCTGCTGTATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAATAA 1983
Db 15940 AATCTGCTGTATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAATAA 15999
Qy 1984 TATCAAACTTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGTAAATAAC 2043
Db 16000 TATCAAACTTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGTAAATAAC 16059
Qy 2044 AAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTC 2103
Db 16060 AAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTC 16119
Qy 2104 TAAATAATCTGTAGTTTATTAATCTTAATCTTAATCTAATCTAATCTAATCTAATCT 2163
Db 16120 TAAATAATCTGTAGTTTATTAATCTTAATCTTAATCTAATCTAATCTAATCTAATCT 16179
Qy 2164 GTCCGAACATGAATAAACAAGGTAACATGATCATGTCAATGTGTTATCATCTATCTT 2223
Db 16180 GTCCGAACATGAATAAACAAGGTAACATGATCATGTCAATGTGTTATCATCTATCTT 16239
Qy 2224 ACATTGGATTTGATTACAGTTGGGAGCTGGGTTGAAATCGAATAGCTTGGCTGCGAGT 2283
Db 16240 ACATTGGATTTGATTACAGTTGGGAGGTTGGGTTGAAATCGAATAGCTTGGGTTGG 16293
Qy 2284 TATCATCATCATATAGACACAGGAAATTAAGTAATCATGATTAATCAAGTTTAAAGCTATGTA 2343
Db 16294 CCTCTAGAGAGCTGACGCTGGATGGCAATAATGATTTTATTTGACTGATAGTACCTG 16353
Qy 2344 ATATTGGCCCATAAACCAATCAATTAATAAATAATAGATCAGTTTAAAGAAAGATCAAGCTC 2403

Db 16354 TTCTGTGCAACAAA----- 16367
Qy 2404 AAAAAAATAAAAGAGAGAAAAGGTCCTTAACCAAGAAAATGAAGGAGAAAACCTAGAAATT 2463
Db 16368 ----- 16367
Qy 2464 TACCTGCACAAGCTTGGATCCTCTAGACCACTTTGTATCAAGAAAGCTGAACAGAAACGT 2523
Db 16368 TTGATAAGCAATGCTTTCTTATATGCAAACTTTGTACAAAGAAAGCTGAACAGAAACGT 16427
Qy 2524 AATATGATATAATATCAATATATTAATATAGATTTTGCATAAATAACAGACTACATAAT 2583
Db 16428 AAAATGATATAATATCAATATATTAATATAGATTTTGCATAAATAACAGACTACATAAT 16487
Qy 2584 ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 2643
Db 16488 ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 16547
Qy 2644 TGTAAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGAATAAATACCTGTGA 2703
Db 16548 TGTAAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGAATAAATACCTGTGA 16607
Qy 2704 CGGAAGATCACTTCGCAAGATAAATAAATCCTGTGTCTCTGTGTATACCGGGAAGCCCT 2763
Db 16608 CGGAAGATCACTTCGCAAGATAAATAAATCCTGTGTCTCTGTGTATACCGGGAAGCCCT 16667
Qy 2764 GGGCCAACTTTTGGCGAAAATGAGACGTTGATCGG-----ATTTTCACAACTCTTATA 2815
Db 16668 GGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGACTACCCATTTTCACAACTCTTATA 16727
Qy 2816 CTTTTCCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTATAACG 2875
Db 16728 CTTTTCCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTATAACG 16787
Qy 2876 TGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTAAGGGAGC 2935
Db 16788 TGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTAAGGGAGC 16847
Qy 2936 CTGACATTTATPATTTCCCGAACAATCAGGTTTAATGGCGTTTTCATGTCAATTTTCGCGGT 2995
Db 16848 CTGACATTTATPATTTCCCGAACAATCAGGTTTAATGGCGTTTTCATGTCAATTTTCGCGGT 16907
Qy 2996 GGTGTAGATCAGCCACTTCTCCCGATTAACGGAGACGGGCACTGGCCATATCGGTGG 3055
Db 16908 GGTGTAGATCAGCCACTTCTCCCGATTAACGGAGACGGGCACTGGCCATATCGGTGG 16967
Qy 3056 TCATCATGCGCGAGCTTTTCATCCCGATATGACCAACCGGGTAAAGTTTCAACGGAGACTT 3115
Db 16968 TCATCATGCGCGAGCTTTTCATCCCGATATGACCAACCGGGTAAAGTTTCAACGGAGACTT 17027
Qy 3116 TATCTGACAGCAGCTGTCATCGCCAGGGGATCAACATCCGTGCGCCGGCGGTGTCAA 3175
Db 17028 TATCTGACAGCAGCTGTCATCGCCAGGGGATCAACATCCGTGCGCCGGCGGTGTCAA 17087
Qy 3176 TAAATATCACTCTGTATCTCAACACAGACCAATACGCTCTCTCTTTTATAGGTGTAAA 3235
Db 17088 TAAATATCACTCTGTATCTCAACACAGACCAATACGCTCTCTCTTTTATAGGTGTAAA 17147
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Qy 3296 AACCGGGCGACCTCAGGCAATCCCTTCTGATTTTTCGCTTTCCAGCGTTCGCGACGACGA 3355
Db 17208 AACCGGGCGACCTCAGGCAATCCCTTCTGATTTTTCGCTTTCCAGCGTTCGCGACGACGA 17267
Qy 3356 CGACGGGCTTCATTTCTGATGTTTGTCTTACAGACCGGAGATTTTACATCATATATG 3415
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Qy 3416 CTTTGAGCAACTGATAGCTGTGCTGTCAAATGTCTGATTAATAGCTGCTTCTATAGCAC 3475
Db 17328 CTTTGAGCAACTGATAGCTGTGCTGTCAAATGTCTGATTAATAGCTGCTTCTATAGCAC 17387

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATATT 85
DB 13121 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATATT 13180
QY 86 AAATTAGATTTTGCATAAAAAAGACACTACATAAATACGTAAACACACATATCCAGTC 145
DB 13181 AAATTAGATTTTGCATAAAAAAGACACTACATAAATACGTAAACACACATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 205
DB 13241 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 13300
QY 206 TGTCTTCGGGTGATGCTCCAACTTGTAGTCGACGACAGCCTTCCAAATGTTCTCTCAA 265
DB 13301 TGTCTTCGGGTGATGCTCCAACTTGTAGTCGACGACAGCCTTCCAAATGTTCTCTCAA 13360
QY 266 ACGGAATCGTGTATCCAGCTACTCGCTATTGTGCTCAATCGGTATTAAATCATATAA 325
DB 13361 ACGGAATCGTGTATCCAGCTACTCGCTATTGTGCTCAATCGGTATTAAATCATATAA 13420
QY 326 AGAAATAAGAAAAAGGTGCGAGCCTCTTTTTTGTGTGACAAAAATAAAAAACATCTACCT 385
DB 13421 AGAAATAAGAAAAAGGTGCGAGCCTCTTTTTTGTGTGACAAAAATAAAAAACATCTACCT 13480
QY 386 ATTCATATACGTGTGTGATAGTCTGAAATCATCTGATCAAGAACAAATTTCAACAC 445
DB 13481 ATTCATATACGTGTGTGATAGTCTGAAATCATCTGATCAAGAACAAATTTCAACAC 13540
QY 446 TCTTATACCTTTCTCTTACAGTCGTTTCGGCTTCTCATCTGATTTTCAGGCTCTATACCTTA 505
DB 13541 TCTTATACCTTTCTCTTACAGTCGTTTCGGCTTCTCATCTGATTTTCAGGCTCTATACCTTA 13600
QY 506 CTAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA 565
DB 13601 CTAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA 13660
QY 566 AGGAGCTGTGACATTTATATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
DB 13661 AGGAGCTGTGACATTTATATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 13720
QY 626 TCSCGTTGGCTGAGATCAGCCTCTCTCCCGATACAGGACCGGACACCTGGCCATA 685
DB 13721 TCSCGTTGGCTGAGATCAGCCTCTCTCCCGATACAGGACCGGACACCTGGCCATA 13780
QY 686 TCSCGTTGGCTGAGATCAGCCTCTCTCCCGATACAGGACCGGACCTGAAAGTTCAAGG 745
DB 13781 TCSCGTTGGCTGAGATCAGCCTCTCTCCCGATACAGGACCGGACCTGAAAGTTCAAGG 13840
QY 746 GAGACTTTATCTGACGACGCTGACCTGCGGAGGGGATCACCATTCGTCGCCCGGGC 805
DB 13841 GAGACTTTATCTGACGACGCTGACCTGCGGAGGGGATCACCATTCGTCGCCCGGGC 13900
QY 806 GTGTCAATAATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTTTATAG 865
DB 13901 GTGTCAATAATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTTTATAG 13960
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DB 13961 GTGTAAACCTTAACTGCAATTTCAAGTCCGCTGTTCTGTCAGCAAAAAGAGCGGTTTCAT 14020
QY 926 TTCATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGGC 985
DB 14021 TTCATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGGC 14080
QY 986 ACGCAGACGAGCGGCTTCAITCTGCATGGTTGTGCTTTACAGACCGGAGATATTGACATC 1045
DB 14081 ACGCAGACGAGCGGCTTCAITCTGCATGGTTGTGCTTTACAGACCGGAGATATTGACATC 14140
QY 1046 ATATATGCTTGAACAATGATAGCTGTGCTGTCACTGTCTGTAATACGCTGCTTC 1105
DB 14141 ATATATGCTTGAACAATGATAGCTGTGCTGTCACTGTCTGTAATACGCTGCTTC 14200

QY 1106 ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTCCGATCAACGCTCTCATTTTCGCAA 1165
DB 14201 ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTCCGATCAACGCTCTCATTTTCGCAA 14260
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QY 1286 GTGACTACAGGTCACTAATACCATCTTAAGTAGTTGATTTCATGACTGCTGATATGTTGT 1345
DB 14381 GTGACTACAGGTCACTAATACCATCTTAAGTAGTTGATTTCATGACTGCTGATATGTTGT 14440
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QY 1406 ATATCATTTTACGTTTCGCTTCAGCTTCTTTGTACAAAGTGG 1448
DB 14501 ATATCATTTTACGTTTCGCTTCAGCTTCTTTGTACAAAGTGGCAITTTAAGAAGCAT 14560
QY 1449 1448
DB 14561 TGTCTTATCAATTTGTTGCAACGACAGGTCACTATCAGTCAAAATATAAATCATTTATTTCG 14620
QY 1449 1493
DB 14621 CATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCTCA-ATTGGTAAGGAATAATATTT 14679
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DB 14680 TCTTTTTCCTTTTAGTATATAAAATAGTTAGTGATGTTAATTAGTATGATATAATA 14739
QY 1554 TAGTTTGTATTAATTCGTAAGAAAAATAATTTATAAATATATTTTACATAAAACACATAGT 1613
DB 14740 TAGTTTGTATTAATTCGTAAGAAAAATAATTTATAAATATATTTTACATAAAACACATAGT 14799
QY 1614 AATGTAAAAAATAATGACAAGTGATGTGTAAAGACGAAGAAGATAAAAGTTGAGAGTAAGT 1673
DB 14800 AATGTAAAAAATAATGACAAGTGATGTGTAAAGACGAAGAAGATAAAAGTTGAGAGTAAGT 14859
QY 1674 ATATTTATTTTATGATTTGATCCGAACATGTAGTATGATATACGATTA 1726
DB 14860 ATATTTATTTTATGATTTGATCCGAACATGTAGTATGATATACGCGCGGTAAAGGTTTC 14919
QY 1727 1726
DB 14920 CAACTTTCACCATATGAATAAGATCACTACCGGGCGTATTTTGTAGTTATCGAGATT 14979
QY 1727 1726
DB 14980 TTCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT 15039
QY 1727 1726
DB 15040 ATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCAGTTGCTCAATGACCTTA 15099
QY 1727 1726
DB 15100 TAACCAGACGTTACGTGATATTTACGGCTTTTAAAGACCGTAAAGAAAAATAAGCA 15159
QY 1727 1726
DB 15160 CAAAGTTTATCCGGCTTTTATTTACATTTCTTCCCGCTGATGAATGCTCATCCGGAAT 15219
QY 1727 1726
DB 15220 CCGTATGGCAATGAAGACGAGTGGTGTGATATGGGATAGTGTTCACCCCTTGTGTACAC 15279
QY 1727 1726

Db 14320 GATTCAATAGTCACTGGATGTAUATGTTGTTTACAGTATATATGTAAGTCTGTTTTTATGCAA 14379
QY 1381 AATCTTAATTAATATATGATATATATATCAATTTTACGTTTCTCGTTCAGCTTCTTCTGTA 1440
Db 14380 AATCTAAATTAATATATGATATATATATCAATTTTACGTTTCTCGTTCAGCTTCTTCTGTA 14439
QY 1441 CAAGTGTCTCGAGGAATTCGTAACCCAGCTTGGTAAGGAATAATATATTTCTTTT 1500
Db 14440 CAAAGTGTCTCGAGGAATTCGTAACCCAGCTTGGTAAGGAATAATATATTTCTTTT 14495
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Db 14496 TCCTTTTAGTATAAATAGTAAAGTGAATGTTAAATAGTATGATATATATATATATATATAT 14555
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QY 1741 ATAATAGTAATTTCTAGCTGTTTGTGATTAATTAATTAATCAATGATAAATACTATATAGTAA 1800
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QY 1801 AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1860
Db 14796 AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 14855
QY 1861 AATATCTATACCAATTAATAATATATTTTGTAAAGTTAAATAATTTTGTAGAAAT 1920
Db 14856 AATATCTATACCAATTAATAATATATTTTGTAAAGTTAAATAATTTTGTAGAAAT 14915
QY 1921 TCCAAATCTGTTGTAATTTATCAATAAACAATAATTAATAAACAAGCTTAAAGTAACAA 1980
Db 14916 TCCAAATCTGTTGTAATTTATCAATAAACAATAATTAATAAACAAGCTTAAAGTAACAA 14975
QY 1981 TAATATCAAACTAATAAGAACAGTAATCTAAATGTAACAAACATATCTAAATGCTAATAT 2040
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QY 2221 CTTACATTTGGATGATTAAGTTGGGAAGCTGGGTTTCGAAATCGATAAGCTTTGGCTGC 2280
Db 15216 CTTACATTTGGATGATTAAGTTGGGAAGCTGGGTTTCGAAATCGATAAGCTTTGGCTGC 15247
QY 2281 AGTTATCATCATCATATAGACACACGAAATAAAGTAATCAGATTATCAGTTAAAGCTAT 2340
Db 15248 ----- 15247
QY 2341 GTAATATTTGGCCATAACCAATCAATTAATAAATAATAGATCAGTTTAAAGAAAGATCA 2400
Db 15248 ----- 15247
QY 2401 CTCAAAAATAAAGAGAAAAAGGGTCTTAACCAAGAAAAATGAAGGAGAAAAAAGTAA 2460
Db 15248 ----- 15247

QY 2461 ATTACCTGCACCAAGCTTGGATCCTCTAGACCACTTTTGTACAAGAAAGCTGAACGAGAA 2520
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Db 15477 TGACGGAGATCACTTCGCAAGATAAATAAATCTGTTGTCCTGTTGATACCGGGAAGC 15536
QY 2761 CCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGGATTCACAACTCTTATACCTTT 2820
Db 15537 CCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGGATTCACAACTCTTATACCTTT 15596
QY 2821 CTCTTAAGTCTGTTTGGCTTCATCTGATTTTTCAGCTCTATCTTACTTAAACGTGATA 2880
Db 15597 CTCTTAAGTCTGTTTGGCTTCATCTGATTTTTCAGCTCTATCTTACTTAAACGTGATA 15656
QY 2881 AAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATAAGGAGAGCTGAC 2940
Db 15657 AAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATAAGGAGAGCTGAC 15716
QY 2941 ATTTATATTTCCCGAACAATCAGGTTAATGCGTTTTTGTAGTGTCAATTTTCGCGTGGCTG 3000
Db 15717 ATTTATATTTCCCGAACAATCAGGTTAATGCGTTTTTGTAGTGTCAATTTTCGCGTGGCTG 15776
QY 3001 AGATCAGCACTTTCTCCCGATAACCGAGACCGCACACTGGCCATATCGTGTGTCAATC 3060
Db 15777 AGATCAGCACTTTCTCCCGATAACCGAGACCGCACACTGGCCATATCGTGTGTCAATC 15836
QY 3061 ATGCGCCAGCTTTCTATCCCGATATGACACACCGGTAAAGTTTACGCGGAGACTTTATCT 3120
Db 15837 ATGCGCCAGCTTTCTATCCCGATATGACACACCGGTAAAGTTTACGCGGAGACTTTATCT 15896
QY 3121 GACAGCAAGTGTCACTGGCCAGGGGGATCAACATCCGTCGCGCGGGGTGTCAATATA 3180
Db 15897 GACAGCAAGTGTCACTGGCCAGGGGGATCAACATCCGTCGCGCGGGGTGTCAATATA 15956
QY 3181 TCACCTCTGTACATCCACAAACAGACGATAAGGCTCTCTCTTTTATAGTGTAAACCTTA 3240
Db 15957 TCACCTCTGTACATCCACAAACAGACGATAAGGCTCTCTCTTTTATAGTGTAAACCTTA 16016
QY 3241 AACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCAATTCATTAACCG 3300
Db 16017 AACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCAATTCATTAACCG 16076
QY 3301 GCGGACCTCAGCCATCCCTTCTGATTTTTCGCTTCCAGGCTTCGCGACGAGACGAG 3360
Db 16077 GCGGACCTCAGCCATCCCTTCTGATTTTTCGCTTCCAGGCTTCGCGACGAGACGAG 16136
QY 3361 GCTTCTATCTGCATGTTGTTGCTTTTACAGACCGGAGATTTGACATCATATATGCTTTG 3420
Db 16137 GCTTCTATCTGCATGTTGTTGCTTTTACAGACCGGAGATTTGACATCATATATGCTTTG 16196
QY 3421 AGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAATACGCTGTCTTCAAGACACTTC 3480
Db 16197 AGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAATACGCTGTCTTCAAGACACTTC 16256
QY 3481 TTTTGTACATCTTCTGTTTGTATGTCAGATGATTTTTCAGGACTATGACACTAGCGTATA 3540
Db 16257 TTTTGTACATCTTCTGTTTGTATGTCAGATGATTTTTCAGGACTATGACACTAGCGTATA 16316

KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
OS Synthetic.
PN WO200259294-A1.
XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU000073.
XX 26-JAN-2001; 2001US-0264067P.
XX 29-NOV-2001; 2001US-0333743P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
XX stranded RNA.
XX Claim 16; Page 83-93; 104pp; English.
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 89.7%; Score 4200; DB 6; Length 17458;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;
QY 1 TTTTCATTTTGGAGGACGCTCGAGCAAGTTTGTACAAAAGCTGAACGAGAAACGT 60
DB 13000 TTTTCATTTTGGAGGACGCTCGAGCAAGTTTGTACAAAAGCTGAACGAGAAACGT 13059
QY 61 AAAATGATATAAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 13060 AAAATGATATAAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 13119
QY 121 ACTGTAAACACCAATATCCAGTCACTATGAATCAACTACTTAGATGTTAGTGACC 180
DB 13120 ACTGTAAACACCAATATCCAGTCACTATGAATCAACTACTTAGATGTTAGTGACC 13179
QY 181 TGTAGTTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAATCTAGTCGACCG 240
DB 13180 TGTAGTTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAATCTAGTCGACCG 13239
QY 241 ACAGCCTTCCAAATGTTCTTCTCAAACGGAAATCGTCGTATCCAGCCTACTCGGTATTGTC 300

DB 13240 ACAGCCTTCCAAATGTTCTTCTCAAACGGAAATCGTCGTATCCAGCCTACTCGGTATTGTC 13299
QY 301 CTCATGCGGTATTAATAATCAATAAAGAAATAGAAAAGAGGTGGAGCCTCTTTTTTG 360
DB 13300 CTCATGCGGTATTAATAATCAATAAAGAAATAGAAAAGAGGTGGAGCCTCTTTTTTG 13359
QY 361 TGTGACAAAATAAACAATCTACCTATTCATATACGCTAGTGTCAATAGTCTGAAATCA 420
DB 13360 TGTGACAAAATAAACAATCTACCTATTCATATACGCTAGTGTCAATAGTCTGAAATCA 13419
QY 421 TCTGATCAAGAACAATTTTCAAACTCTTATATCTTTCTTCAAGTCTCTCGGCTTCA 480
DB 13420 TCTGATCAAGAACAATTTTCAAACTCTTATATCTTTCTTCAAGTCTCTCGGCTTCA 13479
QY 481 TCTGGATTTTTCAGCCTCTATACCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 540
DB 13480 TCTGGATTTTTCAGCCTCTATACCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 13539
QY 541 TCGACCTGACAGCTGCTGTGTATAAGGGAGCCTGACATTTATATTTCCCGAGAACATCAG 600
DB 13540 TCGACCTGACAGCTGCTGTGTATAAGGGAGCCTGACATTTATATTTCCCGAGAACATCAG 13599
QY 601 GTTAATGGCGTTTGTAGTGTCAATTTTCGGGTGCTGAGATCAGCCACTTCTTCCCGAT 660
DB 13600 GTTAATGGCGTTTGTAGTGTCAATTTTCGGGTGCTGAGATCAGCCACTTCTTCCCGAT 13659
QY 661 AACGGAGACGGGACACTGGGCCATATCGTGGTTCATCATCGCCAGCTTTTATCCCGAT 720
DB 13660 AACGGAGACGGGACACTGGGCCATATCGTGGTTCATCATCGCCAGCTTTTATCCCGAT 13719
QY 721 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAG 780
DB 13720 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAG 13779
QY 781 GGGATCACCATCCGTCGGCGGCTGCAATAATATCATCTGTATCATCCACAAACAG 840
DB 13780 GGGATCACCATCCGTCGGCGGCTGCAATAATATCATCTGTATCATCCACAAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACCTTAAACCTTAAACCTTAAACCT 900
DB 13840 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACCTTAAACCTTAAACCTTAAACCT 13899
QY 901 TCTCGTACGAAAAGAGCGTTTCAATTAATAACCGGCGCACTCAGCCTATCCCTTCT 960
DB 13900 TCTCGTACGAAAAGAGCGTTTCAATTAATAACCGGCGCACTCAGCCTATCCCTTCT 13959
QY 961 GATTTTCGGCTTTCAGCGTTTCGGCAGCAGACGCGGCTTCAATTTGCAATGTTGTGC 1020
DB 13960 GATTTTCGGCTTTCAGCGTTTCGGCAGCAGACGCGGCTTCAATTTGCAATGTTGTGC 14019
QY 1021 TTACAGACCGGAGATATTGACATCATATATGCTTGGAGCAACTGATAGCTGTGCTGTC 1080
DB 14020 TTACAGACCGGAGATATTGACATCATATATGCTTGGAGCAACTGATAGCTGTGCTGTC 14079
QY 1081 AACTGTCACTGTATACGCTGCTTCAAGCACTCTTTTGTGACATACTTGGGTAGTG 1140
DB 14080 AACTGTCACTGTATACGCTGCTTCAAGCACTCTTTTGTGACATACTTGGGTAGTG 14139
QY 1141 CCGATCAACGCTCTCAATTTTTCGCAAAAGTTGGCCCGAGGCTTCCCGGTATCAACAGGGAC 1200
DB 14140 CCGATCAACGCTCTCAATTTTTCGCAAAAGTTGGCCCGAGGCTTCCCGGTATCAACAGGGAC 14199
QY 1201 ACCAGATTATTTATTTCTGCGAAGTGTATCTTCGCTCAAGGTAATTTATGCGGCCAAG 1260
DB 14200 ACCAGATTATTTATTTCTGCGAAGTGTATCTTCGCTCAAGGTAATTTATGCGGCCAAG 14259
QY 1261 TCGGTGCGGTGATGCTGCCAATCTAGTCACTTACAGGTCATTAATACCATCTAAGTAGTT 1320
DB 14260 TCGGTGCGGTGATGCTGCCAATCTAGTCACTTACAGGTCATTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTCTGATATGTTGTTTACAGTATTATGATGATGTTGTTTATGTCAT 1380

Db 15495 TGACGGAAGATCACTTCGACGAATAAATAATCTCGTGTCCCTGTGTGATACCGGAAGC 15554
Qy 2761 CCTGGGCCAATCTTTGGGGAATAAGACGCTGTGATCGGAATTCACAACTCTTATACCTTTT 2820
Db 15555 CCTGGGCCAATCTTTGGGGAATAAGACGCTGTGATCGGAATTCACAACTCTTATACCTTTT 15614
Qy 2821 CTCTTACAAAGTCGTTTCGGCTTCATCTGATTTTTCAGCCTCTATATCTTACTTAAACGCTGATA 2880
Db 15615 CTCTTACAAAGTCGTTTCGGCTTCATCTGATTTTTCAGCCTCTATATCTTACTTAAACGCTGATA 15674
Qy 2881 AAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTCGGCTGTGTATAGGAGACCTGTAC 2940
Db 15675 AAGTTTCTGTAATTTCTACTGTATCGACCTCGGCTGTGTATAGGAGACCTGTAC 15734
Qy 2941 ATTATATATCCCGAAGAACATCAGGTAAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTG 3000
Db 15735 ATTATATATCCCGAAGAACATCAGGTAAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTG 15794
Qy 3001 AGATCAGCCACTTCTTCCCGAATAACGGAGACCGGCACACTGGCCATATCGGTGTCTATC 3060
Db 15795 AGATCAGCCACTTCTTCCCGAATAACGGAGACCGGCACACTGGCCATATCGGTGTCTATC 15854
Qy 3061 ATGCGCCAGCTTTCATCCCGGATATGACACCGCGGTAAAGTTTCACGGGAGACTTTATCT 3120
Db 15855 ATGCGCCAGCTTTCATCCCGGATATGACACCGCGGTAAAGTTTCACGGGAGACTTTATCT 15914
Qy 3121 GACGACGACGTGCACTCGCCAGGGGATCAACATCCGTCGCGCGGGGTGTCAATAATA 3180
Db 15915 GACGACGACGTGCACTCGCCAGGGGATCAACATCCGTCGCGCGGGGTGTCAATAATA 15974
Qy 3181 TCACCTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTA 3240
Db 15975 TCACCTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTA 16034
Qy 3241 AACTGCAATTCACAGTCCCTGTTCTGTCAGCAAAAGACCGGTCATTTCAATTAACCG 3300
Db 16035 AACTGCAATTCACAGTCCCTGTTCTGTCAGCAAAAGACCGGTCATTTCAATTAACCG 16094
Qy 3301 GCGACCTCAGGCATCCCTTCCTGATTTTCGCTTCCAGCGTTCGGCAACGACGACG 3360
Db 16095 GCGACCTCAGGCATCCCTTCCTGATTTTCGCTTCCAGCGTTCGGCAACGACGACG 16154
Qy 3361 GCGCTTCATCTCGATGTTGCTTACAGACCGGAGATATTGAATCATATATATGCTTGT 3420
Db 16155 GCGCTTCATCTCGATGTTGCTTACAGACCGGAGATATTGAATCATATATATGCTTGT 16214
Qy 3421 AGCACTGATAGTGTGCTGTCACTGTAATACGCTGCTTCTATGACACACCTC 3480
Db 16215 AGCACTGATAGTGTGCTGTCACTGTAATACGCTGCTTCTATGACACACCTC 16274
Qy 3481 TTTTGTACATCTCTGTTTGTATGACAGATTTTTCAGGACTATGACACTAGCGTATA 3540
Db 16275 TTTTGTACATCTCTGTTTGTATGACAGATTTTTCAGGACTATGACACTAGCGTATA 16334
Qy 3541 TGAATAGGTAGATGTTTTTATTTGTACACAAAGAGGCTCGACCTCTTTTCTTA 3600
Db 16335 TGAATAGGTAGATGTTTTTATTTGTACACAAAGAGGCTCGACCTCTTTTCTTA 16394
Qy 3601 TTTCTTTTATGATTTAATACGGCATTTGAGGACAAATAGCGAGTAGGCTCGATACGACGAT 3660
Db 16395 TTTCTTTTATGATTTAATACGGCATTTGAGGACAAATAGCGAGTAGGCTCGATACGACGAT 16454
Qy 3661 TCGTTTGTAGAGAAACATTTGGAAGGCTGTGCGTTCGACTAAGTTGGCAGCATCACCGGAA 3720
Db 16455 TCGTTTGTAGAGAAACATTTGGAAGGCTGTGCGTTCGACTAAGTTGGCAGCATCACCGGAA 16514
Qy 3721 GAACATTTGGAAGGCTGTGCGTTCGACTACAGGTCACTTAATACCATTAAGTAGTAGTTC 3780
Db 16515 GAACATTTGGAAGGCTGTGCGTTCGACTACAGGTCACTTAATACCATTAAGTAGTAGTTC 16574
Qy 3781 ATAGTGACGTGATGTGTGTTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCT 3840

Db 16575 ATAGTGACGTGATGTGTGTTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCT 16634
Qy 3841 AATTTAATATATTGATATTTTATATCAATTTTACGTTTCTCGTTTACGCTTTTGTGACAAAC 3900
Db 16635 AATTTAATATATTGATATTTATATCAATTTTACGTTTCTCGTTTACGCTTTTGTGACAAAC 16694
Qy 3901 TTTGCTAGAGTCTGCTTTTAAATGAGATATCGAGAGCGCTTATGATCGCATGATATTGCT 3960
Db 16695 TTTGCTAGAGTCTGCTTTTAAATGAGATATCGAGAGCGCTTATGATCGCATGATATTGCT 16754
Qy 3961 TTTCAATTTCTGTTGTCAGCTTTTAAACAACTGAGCATGTGTAGCTCAGATCCTTACCGC 4020
Db 16755 TTTCAATTTCTGTTGTCAGCTTTTAAACAACTGAGCATGTGTAGCTCAGATCCTTACCGC 16814
Qy 4021 CCGTTTCCGTTCTCAATCTTAATGAATATATCACCCGTTTACTATCGTATTTTATGAATAATA 4080
Db 16815 CCGTTTCCGTTCTCAATCTTAATGAATATATCACCCGTTTACTATCGTATTTTATGAATAATA 16874
Qy 4081 TTTCTCCGTTCAATTTACTGATTTGTAACCTTACTTATGTAACAATATTAAATGAATAA 4140
Db 16875 TTTCTCCGTTCAATTTACTGATTTGTAACCTTACTTATGTAACAATATTAAATGAATAA 16934
Qy 4141 CAATATATTGCTGTGAATAGTTTATAGCGACATCTATGATAGCGCCACATATAACAA 4200
Db 16935 CAATATATTGCTGTGAATAGTTTATAGCGACATCTATGATAGCGCCACATATAACAA 16994
Qy 4201 CAATTTGCGTTTATTTATTACAAATTTTAAAAAAGCGGACAGAACCGGTCAAAACCT 4260
Db 16995 CAATTTGCGTTTATTTATTACAAATTTTAAAAAAGCGGACAGAACCGGTCAAAACCT 17054
Qy 4261 AAAAGACTGATTAATATAATCTTATTTCAAAATTTTAAAAAGCGGACAGAACCGGTCTAC 4320
Db 17055 AAAAGACTGATTAATATAATCTTATTTCAAAATTTTAAAAAGCGGACAGAACCGGTCTAC 17114
Qy 4321 GACACACGAGCGCGGAACTAAATAACTTCACTGAAGGAACTCCGCTTCCCGCCGCGCG 4380
Db 17115 GACACACGAGCGCGGAACTAAATAACTTCACTGAAGGAACTCCGCTTCCCGCCGCGCG 17174
Qy 4381 CGCATGGTGAGATTCCTTTGAAGTTGAGTATTTGGCCGTTCCGCTCTACCGAAAGTTACGGG 4440
Db 17175 CGCATGGTGAGATTCCTTTGAAGTTGAGTATTTGGCCGTTCCGCTCTACCGAAAGTTACGGG 17234
Qy 4441 CACCATTTCAACCCGTCAGACACCGCGCGGTTAAACCGACTTCTGCTCCCGGAGATTTAT 4500
Db 17235 CACCATTTCAACCCGTCAGACACCGCGCGGTTAAACCGACTTCTGCTCCCGGAGATTTAT 17294
Qy 4501 GCAGCATTTTTTGTGTATCTGCGGCCCAATGAAGTGCAGGTCAAACTTTGACAGTGA 4560
Db 17295 GCAGCATTTTTTGTGTATCTGCGGCCCAATGAAGTGCAGGTCAAACTTTGACAGTGA 17354
Qy 4561 CGCAAAATTCGTTGGCGGCTCCAGGGCGAATTTTTCGCAACAACTGTTCGAGGCTCAGCAGG 4620
Db 17355 CGCAAAATTCGTTGGCGGCTCCAGGGCGAATTTTTCGCAACAACTGTTCGAGGCTCAGCAGG 17414
Qy 4621 ACCTGACGCAATGAAGTACTAGTATCATATTTCTATAGTCTCAGCTTCACTTAAATCT 4680
Db 17415 ACCTGACGCAATGAAGTACTAGTATCATATTTCTATAGTCTCAGCTTCACTTAAATCT 17474
Qy 4681 GC 4682
Db 17475 GC 17476

RESULT 3

ABQ82142

ID ABQ82142 standard; DNA; 17458 BP.

XX ABQ82142;

AC ABQ82142;

XX 11-DEC-2002 (first entry)

XX

DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.

XX

QY 541 TCGACCTGCAGACTGGCTGTGTATATAAGGGAGCCTGACATTTATATTCGCCAGAACATCAG 600
DB 13540 TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCGCCAGAACATCAG 13599
QY 601 GTTAAATGGCGTTTGTGATGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGCAT 660
DB 13600 GTTAAATGGCGTTTGTGATGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGCAT 13659
QY 661 AACGGAGACCGGCACACTGGCCATATCGGTGCTCATCATGCGGCAGCTTTCATCCCGCAT 720
DB 13660 AACGGAGACCGGCACACTGGCCATATCGGTGCTCATCATGCGGCAGCTTTCATCCCGCAT 13719
QY 721 ATGCACACCGGGTAAAGTTTCA CGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 780
DB 13720 ATGCACACCGGGTAAAGTTTCA CGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 13779
QY 781 GGGGATCACCATTCGGTCCGCCGGGGGTGTCAATATATCATCTGTATCATCCACAAACAG 840
DB 13780 GGGGATCACCATTCGGTCCGCCGGGGGTGTCAATATATCATCTGTATCATCCACAAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTCACCAAGTCCCTGT 900
DB 13840 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTCACCAAGTCCCTGT 13899
QY 901 TCTCGTCAGCAAAAGAGCGCTTCAATTTCAATAAACCGGGGAGCCTCAGCCATCCCTTCCT 960
DB 13900 TCTCGTCAGCAAAAGAGCGCTTCAATTTCAATAAACCGGGGAGCCTCAGCCATCCCTTCCT 13959
QY 961 GATTTTCGGCTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCATTCGATGTTGTGTC 1020
DB 13960 GATTTTCGGCTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCATTCGATGTTGTGTC 14019
QY 1021 TTACAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTCCCTGTC 1080
DB 14020 TTACAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTCCCTGTC 14079
QY 1081 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 1140
DB 14080 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 14139
QY 1141 CGGATCAACGCTCAATTTTCGCCAAAGTTGGCCAGCGGCTTCCGGGTATCAACAGGGAC 1200
DB 14140 CGGATCAACGCTCAATTTTCGCCAAAGTTGGCCAGCGGCTTCCGGGTATCAACAGGGAC 14199
QY 1201 ACCAGGATTTATTTATCTCGGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAG 1260
DB 14200 ACCAGGATTTATTTATCTCGGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAG 14259
QY 1261 TCGCTCGGGTGATGCTGCCAATTAAGTCGATACAGGTCACTAATACCATCTAAGTAGTT 1320
DB 14260 TCGCTCGGGTGATGCTGCCAATTAAGTCGATACAGGTCACTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTCACTGGATATGTTGGTTTACAGTATTATGATGATGCTGTTTTTATGCAA 1380
DB 14320 GATTCATAGTCACTGGATATGTTGGTTTACAGTATTATGATGATGCTGTTTTTATGCAA 14379
QY 1381 AATCTAAATTAATATATTAATTTATATCAATTTTACGTTTCTCGTTCAGCTTCTCTGTA 1440
DB 14380 AATCTAAATTAATATATTAATTTATATCAATTTTACGTTTCTCGTTCAGCTTCTCTGTA 14439
QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTCGGTAAGGAATAATTTATTTCTTTTT 1500
DB 14440 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTCGGTAAGGAATAATTTATTTCTTTTT 14499
QY 1501 TCCCTTTAGTAAATAGTTAAGTCACTTAAGTATGATTAATAGTATGATTAATAATATAGTTGT 1560
DB 14500 TCCCTTTAGTAAATAGTTAAGTCACTTAAGTATGATTAATAGTATGATTAATAATATAGTTGT 14559
QY 1561 TATAATTTGAAAAAATAATTTTATAAATATATTTGTTTACATAAACACATAGTAATGTAA 1620
DB 14560 TATAATTTGAAAAAATAATTTTATAAATATATTTGTTTACATAAACACATAGTAATGTAA 14619

QY 1621 AAAAAATATGCAAGTGATGTGTAAGCAAGAGATATAAAAGTTGAGAGTAAAGTATATAT 1680
DB 14620 AAAAAATATGCAAGTGATGTGTAAGCAAGAGATATAAAAGTTGAGAGTAAAGTATATAT 14679
QY 1681 TTTTAAATGAAATTTGATCGACATGTAGATGATATCTAGCATTTAATATTTGTTTAAATC 1740
DB 14680 TTTTAAATGAAATTTGATCGAATCTGTAGATGATATCTAGCATTTAATATTTGTTTAAATC 14739
QY 1741 ATAATAGTAAATTTCTAGCTGCTTTGATGAATTAATATCAATATGATAAAATCTATAGTAAA 1800
DB 14740 ATAATAGTAAATTTCTAGCTGCTTTGATGAATTAATATCAATATGATAAAATCTATAGTAAA 14799
QY 1801 AATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1860
DB 14800 AATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 14859
QY 1861 AATATCTATACCATTTCTAATAATTTTATGTTTAAAGCTTAAATAATTTTGTGTAGAAAT 1920
DB 14860 AATATCTATACCATTTCTAATAATTTTATGTTTAAAGCTTAAATAATTTTGTGTAGAAAT 14919
QY 1921 TCCAACTGCTGTGTAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAGTAAACAAA 1980
DB 14920 TCCAACTGCTGTGTAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAGTAAACAAA 14979
QY 1981 TAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT 2040
DB 14980 TAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT 15039
QY 2041 AACAAAGCGAAGATCTATCATTTATATATAGTATTTTCAATCAACATCTTTATTAAT 2100
DB 15040 AACAAAGCGAAGATCTATCATTTATATAGTATTTTCAATCAACATCTTTATTAAT 15099
QY 2101 TTTCAATAATATCTGTGTAGTTTATTAACCTTCTAAATGGATGACTAATTAATAAGTAA 2160
DB 15100 TTTCAATAATATCTGTGTAGTTTATTAACCTTCTAAATGGATGACTAATTAATAAGTAA 15159
QY 2161 TTAGTCGAACATGAATAAACAAGGTAAACATGATGATGATCATCTGTTGTTTATCATTCAT 2220
DB 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATGATGATCATCTGTTGTTTATCATTCAT 15219
QY 2221 CTTACATTTGGATTTGATTACAGTTTGGGAAGCTGGGTTTCAAAATCGAATCGATGCTGTC 2280
DB 15220 CTTACATTTGGATTTGATTACAGTTTGGGAAGCTGGGTTTCAAAATCGAATCGAT 15266
QY 2281 AGTTATCATCATCATATAGACACACGAAATAAAGTAAATCAAGTATCAAGTTAAAGCTAT 2340
DB 15267 ----- 15266
QY 2341 GTAATATTTGGCCCATTAACCAATCAATTAATAAATAAGATCAGTTTAAAGAAAGATCAAG 2400
DB 15267 ----- 15266
QY 2401 CTCAAAAATAAAGAGAAAAAGGCTCTTAACCAAAAAATGAAGGAGAAAAAAGTAAAG 2460
DB 15267 ----- 15266
QY 2461 ATTTACCTGCAACAGCTTGGATCTCTAGACCACTTTGTGCAAGAAAGCTGAAACGAGAAA 2520
DB 15267 ----- 15266
QY 2521 CGTAAAAATGATATAAATAATCAATATTTAAATTTAGATTTTGCATAAAAAACAGACTACAT 2580
DB 15315 CGTAAAAATGATATAAATAATCAATATTTAAATTTAGATTTTGCATAAAAAACAGACTACAT 15374
QY 2581 AATCTGTAAAAACCAACATATCCAGTCACATGAATCAACTACTCTAGATGCTATAGTGT 2640
DB 15375 AATCTGTAAAAACCAACATATCCAGTCACATGAATCAACTACTCTAGATGCTATAGTGT 15434
QY 2641 ACCTGTAGTCCAGTAAAGTTGGCAGATCACCCGACGCACTTTTGGCCGGAATAAATACCTG 2700
DB 15435 ACCTGTAGTCCAGTAAAGTTGGCAGATCACCCGACGCACTTTTGGCCGGAATAAATACCTG 15494
QY 2701 TGACGGAAAGATCACTTCGCAAGATAAATAAATCTCGTGTCCCTGTTGATACCGGGAAGC 2760

QY 4081 TTCTCCGTTCAATTTACTGATTGACCCCTACTATTATGTACAAATTAATAATGAAAA 4140
Db 17080 TTCTCCGTTCAATTTACTGATTGACCCCTACTATTATGTACAAATTAATAATGAAAA 17139
QY 4141 CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAAACAAA 4200
Db 17140 CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAAACAAA 17199
QY 4201 CAATGCGTTTATTTATTTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACT 4260
Db 17200 CAATGCGTTTATTTATTTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACT 17259
QY 4261 AAAAGACTGATTACATAAATCTTATTTCAAAATTTCAAAAGGCGCCAGGGGCTAGTATCTAC 4320
Db 17260 AAAAGACTGATTACATAAATCTTATTTCAAAATTTCAAAAGGCGCCAGGGGCTAGTATCTAC 17319
QY 4321 GACACACCGAGCGGGAACCTAATAACGTTCACTGAGGGAACCTCGGTTCCCGCGCGG 4380
Db 17320 GACACACCGAGCGGGAACCTAATAACGTTCACTGAGGGAACCTCGGTTCCCGCGCGG 17379
QY 4381 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACCGG 4440
Db 17380 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACCGG 17439
QY 4441 CACCAATTCAACCCGTCAGACACGCGCGCGGTTAACCGACTTGTCTGCCCGAGAAATTAT 4500
Db 17440 CACCAATTCAACCCGTCAGACACGCGCGCGGTTAACCGACTTGTCTGCCCGAGAAATTAT 17499
QY 4501 GCAGCATTTTGTGTGATGTGGCCCGCCCAATGAGTGCAGGTCAAACTTGCAGGTGA 4560
Db 17500 GCAGCATTTTGTGTGATGTGGCCCGCCCAATGAGTGCAGGTCAAACTTGCAGGTGA 17559
QY 4561 CGACAAATCGTTGGCGGGTCCAGCGCGGAATTTTGGCAAACTGTCGAGGCTCAGCAGG 4620
Db 17560 CGACAAATCGTTGGCGGGTCCAGCGCGGAATTTTGGCAAACTGTCGAGGCTCAGCAGG 17619
QY 4621 ACCTGAGGATGCAAGCTAGCTTACTAGTATGCAATTTCTATAGTGTCACTAAATCT 4680
Db 17620 ACCTGAGGATGCAAGCTAGCTTACTAGTATGCAATTTCTATAGTGTCACTAAATCT 17679
QY 4681 GC 4682
Db 17680 GC 17681

RESULT 2
ID ABQ82141 standard; DNA; 17476 BP.
XX AC ABQ82141;
XX XX
XX XX
XX 11-DEC-2002 (first entry)
XX DE Acceptor vector PHELLSGATE 8 nucleotide sequence SEQ ID NO:24.
XX XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KW recombination site; double stranded RNA; plant; ds.
XX OS Synthetic.
XX XX WO200259294-A1.
XX PN 01-AUG-2002.
XX PD
XX XX 24-JAN-2002; 2002WO-AU0000073.
XX PF
XX XX 26-JAN-2001; 2001US-0264067P.
XX PR 29-NOV-2001; 2001US-0333743P.
XX XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA Wesley S, Waterhouse P, Helliwell C;
XX PI
XX XX

DR MPI; 2002-682669/73.
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX Claim 15; Page 74-83; 104pp; English.
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention.
XX SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
Query Match 91.0%; Score 4262; DB 6; Length 17476;
Best Local Similarity 95.6%; Pred. No. 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3193.6	68.3	18691	6	ABQ82130	Abq82130 Acceptor
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6	1108.8	23.7	4470	7	ABQ55521	Abq55521 Donor pla
7	1108.8	23.7	4470	7	ABZ58767	Abz58767 Destinati
8	1108.8	23.7	4892	8	ADA50329	Ada50329 Plasmid v
9	1108.8	23.7	4939	3	AAC55525	Aac55525 Donor pla
10	1108.8	23.7	5584	3	AAC55632	Aac55632 Donor pla
11	1108.8	23.7	5584	7	ABZ58766	Abz58766 Donor pla
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13	1102.4	23.5	4627	7	ABZ58769	Abz58769 Destinati
14	1102.4	23.5	4627	7	ABZ58770	Abz58770 Destinati
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18	947.8	20.2	4208	3	AAC55523	Aac55523 Donor pla
19	827	17.7	4204	3	AAC55522	Aac55522 Donor pla
20	823.8	17.6	5156	3	AAC55526	Aac55526 Donor pla
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22	780	16.7	786	9	ADD44386	Add44386 Flaveria
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38	597	12.8	5957	3	AAC55467	Aac55467 Destinati
39	597	12.8	5957	3	AAC55464	Aac55464 Destinati
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41	597	12.8	6264	3	AAC55507	Aac55507 Destinati
42	597	12.8	6354	3	AAC55491	Aac55491 Destinati
43	597	12.8	6422	3	AAC55483	Aac55483 Destinati
44	597	12.8	6464	3	AAC55454	Aac55454 Destinati
45	597	12.8	6526	3	AAC55471	Aac55471 Destinati

ALIGNMENTS

RESULT 1
ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector PHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
FN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
(CSIR) COMMONWEALTH SCI & IND RES ORG.
Wesley S, Waterhouse P, Helliwell C;
WPI; 2002-682669/73.
New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
Claim 17; Page 93-102; 104pp; English.

The present invention describes a vector (i) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

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Db      ||||||| 4412 CTGACGGAATTC 4423
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AUTHORS Kardailsky, I. and Weigel, D.
 TITLE Direct Submission
 JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
 Institute for Biological Studies, 10010 N. Torrey Pines Road, La
 Jolla, CA 92037, USA

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 AUTHORS
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Qy	1605	CAACATAGTAATGTAAAAAATAATGACACAGTGATGTGTAAAGACGAAGAGATAAAGATTG	1664
Db	4604	CAACATAGTAATGTAAAAAATAATGACACAGTGATGTGTAAAGACGAAGAGATAAAGATTG	4663
Qy	1665	AGAGTAAGTATATATTTTAAATGAATTTGATCGAACATCTGAAGATGATATCTAGCATTT	1724
Db	4664	AGAGTAAGTATATATTTTAAATGAATTTGATCGAACATCTGAAGATGATATCTAGCATTT	4723
Qy	1725	AATATTGTTTTTAAATCATATAGTAATTTCTAGCTGGTTTGATGAAATTAATATCAATGAT	1784
Db	4724	AATATTGTTTTTAAATCATATAGTAATTTCTAGCTGGTTTGATGAAATTAATATCAATGAT	4783
Qy	1785	AAATACTACTAGTAATAAATAAGAAATAAATAAATTTAAATAAATATTTTTTATCATTAATA	1844
Db	4784	AAATACTACTAGTAATAAATAAGAAATAAATAAATTTAAATAAATATTTTTTATCATTAATA	4843
Qy	1845	GTTTATTATATAATTTAAATATCTATACCATTTACTAAATATTTTTAGTTTAAAAAGTTAATAA	1904
Db	4844	GTTTATTATATAATTTAAATATCTATACCATTTACTAAATATTTTTAGTTTAAAAAGTTAATAA	4903
Qy	1905	ATATTTTGTAGAAATTTCCAAATCTGCTTGTGAATTTTATCAATTAACAAAAATTTAAATTAAC	1964
Db	4904	ATATTTTGTAGAAATTTCCAAATCTGCTTGTGAATTTTATCAATTAACAAAAATTTAAATTAAC	4963
Qy	1965	AAGCTAAAGTAACAAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAAACAT	2024
Db	4964	AAGCTAAAGTAACAAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAAACAT	5023
Qy	2025	AATCTAATGCTAATATATAACAAAGCGGAAGATCTATCAATTTTATATAGTATTTATTTTCAAT	2084
Db	5024	AATCTAATGCTAATATATAACAAAGCGGAAGATCTATCAATTTTATATAGTATTTATTTTCAAT	5083
Qy	2085	CAACATTTCTTAAATTTCTAAATAATACTTTGTAAGTTTATTTAATCTTCTAAATGGATTGA	2144
Db	5084	CAACATTTCTTAAATTTCTAAATAATACTTTGTAAGTTTATTTAATCTTCTAAATGGATTGA	5143
Qy	2145	CTATTAATTTAAATGAATTTAGTCGAACATGAATTAACAAAGTAAACATGATAGATCATGTCGA	2204
Db	5144	CTATTAATTTAAATGAATTTAGTCGAACATGAATTAACAAAGTAAACATGATAGATCATGTCGA	5203
Qy	2205	TTGTGTTATCATTTGATCTTACATTTGATTCAGATTCAGATTTGGGAAGCTGGTTCGAATTC	2264
Db	5204	TTGTGTTATCATTTGATCTTACATTTGATTCAGATTCAGATTTGGGAAGCTGGTTCGAATTC	5263
Qy	2265	GATAAGCTTG 2274	
Db	5264	GATAAGCTTG 5273	
RESULT 11			
BD194641			
LOCUS	BD194641	786 bp	DNA linear
DEFINITION	Method and means of obtaining improved phenotype.		
ACCESSION	BD194641		
VERSION	BD194641.1	GI:33004386	
KEYWORDS	JP 2002511258-A/7.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 786)		
AUTHORS	Waterhouse, P.M., Wang, M.B. and Graham, M.W.		
TITLE	Method and means of obtaining improved phenotype		
JOURNAL	PATENT: JP 2002511258-A 7 16-APR-2002;		
COMMENT	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION		
	PN	JP 2002511258-A/7	
	PD	16-APR-2002	
	PF	07-APR-1999	JP 2000543598
	PR	08-APR-1998	US 09/056767, 03-AUG-1998
	PETER MICHAEL WATERHOUSE, MIN BO WANG, MICHAEL WAIN GRAHAM PC		
	C12N15/09, A01H5/00, C12N5/10, C12N5/00, C12N5/00 CC Description of		

4245	Db	TAATTAATTTCTTTTTCCTTTTAGTATATAAATAGTTAAAGTGAATTAATAGTATGATT	4303
1545	QY	ATAATAATAATAGTGTGTTTAATAATGTGGAATAATAATTTATAATAATATTTGTGTACATAAA	1504
4305	Db	ATAATAATAATAGTGTGTTTAATAATGTGGAATAATAATTTATAATAATATTTGTGTACATAAA	4364
1605	QY	CAACATAGTAATGTAAAAAATAATGACAAAGTGAATGTGAAGACGAAGAGATAAAAAGTTG	1664
4365	Db	CAACATAGTAATGTAAAAAATAATGACAAAGTGAATGTGAAGACGAAGAGATAAAAAGTTG	4424
1665	QY	AGAGTAAGTATATTAATTTTAATGAAATTTGATCGAACAATGTAAGATGATATATCTAGCAATT	1724
4425	Db	AGAGTAAGTATATTAATTTTAATGAAATTTGATCGAACAATGTAAGATGATATATCTAGCAATT	4484
1725	QY	AATATTTGTTTTTAATCAATATAGTAATTTCTAGCTGGTTTGTAGCAATTAATAATCAATGAT	1784
4485	Db	AATATTTGTTTTTAATCAATATAGTAATTTCTAGCTGGTTTGTAGCAATTAATAATCAATGAT	4544
1785	QY	AAAACTACTAGTAAAAAATAAGAAATAAAATAAAATAAAATAATTTTTTTATGATTAAATA	1844
4545	Db	AAAACTACTAGTAAAAAATAAGAAATAAAATAAAATAAAATAATTTTTTTATGATTAAATA	4604
1845	QY	GTTTATATATAATTAATAATATCTATPACCAATCTACTAAATATTTTAGTTTAAAAAGTTAATAA	1904
4605	Db	GTTTATATATAATTAATAATATCTATPACCAATCTACTAAATATTTTAGTTTAAAAAGTTAATAA	4664
1905	QY	ATATTTTGTGTAGAAATTCCAAATCTGCTGTGTAATTTATCAATAAAACAAAAATTTAAATAAAC	1964
4665	Db	ATATTTTGTGTAGAAATTCCAAATCTGCTGTGTAATTTATCAATAAAACAAAAATTTAAATAAAC	4724
1965	QY	AGCTAAAGTAACAAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACAT	2024
4725	Db	AGCTAAAGTAACAAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACAT	4784
2025	QY	AATCTAATGCTAATATACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAAT	2084
4785	Db	AATCTAATGCTAATATACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAAT	4844
2085	QY	CAACATTTCTATTAAATTTCTAAATAATCTGTGTAGTTTATTAACTCTTAAATGGATTGA	2144
4845	Db	CAACATTTCTATTAAATTTCTAAATAATCTGTGTAGTTTATTAACTCTTAAATGGATTGA	4904
2145	QY	CTATTAAATTAATGAATTAAGTCGAACATGAATAAACAAGGTACATGATAGATCATGTCA	2204
4905	Db	CTATTAAATTAATGAATTAAGTCGAACATGAATAAACAAGGTACATGATAGATCATGTCA	4964
2205	QY	TTGTGTTATCAATTGATCTTACATTTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATC	2264
4965	Db	TTGTGTTATCAATTGATCTTACATTTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATC	5024
2265	QY	GATAAGCTTG 2274	
5025	Db	GATAAGCTTG 5034	
RESULT 10			
CVE311873			
LOCUS		5063 bp	DNA
DEFINITION			circular SYN 09-JUL-2002
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			

3844	Db	GGCACA	CTGCCATATCGGTGTCATCATCGCGCAGCTTTCATCCCGATATCACACC	3788
731	QY	GGTAAAGTTCA	CGGAGACTTTATCTGACAGCAGACGTGCATCGCCAGGGGGATCAC	790
3784	Db	GGTAAAGTTCA	CGGAGACTTTATCTGACAGCAGACGTGCATCGCCAGGGGGATCAC	3725
791	QY	ATCCGTCGCGCGCGCTGTC	CAATAATATCACTCTGTACATCCCAACACGACATACCG	850
3724	Db	ATCCGTCGCGCGCGCGCTGTC	CAATAATATCACTCTGTACATCCCAACACGACATACCG	3665
851	QY	CTCTCTCTTTTATAGGTG	TAAACCTTAACTGCATTTACCACTGCCCTGTTCTCGTCAGC	910
3664	Db	CTCTCTCTTTTATAGGTG	TAAACCTTAACTGCATTTACCACTGCCCTGTTCTCGTCAGC	3605
911	QY	AAAAGAGCGCTTCATTTCA	TAAACCGGGGCACTCAGCCATCCCTTCCTGATTTTCCGC	970
3604	Db	AAAAGAGCGCTTCATTTCA	TAAACCGGGGCACTCAGCCATCCCTTCCTGATTTTCCGC	3545
971	QY	TTTCCAGCGTTCCGACG	ACGACGAGCGGCTTCATTCTGCATGTTGTGCTTACCAAGACC	1030
3544	Db	TTTCCAGCGTTCCGACG	ACGACGAGCGGCTTCATTCTGCATGTTGTGCTTACCAAGACC	3485
1031	QY	GGAGATATTGACATCATAT	TATGCTTGAGCAACTGATAGCTGTCGTGCTCAACTGTCCT	1090
3484	Db	GGAGATATTGACATCATAT	TATGCTTGAGCAACTGATAGCTGTCGTGCTCAACTGTCCT	3425
1091	QY	GTAAATCGCTGCTTCATAG	CACACCTCTTTTTCACATACCTTCGGGTA	1137
3424	Db	GTAAATCGCTGCTTCATAG	CACACCTCTTTTTCACATACCTTCGGGTA	3378
RESULT 8				
BD263382/c				
LOCUS	5156 bp DNA linear PAT 17-JUL-2003			
DEFINITION	Compositions and methods for use in recombinational cloning of nucleic acids.			
ACCESSION	BD263382			
VERSION	BD263382.1 GI:33073150			
KEYWORDS	JP 2002537790-A/160.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1 (bases 1 to 5156).			
AUTHORS	Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.			
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids			
JOURNAL	Patent: JP 2002537790-A 160 12-NOV-2002;			
COMMENT	INVITROGEN CORP			
OS	Artificial Sequence			
PN	JP 2002537790-A/160			
PD	12-NOV-2002			
PR	02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR			
PI	JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC			
	C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/00			
CC	pDONR206			
CC	May be any nucleotide			
CC	May be any nucleotide			
FH	Key			
FT	misc feature (1102) . (1102)			
FT	misc-feature (3080) . (3080) .			
FEATURES	Location/Qualifiers			
source	1..5156			
	/organism="synthetic construct"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:32630"			
ORIGIN				
Query Match	17.6%; Score 823.8; DB 6; Length 5156;			
Best Local Similarity	99.8%; Pred. No. 4.2e-109;			
Matches 825; Conservative	0; Mismatches 2; Indels 0; Gaps 0;			

QY	3206	GATAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCATTTTACCAAGTCCCTGTTC	3263
DB	2904	GATAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCATTTTACCAAGTCCCTGTTC	2963
QY	3266	TGCTCAGCAAAAGAGCGGTTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTCTGA	3325
DB	2964	TGCTCAGCAAAAGAGCGGTTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTCTGA	3023
QY	3326	TTTTTCGGCTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCATCTGCATGGTTGCTT	3385
DB	3024	TTTTTCGGCTTTCAGCGTTTCGGCAGCAGACGAGCGGCTTCATCTGCATGGTTGCTT	3083
QY	3386	ACCAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTCGCTGTCAA	3445
DB	3084	ACCAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTCGCTGTCAA	3143
QY	3446	CTGTCACTGTAATACGCTGCTTCATGACACACCTCTTTTGTGACATCTTCTGTTCTTGTAT	3505
DB	3144	CTGTCACTGTAATACGCTGCTTCATGACACACCTCTTTTGTGACATCTTCTGTTCTTGTAT	3203
RESULT 6			
BD263379			
LOCUS			
DEFINITION			
BD263379 4208 bp DNA linear PAT 17-JUL-2003			
Compositions and methods for use in recombinational cloning of nucleic acids.			
ACCESSION			
BD263379			
VERSION			
BD263379.1 GI:33073147			
KEYWORDS			
JP 2002537790-A/157.			
SOURCE			
ORGANISM			
synthetic construct			
artificial sequences.			
REFERENCE			
1 (bases 1 to 4208)			
Hartley,J.L., Bransch,M.A., Temple,G.F. and Cheo,D.			
AUTHORS			
TITLE			
Compositions and methods for use in recombinational cloning of nucleic acids			
JOURNAL			
Patent: JP 2002537790-A 157 12-NOV-2002;			
COMMENT			
INVITROGEN CORP			
OS			
Artificial Sequence			
PN			
JP 2002537790-A/157			
PD			
12-NOV-2002			
PF			
02-MAR-2000 JP 2000602252			
PR			
02-MAR-1999 US 60/123389, 23-MAR-1999 US 60/126049			
PM			
28-MAY-1999 US 60/136744			
PI			
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO			
PC			
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N5/10, C12N15/00, C12N5/00			
CC			
pDONR203			
CC			
inactivated ccdA			
CC			
Cmr			
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CC			
ccdB			
FH			
Key			
Location/Qualifiers			
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gene			
(251)..(910)			
FT</			

Qy	986	ACCGAGACGACGGGCTTCATCTTCGATGAGTGTGCTTACAGACCGGAGATATTGACATC	1045
Db	4596	ACCGAGACGACGGGCTTCATCTTCGATGAGTGTGCTTACAGACCGGAGATATTGACATC	4655
Qy	1046	ATATATGCCCTTTGAGCAACTGATAGCTGTGCGCTGTCAACTGTCACTGTAAATAGAGCTGCTTC	1105
Db	4656	ATATATGCCCTTTGAGCAACTGATAGCTGTGCGCTGTCAACTGTCACTGTAAATAGAGCTGCTTC	4715
Qy	1106	ATAGACACACTCTTTTGTGACATATCTGGGTA	1137
Db	4716	ATAGACACACTCTTTTGTGACATATCTGGGTA	4747
RESULT 4			
BD263402/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<p>BD263402 5584 bp DNA linear PAT 17-JUL-2003</p> <p>Compositions and methods for use in recombinational cloning of nucleic acids.</p> <p>BD263402</p> <p>BD263402.1 GI:33073170</p> <p>JP 2002537790-A/180.</p> <p>synthetic construct</p> <p>artificial sequences.</p> <p>1 (bases 1 to 5584)</p> <p>Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.</p> <p>Compositions and methods for use in recombinational cloning of nucleic acids</p> <p>Patent: JP 2002537790-A 180 12-NOV-2002;</p> <p>INVITROGEN CORP</p> <p>OS Artificial Sequence</p> <p>PN JP 2002537790-A/180</p> <p>PD 12-NOV-2002</p> <p>PF 02-MAR-2000 JP 2000602252</p> <p>PR 02-MAR-1999 US 60/123389,23-MAR-1999 US 60/126049 PR</p> <p>PI 28-MAY-1999 US 60/136744</p> <p>CI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC</p> <p>C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N5/10,C12N15/ PC</p> <p>00,C12N5/00</p> <p>CC pDONR207</p> <p>PH Key</p> <p>FT source</p> <p>FT Location/Qualifiers</p> <p>FT 1..5584</p> <p>Location/Qualifiers</p> <p>/organism="Artificial Sequence".</p>			
FEATURES			
source			
ORIGIN			
Query Match 23.7%; Score 1108.8; DB 6; Length 5584;			
Best Local Similarity 99.8%; Pred. No. 4.4e-150;			
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	26	GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAATATGATATAATCAATATATT	85
Db	5483	GCCAACTTTGTACAAAAAAGCTGACGAGAAACGTAAATATGATATAATCAATATATT	5424
Qy	86	AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTC	145
Db	5423	AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTC	5364
Qy	146	ACTATGATCAACTACTAGTATGATATAGTACCTGTAGTCGACGACGAGCCTTCCAAA	205
Db	5363	ACTATGATCAACTACTAGTATGATATAGTACCTGTAGTCGACGACGAGCCTTCCAAA	5304
Qy	206	TGTTCTTCGGGTGATGTGCGCAACTTAGTGCACCGACAGCCTTCCAAATGTTCTTCAA	265
Db	5303	TGTTCTTCGGGTGATGTGCGCAACTTAGTGCACCGACAGCCTTCCAAATGTTCTTCAA	5244
Qy	266	ACGGAATCGTCGATTCAGCGCTACTCGCTATGTGTCCTCAATGCGGTATTAATCATATAA	325
Db	5243	ACGGAATCGTCGATTCAGCGCTACTCGCTATGTGTCCTCAATGCGGTATTAATCATATAA	5184

566 AGGAGGCTGACATTTATATCCCGAAGACATCAGGTTAATGGGTTTTTGATGTCAATTT 625
642 AGGAGGCTGACATTTATATCCCGAAGACATCAGGTTAATGGGTTTTTGATGTCAATTT 701
626 TCGCGGTGGCTGAGATCAGCACATTTCTCCCGATTAACGAGACCGGCACACTGGGCATA 685
702 TCGCGGTGGCTGAGATCAGCACATTTCTCCCGATTAACGAGACCGGCACACTGGGCATA 761
686 TCGGTGCTCATCATCGCGCAGCTTTCTCCCGATTAACGAGACCGGCACACTGGGCATA 745
762 TCGGTGCTCATCATCGCGCAGCTTTCTCCCGATTAACGAGACCGGCACACTGGGCATA 821
746 GAGACTTTATCTGACAGCAGACGTCGACATCGCGCAGGCGGATCAACATCCGTCCGCCGGGC 805
822 GAGACTTTATCTGACAGCAGACGTCGACATCGCGCAGGCGGATCAACATCCGTCCGCCGGGC 881
806 GTGTCAATAATATCACTCTGACATTCACCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 865
882 GTGTCAATAATATCACTCTGACATTCACCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 941
866 GTGTAAACCTTAACTGATTTCAACAGTCCCTGCTCTCGTCAGCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 925
942 GTGTAAACCTTAACTGATTTCAACAGTCCCTGCTCTCGTCAGCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 1001
926 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCGATTTTTCGCTTTCCAGCGTTCCGGC 985
1002 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCGATTTTTCGCTTTCCAGCGTTCCGGC 1061
986 ACGCAGACGCGGCTTCACTTCGATGTTGCTGTTACACGAGCGGAGATTAACGAGACCGGCACACTGGGCATA 1045
1062 ACGCAGACGCGGCTTCACTTCGATGTTGCTGTTACACGAGCGGAGATTAACGAGACCGGCACACTGGGCATA 1121
1046 ATATATGCTTTGAGCACTGATAGCTGCTGCTGCTCAACTGTCATCTGTAATAACGCTGCTTC 1105
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1106 ATAGCACACCTTTTGGACATCTTCGGGTA 1137
1182 ATAGCACACCTTTTGGACATCTTCGGGTA 1213

RESULT 3
BD263381
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PN
PD
PR
PI
CC
PH
FT
FT

BD263381
4939 bp
DNA
linear
PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of nucleic acids.
BD263381
BD263381.1 GI:33073149
JP 2002537790-A/159.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 4939)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of nucleic acids
Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP
OS
PN
PD
PR
PI
CC
PH
FT
FT

Artificial Sequence
JP 2002537790-A/159
12-NOV-2002
02-MAR-2000 JP 200602252
02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N15/00, C12N5/00
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Key
source
Location/Qualifiers
Location/Qualifiers
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Artificial Sequence

/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN

Query Match 23.7%; Score 1108.8; DB 6; Length 4939;
Best Local Similarity 99.8%; Pred. No. 4.5e-150;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAAGCTAAATATGATATAATATCAATATATT 85
DB 3636 GCCAACTTTGTACAAAAAGCTGAACGAGAAAGCTAAATATGATATAATATCAATATATT 3695
QY 86 AAATTAGATTTTGCATAAAAAAAGAGCTAATAATATGATATAATATCAATATATT 145
DB 3696 AAATTAGATTTTGCATAAAAAAAGAGCTAATAATATGATATAATATCAATATATT 3755
QY 146 ACTATCAATCACTACTAGATGTTATAGTACCTGTAGTCAGCCGACAGCCTTCCAAA 205
DB 3756 ACTATGAATCAACTACTAGATGTTATAGTACCTGTAGTCAGCCGACAGCCTTCCAAA 3815
QY 206 TGTTCCTCGGGTGCATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 265
DB 3816 TGTTCCTCGGGTGCATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA 3875
QY 266 ACGGAATCGTCGATCCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAATATCAATAAAA 325
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QY 326 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATATAAAACATCTACCT 385
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QY 386 ATTCAATACGCTAGTGTCTAGTCCCTGAAATATCATCTGCATCAAGAACAAATTTCAACAC 445
DB 3996 ATTCAATACGCTAGTGTCTAGTCCCTGAAATATCATCTGCATCAAGAACAAATTTCAACAC 4055
QY 446 TCTTATACCTTTCTTCAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 505
DB 4056 TCTTATACCTTTCTTCAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 4115
QY 506 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGATCGACTGACACTGGCTGTGATA 565
DB 4116 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGATCGACTGACACTGGCTGTGATA 4175
QY 566 AGGAGCCTGACATTTATTTCCCGAAGACATCAAGTTAATGGGTTTTTGATGTCAATTT 625
DB 4176 AGGAGCCTGACATTTATTTCCCGAAGACATCAAGTTAATGGGTTTTTGATGTCAATTT 4235
QY 626 TCGCGGTGGCTGAGATCAGCACATTTCTCCCGATTAACGAGACCGGCACACTGGGCATA 685
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QY 686 TCGGTGCTCATCATCGCGCAGCTTTCTATCCCGATGATGACACCGGCTAAAGTTTCACGG 745
DB 4296 TCGGTGCTCATCATCGCGCAGCTTTCTATCCCGATGATGACACCGGCTAAAGTTTCACGG 4355
QY 746 GAGACTTTATCTGACAGCAGACGTCGACATGGCGAGGCGATCACCATCCGTCCGCCGGGC 805
DB 4356 GAGACTTTATCTGACAGCAGACGTCGACATGGCGAGGCGATCACCATCCGTCCGCCGGGC 4415
QY 806 GTGTCAATAATATCACTCTGATACCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 865
DB 4416 GTGTCAATAATATCACTCTGATACCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 4475
QY 866 GTGTAAACCTTAACTGATTTCAACAGTCCCTGCTCTCGTCAGCAAAAGAGATTAACGAGACCGGCACACTGGGCATA 925
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DB 4536 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCGATTTTTCGCTTTCCAGCGTTCCGGC 4595

15760 ATAGTAATCTAGCTGTTTGATGAATTAAATATCAATGATATAAAATACATATAGTAAAAAT 15819 Db
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15820 AAGAATAAAATAAAATAAATATTTTATGATTAATAGTTATATATATATATATATATATAT 15879 Db
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15880 ATCTATACCAATCTAATAATATTTAGTTTAAAGTTAAATATATATATATATATATATATAT 15939 Db
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Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
J. 27 (6), 581-590 (2001)
MEDLINE
21461301
PUBMED
11576441
REFERENCE
2 (bases 1 to 18691)
Waterhouse, P.M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL
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ORIGIN

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Db 13121 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAATATCAATATATT 13180
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11650.2 Seconds
(without alignments)
17418.703 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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6	947.8	20.2	4208	6	BD263379
7	827	17.7	4204	6	BD263378
8	823.8	17.6	5156	6	BD263382
9	810.8	17.3	5824	12	CVE3111872
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14	735	15.7	10138	12	AF187951
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16	728.8	15.6	7566	6	AR074388
17	728.8	15.6	7639	6	A24782
18	728.8	15.6	7639	6	AR074387
19	722.8	15.4	11405	12	AY310901
20	719.4	15.4	22574	12	CVE18556
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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gene; promoter; spec gene; spectinomycin resistance protein;
transposon Tn7.
Cloning vector pHELLSGATE
Cloning vector pHELLSGATE
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Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,

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Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopol@med.nyu.edu
No Blast Hits ().

FEATURES
source
1. 1037
/organism="Plasmodium yoelii yoelii"
/mol_type="mrna"
/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.OTOP; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exoerythrocytic malaria parasites does not require host
cells' (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN
Query Match 6.1%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 5.4e-38;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 571 GCGTACATTTATATCCCGAGACATCAGGTTAATAGCGTTTGTGATGTCATTTTCGG 630
Db 496 GCGTACATTTATATCCCGAGACATCAGGTTAANGGGGTTTGTGATGTCATTTTCGG 437
QY 631 GTGGCTGAGATCAGCCACTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 690
Db 436 GTGGCTGAGATCAGCCACTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 377
QY 691 GGTATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTCACGGAGAC 750
Db 376 GGTATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTCACGGAGAC 317
QY 751 TTTATCTGACAGCAGCGTGCACCTGCGGAGGATGACATCCGTCGCGCGCGGTGTC 810
Db 316 TTTATCTGACAGCAGCGTGCACCTGCGGAGGATGACATCCGTCGCGCGCGGTGTC 257
QY 811 AATAATATCATCTGTACATCCCAACAG--ACGATAAGGCTCTCTTTTATAGGTG 868
Db 256 AATAAGATCACTGTACATCCCAACAG--ACGATAAGGCTCTCTTTTATAGGTG 197
QY 869 TAAACCTTAAACTGCATTTC 888
Db 196 AAACCTTNNACNCCGNTTC 177

RESULT 15
AG000791
LOCUS
DEFINITION
Homo sapiens genomic DNA, 724 bp DNA linear GSS 06-FEB-1999
survey sequence.
ACCESSION
AG000791
VERSION
AG000791.1 GI:2579599
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 724)

AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 724)
AUTHORS
TITLE
JOURNAL

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1997)
Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
Direct Submission
Submitted (31-Oct-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@ngc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
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ORIGIN

Query Match 5.9%; Score 264.4; DB 29; Length 724;
Best Local Similarity 98.6%; Pred. No. 1.2e-36;
Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 847 ACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACCACTCCCTGTTCTCG 905
Db 27 ACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACCACTCCCTGTTCTCG 86
QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATT 965
Db 87 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATT 146
QY 966 TCCGCTTTCAGCGTTCCGACGAGAGCGGCTTCATTCGATGTTGCTTACC 1025
Db 147 TCCGCTTTCAGCGTTCCGACGAGAGCGGCTTCATTCGATGTTGCTTACC 206
QY 1026 AGACGGAGATTTGACATCATATATGCTTGGCACTGATGCTGCTGCTCACTG 1085
Db 207 AGACGGAGATTTGACATC--ATATGCTTGGCACTGATGCTGCTGCTCACTG 264
QY 1086 TCACGTGTAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTCGGGTA 1137
Db 265 TCACGTGTAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTCGGGTA 316

Search completed: May 9, 2004, 21:55:53
Job time : 6918.79 secs

COMMENT

Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source
Location/Qualifiers
1..337
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="jmi8n08"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

ORIGIN

Query Match 6.8%; Score 301.4; DB 12; Length 337;
Best Local Similarity 99.4%; Pred. No. 4.8e-43;
Matches 313; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 546 CTGCAGCTGGCTGTATAGGAGAGCTGACATTTATATCCCGAGACATCAGGTAA 605
DB 24 CTGCAGCTGGCTGTATAGGAGAGCTGACATTTATATCCCGAGACATCAGGTAA 83
QY 606 TGGCGTTTGTATGATCATTTTCGGCGTGTGATGATCAGCCACTTCTTCCCGATAACGG 665
DB 84 TGGC-TTTTGTGATGCAATTTTCGGGTGTGATGATCAGCCACTTCTTCCCGATAACGG 142
QY 666 AGACCGGCACACTGGCCATATCGGTGGTATCATGCGCAGCTTTATCCTCCCGATATGCA 725
DB 143 AGACCGGCACACTGGCCATATCGGTGGTATCATGCGCAGCTTTATCCTCCCGATATGCA 202
QY 726 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGAGAGTGCACCTGGCCAGGGGA 785
DB 203 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGAGAGTGCACCTGGCCAGGGGA 262
QY 786 TCACCATCCGTGCGCGCGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT 845
DB 263 TCACCATCCGTGCGCGCGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT 322
QY 846 AACGGCTCTCTTT 860
DB 323 AACGGCTCTCTTT 337

RESULT 13

CF469981/c 1068 bp mRNA linear EST 05-SEP-2003
LOCUS P7-E11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium
DEFINITION yoelii cDNA, mRNA sequence.

ACCESSION CF469981 GI:34487353

VERSION EST.

KEYWORDS Plasmodium yoelii yoelii

SOURCE Plasmodium yoelii yoelii

ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 1068)

AUTHORS Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,

Nussenzweig, V., and Bhanot, P.

TITLE Expressed sequence tags from Plasmodium yoelii hepatic stages in

axenic culture

JOURNAL Unpublished (2003)

COMMENT Contact: Bhanot P

Department of Pathology

New York University School of Medicine

550 First Avenue, MSB 131, New York, NY 10016, USA

Tel: 212 263 5346

Fax: 212 263 8179

Email: bhanop01@med.nyu.edu

similar to NR|GI-23483806 hypothetical protein [Plasmodium yoelii

yoelii] (e-108).

FEATURES

source
Location/Qualifiers
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/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
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/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium Yoelii 17X axenic hepatic stages"
/notes="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
excoerythrocytic malaria parasites does not require host
cells', (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BD Biosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN

Query Match 6.1%; Score 273.2; DB 14; Length 1068;
Best Local Similarity 90.0%; Pred. No. 3e-38;
Matches 278; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 571 GCCTGACATTTATATCCCGAGACATCAGCTTAATGCGTTTGTATGATTCATTTCCG 630
DB 562 GCCTGACATTTATATCCCGAGACATCAGCTTAATGCGTTTGTATGATTCATTTCCG 503
QY 631 GTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGACACTGGCCATATCGGT 690
DB 502 GTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGACACTGGCCATATCGGT 443
QY 691 GGTATCATGCGCCAGCTTTCATCCCGATATGACACCGGTAAGTTCACGGGAGAC 750
DB 442 GGNCATCATGCGCCAGCTTTCATCCCGATATGACACCGGTAAGTTCACGGGAGAC 383
QY 751 TTTATCTCAGCAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCGGGCGGTGC 810
DB 382 TTTATCTCAGCAGCAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCGGGCGGTGC 323
QY 811 AATAATATCATCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTATAGTGT 870
DB 322 AANAATATCGCTCGGNNCATCCACNANNCNANANCGGCTNTNTTTTTCACAGGTGNA 263
QY 871 AACCTTAA 879
DB 262 AACNTTGAA 254

RESULT 14

CF469119/c

LOCUS

DEFINITION

Pl6A8 Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii

yoelii cDNA, mRNA sequence.

ACCESSION CF469119 GI:34486491

VERSION EST.

KEYWORDS Plasmodium yoelii yoelii

SOURCE Plasmodium yoelii yoelii

ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 1037)

AUTHORS Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,

Nussenzweig, V., and Bhanot, P.

TITLE Expressed sequence tags from Plasmodium yoelii hepatic stages in

axenic culture

JOURNAL Unpublished (2003)

COMMENT Contact: Bhanot P

Department of Pathology

philippe_vaglio@dfci.harvard.edu
POLYA=No.

FEATURES

```

location/Qualifiers
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/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/name="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

```

ORIGIN

Query Match	7.6%;	Score 340.2;	DB 12;	Length 394;
Best Local Similarity	97.7%;	Pred. No. 6.7e-50;		
Matches 345;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	101	TAATAAACACAGACTACATAAATACTCTAAACACACACATATCCAGTCACCTATGTAATCAACTA	160	
Db	32	TAATACACAGACTACATAAATACTCTAAACACACATATCCAGTCACCTATGTAATCAACTA	91	
QY	161	CTTAGATGGTATTAGTCAGCCTGTAGTCGACCGACGAGCCTTCCAAATGTTCTTCGGGGTCAT	220	
Db	92	CTTAGATGGCTTTAGTCAGCCTGTAGTCGACCGACGAGCCTTCCAAATGTTCTTCGGGGTCAT	151	
QY	221	GCTGCCAACCTTAGTCGACCGAGAGCCTTCCAAATGTTCTTCTCCAAACGGAAATCGTCGTAT	280	
Db	152	GCTGCCAACCTTAGTCGACCGAGAGCCTTCCAAATGTTCTTCTCCAAACGGAAATCGTCGTAT	211	
QY	281	CGAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAAAGAAATAAGAAAAG	340	
Db	212	CCAACCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAAAGAAATAAGAAAAG	271	
QY	341	AGGTGCGAGCCTCTTTTGTGTGCACAAAATAAAAAACATCCACCTATTCATATACGCTAG	400	
Db	272	AGGTGCGAGCCTCTTTTGTGTGCACAAAATAAAAAACATTCATATACGCTAG	331	
QY	401	TGTCATAGTCCTGAAAAATCATCTCGCATCAAGAACAAATTCACACTCTTTATAC	453	
Db	332	TGTCATAGTCCTGAAAAATCATCTCGCATCAAGAACAAATTCACACTCTTTTATAC	384	

RESULT 11
BI174407/c

LOCUS	B1174407	384 bp	mrna	linear	EST 09-JUL-2001			
DEFINITION	OSTF043E11.1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to Flt1F.5, mRNA sequence.							
ACCESSION	B1174407							
VERSION	B1174407.1	GI:11640210						
KEYWORDS	EST.							
SOURCE	Caenorhabditis elegans							
ORGANISM	Caenorhabditis elegans							
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.							

REFERENCE
AUTHORS

TITLE Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in *C. elegans*

JOURNAL Nat. Genet. 27 (3), 332-336(2001)

MEDLINE
PURMED

11242119 FORMED
COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@fci.harvard.edu

Email: jerome_reboulet@ci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORF clone used for this study is available from the ORF clone library of the cloning project : Contact jerome_reboulet@ci.harvard.edu or philippe_vaglio@ci.harvard.edu
POLYA=No

FEATURES source

1. Location/Qualifiers
1. 384

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   /strain="N2"
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   /clone_lib="AD-wrmCDNA"
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         cDNAs were cloned into pPCR6"
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ORIGIN

Query Match	7.3%;	Score 325.4;	DB 12;	Length 384;
Best Local Similarity	98.2%;	Pred. No. 2.7e-47;		
Matches 329;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	3273	TGTTCTTGATGCGAGATGATTTTCAGAGACATATGACACTAGCGTATATGAATAGTAGTATGT	3332	
Db	366	TGTTCTTGATGCGAGATGATTTTCAGAGACTATGACACTAGCGTATATGAATAGTAAATGT	307	
Qy	3333	TTTTTATTTTGTACACAAAAAGAGGCTCGCACTCTTTTTCCTATTTCCTTTTATGATTT	3392	
Db	306	TTTTTATTTTGTACACAAAAAGAGGCTCGCACTCTTTTTCCTATTTCCTTTTATGATTT	247	
Qy	3393	TAATACGGCATTGAGGACAAATACGCGATGAGCTGGATACGACGATTCGGTTTCGAGAAGAA	3452	
Db	246	TAATACGGCATTGAGGACAAATACGCGATGAGCTGGATACGACGATTCGGTTTCGAGAAGAA	187	
Qy	3453	CATTTCGAAAGCGCTGTCGGTCGCATTAAGTTGGCGAGCATCACCCGAGACATTTGGAGGC	3512	
Db	186	CATTTCGAAAGCGCTGTCGGTCGCATTAAGTTGGCGAGCATCACCCGAGACATTTGGAGGC	127	
Qy	3513	TGTCGGTCGACTACAGGTCACTAATACCATCTAAAGTAGTTGATTCATAGTGCCTGGATAT	3572	
Db	126	TGTCGGTCGACTACAGGTCACTAAGGCCATCTAAGTAGTTGATTCATAGTGCCTGGATAT	67	
Qy	3573	GTGTGTTTTTACAGTATTATGTAGTCGTGTTTTTA	3607	
Db	66	GTGTGTTTTTACAGTATTATGTAGTCGTGTTATTA	32	

RESULT 12
PTEEE990

BU555980	BU555980	337 bp	mRNA	linear	EST 18-DEC-2002
LOCUS	BU555980				
DEFINITION	Ipomoea nil mixture of flower and flower bud Ipomoea nil				
	cDNA clone jml8n08.5', mRNA sequence.				
ACCESSION	BU555980				
VERSION	BU555980.1	GI:27237800			
KEYWORDS	EST.				
SOURCE	Ipomoea nil (Japanese morning glory)				
ORGANISM	Ipomoea nil				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; asterids; lamids; Solanales; Convolvulaceae; Ipomoea.				
REFERENCE	1 (bases 1 to 337)				
AUTHORS	Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Natsaka,E., Shinozaki,K., Hayaashizaki,Y., Kohara,Y. and Iida,S.				
TITLE	ESTs of Japanese morning glory				
JOURNAL	Unpublished (2002)				

QY 60 TAAATGATATAAATCAATATATTAATAGATTTTGCATATAAAACAGACTACATAA 119
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 Db 487 TAAATGATATAAATCAATATATTAATAGATTTTGCATATAAAACAGACTACATAA 428
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 QY 120 TACTGTAAACACAAACATATCCAGTCACTATGAATCAACTACTTATAGTGGTATAGTGAC 179
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 Db 427 TACTGTAAACACAAACATATCCAGTCACTATGAATCAACTACTTATAGTGGTATAGTGAC 368
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 QY 180 CTGTAGTGCACGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAAGTATAGTGCACC 239
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 Db 367 CTGTAGTGCACGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAAGTATAGTGCACC 308
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 QY 240 GACAGCTTCCAAATGTTCTTCTCAAAGGAATCGTGTATCCAGCTACTCGCTATTGTT 299
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 Db 307 GACAGCTTCCAAATGTTCTTCTCAAAGGAATCGTGTATCCAGCTACTCGCTATTGTT 248
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 QY 300 CTTCAATGCGTATTAATCATATAAAAGAAATAGAAAGAGGTGGAGCTCTTTT 359
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 Db 247 CTTCAATGCGTATTAATCATATAAAAGAAATAGAAAGAGGTGGAGCTCTTTT 188
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 Db 187 GTGTGACAAATATAAGGCACTACAAATATCAATATCAATTTAGTGTATGCTCCAGTAT 128
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 QY 419 CATCTGCATCAAGAAACAATTCACAACTCTTATATCTTTCTCTTACAAG 467
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 Db 127 CTTCCGTCATCATGAACAGAGCTTTTATATGCTATCTCTGCAAG 79
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RESULT 9
 CB395230
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 DEFINITION OSTR151B2_1 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence.
 CB395230
 ACCESSION
 VERSION CB395230.1 GI:30736941
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
 AUTHORS Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
 Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
 Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
 Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
 Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
 Doucette-Stamm,L., Hill,D.E. and Vidal,M.
 C. elegans ORFeome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression
 Nat. Genet. (2003) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 658, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact david.hill@dfci.harvard.edu or
 marc.vidal@dfci.harvard.edu
 POLYA=No.

FEATURES
 source
 1. .487
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 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"

/clone_lib="AD-wrmCDNA"

/note="The AD-wrmCDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.8%; Score 347.4; DB 14; Length 487;
 Best Local Similarity 96.8%; Pred. No. 3.3e-51;
 Matches 365; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
 QY 3273 TGTTCCTGATGACAGATGATTTTCAGGACTATGACACTAGCGTATATGAAATG-GTAGATG 3331
 Db 111 TGTTCATGATCGGAAGATATCTCGGACTATGACACTAAAGTATATGAATATCTAGATG 170
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 QY 3332 TTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 3391
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 Db 171 CTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 230
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 QY 3392 TTAATACGGCAATTGAGGACAAATAGCGAGTAGGCTGGATACGACGATTCGGTTGAGAAGA 3451
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 Db 231 TTAATACGGCAATTGAGGACAAATAGCGAGTAGGCTGGATACGACGATTCGGTTGAGAAGA 290
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 QY 3452 ACATTTGGAAGGCTGTCGCTGACCTAAGTTGGGAGCATCACCAGAACATTTTGGAGG 3511
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 Db 291 ACATTTGGAAGGCTGTCGCTGACCTAAGTTGGGAGCATCACCAGAACATTTTGGAGG 350
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 QY 3572 TGTGTGTTTTACAGTATATATGATGCTGTTTTATGCAAAATCTAATTTAATATATG 3631
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 Db 411 TGTGTGTTTTACAGTATATATGATGCTGTTTTATGCAAAATCTAATTTAATATATG 470
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 QY 3632 ATATTTATATCATTTTA 3648
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 Db 471 ATATTTATATCATTTTA 487
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RESULT 10

BI174407
 LOCUS
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 F11F1.5, mRNA sequence.
 BI174407
 ACCESSION
 VERSION BI174407.1 GI:14640210
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
 AUTHORS Rebol,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
 Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
 Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
 Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
 Open-reading-frame sequence tags (OSTs) support the existence of at
 least 17,300 genes in C. elegans
 Nat. Genet. 27 (3), 332-336 (2001)
 21135039
 11242119

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Rebol J, Vaglio P
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 44 Binney Street, Boston, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 2425
 Email: Jerome.Rebol@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFeome
 cloning project : Contact jerome_rebol@dfci.harvard.edu or
 marc.vidal@dfci.harvard.edu

```

QY 786 TCACCATCCGTCGCGCGGGTGTCATATAATATACATCTGTACATCCACAAAACAGACGAT 845
Db 263 TCACCATCCGTCGCGCGGGTGTCATATAATATACATCTGTACATCCACAAAACAGACGAT 322
QY 846 AACGGCTCTCTCTTTTATAGTGTAACACCTTTAAACTGCAATTTACACAGTCCCTGTTCTCG 905
Db 323 AACGGCTCTCTC-TTTATAGTGTAACACCTTTAAACTGCAATTTACACAGTCCCTGTTCTCG 381
QY 906 TCAGCAAAAGAGCGGTCATTTCAATAAACCGGGGAGCTCAGGCATCC-TTCTGATT 964
Db 382 TCAGCAAAAGAGCGGTCATTTCAATAAACCGGGGAGCTCAGGCATCCCTTTCCTGATT 441
QY 965 TTTCGGCTTTCCAGCGTTCCGACGACGACGAC 996
Db 442 TTTCGGCTTTCCAGCGTTTCGCGACGCGCAGAC 473

RESULT 7
AG000763/c
LOCUS AG000763 722 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgci.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

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     /clone="64E11X4"

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Best Local Similarity 92.2%; Pred. No. 3e-60;
Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 601 GTTAATGGCGTTTGTGATGTCATTTTCGGTGCTGAGATCAGCCATCTTCCCGGAT 660
Db 722 GTTAAGGCGCTTTTGGANGNCAATTTTCGGGTGGC---GAGATCGCCAATTNTTCCCGA 667
QY 661 AACGGAGACCGGCACACTGGCCATATCGTGTGTCATATCGCCAGCTTTCATCCCGAT 720
Db 666 TAAGGAGACCGGCACA-TGGGCNTAACGGTGTGCATCA-GGCCAGCTTTCATCA-CCCGGAT 610
QY 721 ATGCACACCGGGTAAAGTTTCAACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 780
Db 609 ATGCACACCGGGTAAAGTTTCAACGGGAGACTTTATACGACAGCAGACGTGCACTGGCCAG 550
QY 781 GGGGATACACATCCCTGCGCCCGGGCGTGTCAATAATATATCTCTGTATCCACAAAACAG 840
Db 549 GGGGAATCACCATCCCTGCGCCCGGGCGTGTCAATAATATATCTCTGTATCCACAAAACAG 490
QY 841 ACGATAAGCGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTCCACGAGTCCCTGT 900

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Db 489 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTTCCACGAGTCCCTGT 430
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Db 429 TCTCTGTCAGC-AAAGAGCGGTTTCATTTCAATAAACCGGGGAGCTCAGCCATCCCTTCCCT 371
QY 961 GATTTTCCGCTTTCCAGCGTTTCGGACGACGACGACGCGGCTTCATTTGTCATGTTGTGC 1020
Db 370 GATTTTCCGCTTTCCAGCGTTTCGGACGACGACGACGCGGCTTCATTTGTCATGTTGTGC 311
QY 1021 TTACCGAGACGGAGATTTGACATCATATATATGCTTGAGCAACTGATAGTGTGCTGTC 1080
Db 310 TTACCGAGACGGAGATTTGACATC--ATATGCTTTGAGCAACTGATAG-TGTGCTGTC 254
QY 1081 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
Db 253 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 197

RESULT 8
CB395230/c
LOCUS CB395230 487 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Rebol,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS 1 (bases 1 to 487)
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Janna,S., Chevet,E., Papasotiropoulos,V., Tolias,P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,J., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david.hill@dfci.harvard.edu or marc.vidal@dfci.harvard.edu
POLYA=No.

FEATURES             Location/Qualifiers
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ORIGIN
Query Match      8.0%; Score 357; DB 14; Length 487;
Best Local Similarity 93.6%; Pred. No. 6.8e-53;
Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
JOURNAL Published Only in DataBase (1998)
TITLE Homo sapiens genomic DNA, chromosome 21q
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
JOURNAL Direct Submission
Submitted (07-SEP-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagami-hara 228, Japan (E-mail: hattori@hgc.ims.u-tokyo.ac.jp, Tel: 0427-78-9732, Fax: 0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
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Best Local Similarity 90.2%; Pred. No. 5.2e-62;
Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;
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DB |||||
723 TTATATCCCGAGACATCAGTTAATGCGTTTGTGATGTCATTTTCGGTGGCTGAG 664
QY 640 ATCAGGCACTTCTTCCCGATACGAGACCGGACACCTGCGGCATATCGTGTCTCATCAT 699
DB |||||
663 ATCAGGCACTTCTTCCCGATACGAGACCGGACACCTGCGGCATATCGTGTCTCATCAT 604
QY 700 GCGCAGCTTTCATCCCGATATGACACCGGTAAGTTTACCGGAG-ACCTTATCTG 758
DB |||||
603 GCGCAGCTTTCATCCCGATATGACACCGGTAAGTTTACCGGAG-ACCTTATCTG 545
QY 759 ACAGCAGAGCTGCTACCTGCGC-AGGGGGATCACCATCCGTCGCGCGGCTGTCAATAATA 817
DB |||||
544 ACAGCAGAGCTGCTACCTGCGC-AGGGGGATCACCATCCGTCGCGCGGCTGTCAATAATA 486
QY 818 TCACCTCTGTACATCCCAACAGACGATACCGGCTCTCTTTTATAGTGTAACCTTA 877
DB |||||
485 TCACCTCTGTACATCCCAACAGACGATACCGGCTCTCTTTTATAGTGTAACCTTA 427
QY 878 AACTGATTTACAGTCCCTGTTTCGTCAGCAAAAGAGCGGTCATTTCAATAAACCG 937
DB |||||
426 AACTGATTTACAGTCCCTGTTTCGTCAGCAAAAGAGCGGTCATTTCAATAAACCG 367
QY 938 GCGCCTCAGCCTCCCTCTCTGATTTTCGCTTCCAGCGTTCGCGCAGCAGCAGC 997
DB |||||
366 GCGCCTCAGCCTCCCTCTCTGATTTTCGCTTCCAGCGTTCGCGCAGCAGCAGC 307
QY 998 GGCTTCATTTCTGATGGTTGTGTTTACAGACCGGAGATATTGACATCATATATGCTTGT 1057
DB |||||
306 GGCTTCATTTCTGATGGTTGTGTTTACAGACCGGAGATATTGACATC--ATATGCTTGT 249
QY 1058 AGCACTGATAGTGTGCTGTCACTGTAATACGCTGCTTCAATAGCAGCAGCTTC 1117
DB |||||
248 AGCACTGATAGTGTGCTGTCACTGTAATACGCTGCTTCAATAGCAGCAGCTTC 190
QY 1118 TTTTTCACATACCTTCGGGTA 1137

DB 189 TTTTTCACATACCTTCGGGTA 170
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CB997937
LOCUS
DEFINITION CB997937 522 bp mRNA linear EST 01-MAY-2003
IMAGE:30348484 5', mRNA sequence.
ACCESSION CB997937
VERSION CB997937.1 GI:30292457
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: e column: 05
High quality sequence start: 58
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ORIGIN
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Best Local Similarity 96.2%; Pred. No. 3.5e-61;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 546 CTGCAGACTGCTGTATAGGAGCGCTGACATTTATTTCCCGAACATCAGGTTAA 605
DB |||||
23 CTGCAGACTGCTGTATAGGAGCGCTGACATTTATTTCCCGAACATCAGTAA 82
QY 606 TGGCGTTTTTGCATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGTAACGG 665
DB |||||
83 TGGCGTTTTTGCATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGTAACGG 142
QY 666 AGACCGGCACACTGCCCATATCGGTGTCATCATCGCCAGCTTCATCCCGATATGCA 725
DB |||||
143 AGACCGGCACACTGCCCATATCGGTGTCATCATCGCCAGCTTCATCCCGATATGCA 202
QY 726 CCACCGGTTAAAGTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCGAGGGGA 785
DB |||||
203 CCACCGGTTAAAGTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCGAGGGGA 262

Email: csapbe-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDA387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.
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 /clone_lib="NIH MGC 147"
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 5'-TTTTTTTTTTTTTTTT-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

ORIGIN

Query Match 9.8%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 4.8e-67;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

Qy 546 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATTCAGGTTAA 605
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Qy 606 TGGCGTTTTTGCATCTTTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 665
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Qy 666 AGACCGGCACACTGGCCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCA 725
 Db 143 AGACCGGCACACTGGCCCATATCGGTGGTGCATCATCGGTGCATCTTTCATCCCGATATGCA 202

Qy 726 CCACCGGTTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGTGCTGCGCCAGGGGGA 785
 Db 203 CCACCGGTTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGTGCTGCGCCAGGGGGA 262

Qy 786 TCACCATCCGTCGCGCGGGCGTGCATTAATATCACTCTGTACATCCCAACACAGCAT 845
 Db 263 TCACCATCCGTCGCGCGGGCGTGCATTAATATCACTCTGTACATCCCAACACAGCAT 322

Qy 846 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTCTCG 905
 Db 323 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTCTCG 382

Qy 906 TCAGCAAAAGAGCCGTTCAATTAACCGGGGAGCTCAGCCATCCCTTCCTGATT 965
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Qy 966 TCCGTTTCCCA-GCGTTCGGCAGCAGAGC-ACGGGCTTCATTTC-TGCATGGTTGTGCT 1021
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Qy 1022 TACCAGACCGG-AGATATTGACATCATATATGCCTT 1056
 Db 503 TACCAGACCGGAGATATTGACATCATATATGCCTT 538

RESULT 4

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 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 TITLE Homo sapiens genomic DNA, chromosome 21q
 JOURNAL Published Only in DataBase (1997)
 REFERENCE 2 (bases 1 to 723)
 AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@bc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
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 Best Local Similarity 98.1%; Pred. No. 1.3e-62;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 546 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATTCAGGTTAA 605
 Db 450 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATTCAGGTTAA 391

Qy 606 TGGCGTTTTTGCATCTTTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 665
 Db 390 TGGCGTTTTTGCATCTTTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 331

Qy 666 AGACCGGCACACTGGCCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCA 725
 Db 330 AGACCGGCACACTGGCCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCA 271

Qy 726 CCACCGGTTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGTGCTGCGCCAGGGGGA 785
 Db 270 CCACCGGTTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGTGCTGCGCCAGGGGGA 211

Qy 786 TCACCATCCGTCGCGCGGGCGTGCATTAATATCACTCTGTACATCCCAACACAGCAT 845
 Db 210 TCACCATCCGTCGCGCGGGCGTGCATTAATATCACTCTGTACATCCCAACACAGCAT 151

Qy 846 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTCTCG 905
 Db 150 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTCTCG 91

Qy 906 TCAGCAAAAGAGCCGTTCAATTAACCGGGGAGCTCAGCCATCCCTTCCTGATT 965
 Db 90 TCAGCAAAAGAGCCGTTCAATTAACCGGGGAGCTCAGCCATCCCTTCCTGATA 31

Qy 966 TCCG 969
 Db 30 TCAG 27

RESULT 5

AG013450/c
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ORIGIN

Query Match 11.6%; Score 518.4; DB 29; Length 698;
Best Local Similarity 98.9%; Pred. No. 2.2e-81;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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QY 639 GATCAGCCACTTCTTCCCGGATPAAGGAGACGGGACACTGGCCATATCGGTGGTCATCA 698
Db 94 GATCAGCCACTTCTTCCCGGATPAAGGAGACGGGACACTGGCCATATCGGTGGTCATCA 153
QY 699 TCGCCAGCTTTTCATCCCGGATATGACACACGGGTAAAGTTTCAGGGAGACTTTATCTG 758
Db 154 TCGGCCA-NTTTCATCCCGGATATGACACACGGGTAAAGTTTCAGGGAGACTTTATCTG 212
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Db 273 CACTCTGTACATCCACAAACAGACGATACCGGCTCTCTCTTTTATAGGTGTAACCTTAA 332
QY 879 ACTGATTTTACAGCAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTAACACGG 938
Db 333 ACTGATTTTACAGCAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTAACACGG 392
QY 939 GCGACTCAGCCATCCCTTCTGATTTTCCGCTTTCAGCGTTTCGCGACGACGACGCG 998
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QY 999 GCTTCATTTGATGATGTTGTGTTTACCGACCGGAGATATGACATCATATATGCTTGA 1058
Db 453 GCTTCATTTGATGATGTTGTGTTTACCGACCGGAGATATGACATC--ATATGCTTGA 510
QY 1059 GCAACTGATAGTGTGCTGTCACTGTCATGTAATAGCTTTCATAGCAGACCTCT 1118
Db 511 GCAACTGATAGC-GTGGCTGTCACTGTCACTGTATAGCTGTGTTATAGCAGACCTCT 569
QY 1119 TTTTGACATCTTCGGGTA 1137
Db 570 TTTTGACATCTTCGGGTA 588

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RESULT 2
AG000762/c
LOCUS
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000762
VERSION AG000762.1 GI:2579570
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Hattori.M., Ishii.K., Shiba.T. and Sakaki.Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE
AUTHORS Hattori.M., Ishii.K., Shiba.T. and Sakaki.Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-78-9561)
Location/Qualifiers
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Query Match 11.1%; Score 496.6; DB 29; Length 713;  
Best Local Similarity 94.2%; Pred. No. 1.5e-77;  
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;  

QY 583 TATTCCCGCAGAACATCAGGTTAATGGCGTTTTCATGTCATTTTCGGGTGGCTGAGATC 642
Db 599 TATATCCCGGANCATCNGTTAATGCCGTTTTCGAGGNATTTTCGCCGTGGCTGAGAT 540
QY 643 AGCCACTTCTTCCCGGATPAAGGAGACGGGACACTGGCCATATCGGTGGTCATCATGCG 702
Db 539 CACCAACTTTTTCGCCGATTACGNAGACGGCAGCATGCCATATCGGTGGTCATCATGCG 480
QY 703 CCAGCTTTTCATCCCGGATATGACACACGGGTAAAGTTTCAGGGAGACTTTTATCTGACG 762
Db 479 CCAGCTTTTCATCCCGGATATGACACACGGGTAAAGTTTCAGGGAGACTTTTATCTGACG 420
QY 763 CAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACT 822
Db 419 CAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACT 360
QY 823 CTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTG 882
Db 359 CTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTG 300
QY 883 CATTTCCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTAACACCGGGCGA 942
Db 299 CATTTCCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTAACACCGGGCGA 240
QY 943 CCTCAGGCATCCCTTCTCGATTTTCGCTTTTCAGCGTTTCGCGACGACGAGCGGCTT 1002
Db 239 CCTCAGGCATCCCTTCTCGATTTTCGCTTTTCAGCGTTTCGCGACGACGAGCGGCTT 180
QY 1003 CATTTCTGATGGTGTGCTTACCGACCGGAGATATTGACATCATATATGCTTGAACAA 1062
Db 179 CATTTCTGATGGTGTGCTTACCGACCGGAGATATTGACATC--ATAAGCTTGAACAA 122
QY 1063 CTGATAGCTGTGCTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGT 1122
Db 121 CTGAATANTGTGCTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGTCACTGT 62
QY 1123 GACATACTTCGGGTA 1137
Db 61 GACATACTTCGGGTA 47

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RESULT 3

CD109790
LOCUS
DEFINITION AGENCOURT 13988518 NIH MGC 147 Homo sapiens cDNA clone IMAGE:30346919 5', mRNA sequence.
ACCESSION CD109790
VERSION CD109790.1 GI:30753999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 542)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
REFERENCE
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 6916.59 Seconds

(without alignments)
19251.609 Million cell updates/sec

Title: US-10-055-001B-25_COPY_13000_17458

Perfect score: 4459

Sequence: 1 tttcatttggagagacacg.....atagtgcacataatctgc 4459

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518.4	11.6	698	29	AG012840 Homo sapi
c 2	496.6	11.1	713	29	AG000762 Homo sapi
3	437.2	9.8	542	14	CD109790 AGENCOURT
c 4	411.8	9.2	723	29	AG000761 Homo sapi

c	5	408.4	9.2	725	29	AG013450
c	6	404	9.1	522	14	CB997937
c	7	398.4	8.9	722	29	AG000763
c	8	357	8.0	487	14	CB395230
c	9	347.4	7.8	487	14	CB395230
c	10	340.2	7.6	384	12	B1174407
c	11	325.4	7.3	384	12	B1174407
c	12	301.4	6.8	337	12	BUS55980
c	13	273.2	6.1	1068	14	CF469981
c	14	271.8	6.1	1037	14	CF469119
c	15	264.4	5.9	724	29	AG000791
c	16	262.4	5.9	816	14	CF469496
c	17	257.4	5.8	557	12	BG220129
c	18	255.8	5.7	656	14	CK231800
c	19	254	5.7	569	14	CF469084
c	20	252.4	5.7	819	14	CF469247
c	21	247.4	5.5	320	29	CG206516
c	22	246	5.5	329	28	BH739300
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c	26	239.2	5.4	659	14	CK287298
c	27	235.6	5.3	859	14	CF468865
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c	29	234.8	5.3	657	14	CF468948
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c	31	227.2	5.1	968	14	CF469474
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c	43	203.4	4.6	1013	14	CF469353
c	44	203.2	4.6	973	14	CF469399
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ALIGNMENTS

RESULT 1
AG012840
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
TITLE
AUTHORS
JOURNAL
JOURNAL
AUTHORS
TITLE
JOURNAL
JOURNAL

AG012840 Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840.1 GI:3435047 GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published only in DataBase (1998)

2 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission

Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228 Japan (E-mail:hattori@jst.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

1. .698

/organism="Homo sapiens"

/mol_type="genomic DNA"

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Db 750 TCGGTGGTTCATCATGCGCGAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTCACGG 809
Qy 746 GAGACTTTATCTGACAGCAGAGTGCACTGCGCCAGGGGGATCACCATCCGTGCGCCCGGGC 805
Db 810 GAGACTTTATCTGACAGCAGAGTGCACTGCGCCAGGGGGATCACCATCCGTGCGCCCGGGC 869
Qy 806 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAAAGCGCTCTCTTTTATAG 865
Db 870 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAAAGCGCTCTCTTTTATAG 929
Qy 866 GTGTAAACCTTAAACCTGCAATTTACCAAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCA 925
Db 930 GTGTAAACCTTAAACCTGCAATTTACCAAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCA 989
Qy 926 TTCAATAAACCGGGCGAGCTCAGCCATCCCTCTCTGATTTTCCGTTTCCAGCGGTTCCGC 985
Db 990 TTCAATAAACCGGGCGAGCTCAGCCATCCCTCTCTGATTTTCCGTTTCCAGCGGTTCCGC 1049
Qy 986 AGCGACAGCAGCGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC 1045
Db 1050 AGCGACAGCAGCGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC 1109
Qy 1046 ATATATGCTTGGACAACTGATAGTGTGCTGCTCAACTGTCACCTGTAATACGCTGCTTC 1105
Db 1110 ATATATGCTTGGACAACTGATAGTGTGCTGCTCAACTGTCACCTGTAATACGCTGCTTC 1169
Qy 1106 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1137
Db 1170 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1201
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RESULT 15

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US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R. N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64
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Query Match 24.7%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 7.4e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 26 GACAAAGTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAATAATATCAATATATT 85
Db 90 GCCAACTTTGTACAAAAGCTGATATCGAAACGTAATAATGATATAATAATATCAATATATT 149
Qy 86 AAATTAGATTTTGCATAAAACACAGACTACATAATCTGTAAACACACACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAACACAGACTACATAATCTGTAAACACACACATATCCAGTC 209
Qy 146 ACTATGAATCAACTACTTATAGTGGTATTAGTACCTGTAGTACCTGTAGTACCGGACGCGCTTCCAAA 205
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Search completed: May 10, 2004, 00:05:56
Job time : 1230.96 secs

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGAAGCTGTAGTCGACCGCAGCCCTTCCAAA 205
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QY 206 TGTCTCTCGGTGATGTCGCAACTAGTCGACCGCAGCCCTTCCAAATGTTCTTCAAA 265
DB 1119 TGTCTCTCGGTGATGTCGCAACTAGTCGACCGCAGCCCTTCCAAATGTTCTTCAAA 1178
QY 266 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
DB 1179 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 1238
QY 326 AGAATTAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATAAATAAATCAATCACT 385
DB 1239 AGAATTAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATAAATAAATCAATCACT 1298
QY 386 ATTCAATACGCTAGTGTCTGATGCTGAAATCATCTGCATCAAGACAAATTTTCAAC 445
DB 1299 ATTCAATACGCTAGTGTCTGATGCTGAAATCATCTGCATCAAGACAAATTTTCAAC 1358
QY 446 TCTTATACCTTTCTCTTCAAGTCTGTCGGCTTCACTCTGATTTTTCAGCCCTCTACTTA 505
DB 1359 TCTTATACCTTTCTCTTCAAGTCTGTCGGCTTCACTCTGATTTTTCAGCCCTCTACTTA 1418
QY 506 CTAACAGTGATTAAGTTTCTGTAAATTTCTACTGTATCGAAGCTGAGCTGGCTGTGTATA 565
DB 1419 CTAACAGTGATTAAGTTTCTGTAAATTTCTACTGTATCGAAGCTGAGCTGGCTGTGTATA 1478
QY 566 AGGAGCGCTGACATTTATATCCCGAGAAATCAGGTTTAAAGGCTTTTTCATGTCATTT 625
DB 1479 AGGAGCGCTGACATTTATATCCCGAGAAATCAGGTTTAAAGGCTTTTTCATGTCATTT 1538
QY 626 TCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATAACCGGAGACCGGCACACTGSCCATA 685
DB 1539 TCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATAACCGGAGACCGGCACACTGSCCATA 1598
QY 686 TCGGTGGTTCATCATGCGCGCAGCTTTCATCCCGGATATGACCAACCGGTAAGTTCACGG 745
DB 1599 TCGGTGGTTCATCATGCGCGCAGCTTTCATCCCGGATATGACCAACCGGTAAGTTCACGG 1658
QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACCATCCGTCGCGCGGCG 805
DB 1659 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACCATCCGTCGCGCGGCG 1718
QY 806 GTGTCAATTAATACCTCTGTATATCCCAACAGACGATAAAGCTCTCTCTTTTATAG 865
DB 1719 GTGTCAATTAATACCTCTGTATATCCCAACAGACGATAAAGCTCTCTCTTTTATAG 1778
QY 866 GTGTAAACCTTAACTGATTTTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925
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QY 986 ACGCAGACGAGCGGCTTCACTTGTGATGCTTACCAACCGGAGATTAATGACATC 1045
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DB 2019 ATAGCACACCTCTTTTGTGACATCTTGGGTA 2050

RESULT 14

US-10-151-690-63

; Sequence 63, Application US/10151690

; Publication No. US20030124555A1

; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID M
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match 24.7%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 7.4e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 26 GACAAAGTTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAATATCAATATATT 85
DB 90 GCCAACTTTGTACAAAAGCTGATATCGAAACGTAATAATGATATAATATCAATATATT 149
QY 86 AAATTAGATTTTGCATAAAAAAGACACTACATATACTGTAAAAACAAACATATCCAGTC 145
DB 150 AAATTAGATTTTGCATAAAAAAGACACTACATATACTGTAAAAACAAACATATCCAGTC 209
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGAAGCTGTAGTCGACCGCAGCCCTTCCAAA 205
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QY 266 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
DB 330 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 389
QY 326 AGAATTAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATAAATAAATCAATCACT 385
DB 390 AGAATTAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATAAATAAATCAATCACT 449
QY 386 ATTCAATACGCTAGTGTCTGATGCTGAAATCATCTGCATCAAGACAAATTTTCAAC 445
DB 450 ATTCAATACGCTAGTGTCTGATGCTGAAATCATCTGCATCAAGACAAATTTTCAAC 509
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QY 506 CTAACAGTGATTAAGTTTCTGTAAATTTCTACTGTATCGAAGCTGGCTGTGTATA 565
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QY 566 AGGAGCGCTGACATTTATATTTCCCGAGAAATCAGGTTTAAAGGCTTTTTCATGTCATTT 625
DB 630 AGGAGCGCTGACATTTATATTTCCCGAGAAATCAGGTTTAAAGGCTTTTTCATGTCATTT 689
QY 626 TCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATAACCGGAGACCGGCACACTGSCCATA 685
DB 690 TCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATAACCGGAGACCGGCACACTGSCCATA 749
QY 686 TCGGTGGTTCATCATGCGCGCAGCTTTCATCCCGGATATGACCAACCGGTAAGTTCACGG 745

Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 24.9%; Score 1108.8; DB 15; Length 5584;
Best Local Similarity 99.8%; Pred. No. 8.6e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY	206	TGTTCTTCGGGTGATCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTCTCAA	265
DB	5303	TGTTCTTCGGGTGATCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTCTCAA	5244
QY	266	ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGATTAATCAATAA	325
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QY	326	AGAAATAAGAAAAGAGGTGCGAGCTCTTTTGTGTGACAAATAAATAATCACTACCT	385
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DB	5123	ATTATATACGCTAGTGTATAGTCTGAAAATCATCTGATCAAGAACAAATTCACAA	5064
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QY	866	GTGTAAACCTTAACTGCACTTACAGTCCCTGCTTCTGCTCAGCAAAAGAGCGGTTTCA	925
DB	4643	GTGTAAACCTTAACTGCACTTACAGTCCCTGCTTCTGCTCAGCAAAAGAGCGGTTTCA	4584
QY	926	TTCAATAAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGC	985
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QY	986	ACGAGACGACGGGCTTCATTTCTGATGTTGCTTACAGACCGGAGATATTGACATC	1045
DB	4523	ACGAGACGACGGGCTTCATTTCTGATGTTGCTTACAGACCGGAGATATTGACATC	4464
QY	1046	ATATATGCTTGTGCAACTGATAGCTGTCGCTGCAACTGTCACTGTAATACGCTGCTTC	1105
DB	4463	ATATATGCTTGTGCAACTGATAGCTGTCGCTGCAACTGTCACTGTAATACGCTGCTTC	4404
QY	1106	ATAGCACACCTCTTTTGTGACATATCTCGGGTA	1137
DB	4403	ATAGCACACCTCTTTTGTGACATATCTCGGGTA	4372

RESULT 13

US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match 24.7%; Score 1102.4; DB 15; Length 4428;
Best Local Similarity 99.5%; Pred. No. 7.3e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	26	GACAAAGTTTGTACAAAAGCTGAAACGAGAAACGTAAATAATGATATAATATCAATATATT	85
DB	939	GCCAACTTTGTACAAAAGCTGATATCGAAACGTAAATAATGATATAATATCAATATATT	998
QY	86	AAATTAGATTTTGCATAAAAACAGACTACATTAATCTGTAAACACACACATATCCAGTC	145
DB	999	AAATTAGATTTTGCATAAAAACAGACTACATTAATCTGTAAACACACACATATCCAGTC	1058

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Db 1182 ATAGCACACCTCTCTTTTGGACATACCTTCGGGTA 1213
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RESULT 11
US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US20030219902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; FILE REFERENCE: WSR-1-20291
; CURRENT FILING DATE: 2003-01-31
; CURRENT APPLICATION NUMBER: 60/354,063
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4892
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (73)..(100)
; OTHER INFORMATION: T2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(563)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (959)..(1264)
; OTHER INFORMATION: ccdB gene
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1606)..(2265)
; OTHER INFORMATION: Cam(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2513)..(2744)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2868)..(3677)
; OTHER INFORMATION: Kan(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3794)..(4537)
; OTHER INFORMATION: pUC oriV / RK2 oriT
US-10-357-268-1
Query Match 24.9%; Score 1108.8; DB 16; Length 4892;
Best Local Similarity 99.8%; Pred. No. 8.2e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAACTTCTGACAAAAGCTGACGAGAAAGCTAAATGATATAATATCAATATATT 85
Db 102 GCCAACTTTGTACAAAAGAGCTGAACGAGAAAGCTAAATGATATAATATCAATATATT 161
QY 86 AAATTAGATTTCATATAAAGACAGACTACATATACTGTAAACACAAACATATCCAGTC 145
Db 162 AAATTAGATTTCATATAAAGACAGACTACATATACTGTAAACACAAACATATCCAGTC 221
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QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGCTTCCAAA 205
Db 222 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGCTTCCAAA 281
QY 206 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCA 265
Db 282 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCA 341
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAATCATA 325
Db 342 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAATCATA 401
QY 326 AGAAATAGAAAAGAGTGCGAGCCTCTTTTGTGTGACAAATAAATAACATCTAC 385
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QY 386 ATTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGAAACAATTTCA 445
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Db 522 TCTTATACCTTTCTCTTCAAAAGTCGTTGGCTTCATCTGGAATTTAGCCTCTA 581
QY 506 CTAAACGTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGACACTGGCTGT 565
Db 582 CTAAACGTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGACACTGGCTGT 641
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Db 642 AGGAGCCTGACATTTATTTCCCGAGAAATCAAGTTAATGGCGTTTTTGATGTC 701
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Db 702 TCGCGGTGCTGAGATCAGCCACTTTCTCCCGATTAACGGAGACCGGCACACT 761
QY 686 TCGGTGCTCATCATCGCGCAGCTTTTCATCCCGATTAACGGAGACCGGCACACT 745
Db 762 TCGGTGCTCATCATCGCGCAGCTTTTCATCCCGATTAACGGAGACCGGCACACT 821
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Db 1002 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTGATTTCCGCTTTCCAGCT 1061
QY 986 ACGCAGACGACCGGCTTCAATCTGATGTTGTCTTACACACCGGAGATATGAC 1045
Db 1062 ACGCAGACGACCGGCTTCAATCTGATGTTGTCTTACACACCGGAGATATGAC 1121
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Db 1182 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1213
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RESULT 12
US-10-151-690-61/c
; Sequence 61, Application US/10151690

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Db	13198	AGGCTGTCGGTCGACTACAGCTCACTAATACCACTAAGTAGTGTGATTCATAGTACTGG	13139
QY	3569	ATATGTTGTTTACAGATATATAGTACTGTTTATGCAAAATCAATTTAATATA	3628
Db	13138	ATATGTTGTTTACAGATATATAGTACTGTTTATGCAAAATCAATTTAATATA	13079
QY	3629	TTGATATTATATCAATTTAGTCTTCGTTTCAGCTTTTGTACAAACTTGTCTAGAG	3687
Db	13078	TTGATATTATATCAATTTAGTCTTCGTTTCTGTTTCAGCTTTTGTACAAACTTGTCTAGAG	13020
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US-10-151-690-21			
; Sequence 21, Application US/10151690			
; Publication No. US20030124555A1			
; GENERAL INFORMATION:			
; APPLICANT: BRASCH, MICHAEL A.			
; APPLICANT: CHEO, DAVID			
; APPLICANT: LI, XIAO			
; APPLICANT: ESPOSITO, DOMINIC			
; APPLICANT: BYRD, DEVON R.N.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO			
; FILE REFERENCE: 0942.5120001			
; CURRENT APPLICATION NUMBER: US/10/151,690			
; CURRENT FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: US 10/151,690			
; PRIOR FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: US 60/291,973			
; PRIOR FILING DATE: 2001-05-21			
; NUMBER OF SEQ ID NOS: 64			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 21			
; LENGTH: 4470			
; TYPE: DNA			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: plasmid pDONR201			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (29)..(260)			
; OTHER INFORMATION: attP1			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (656)..(961)			
; OTHER INFORMATION: ccdB			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (1099)..(1184)			
; OTHER INFORMATION: ccdA			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (1303)..(1962)			
; OTHER INFORMATION: Cmr			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (2210)..(2442)			
; OTHER INFORMATION: attP2			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (2565)..(3374)			
; OTHER INFORMATION: Km ^r			
; FEATURE:			
; NAME/KEY: gene			
; LOCATION: (3495)..(4134)			
; OTHER INFORMATION: ori			
US-10-151-690-21			
Query Match 24.9%; Score 1108.8; DB 15; Length 4470;			
Best Local Similarity 99.8%; Pred. No. 7.9e-158;			
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			

Db 15405 AGTGACTGGATATGTTGTTTACAGTATTATAGTAGTCTGTTTTTATGCAAAATCTAA 15346
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Db 15345 TTTAATATATGATATTTATATCATTTTACGTTTCTCGTTACGTTTCTTTGACAAAGTG 15286
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Db 15285 GTCTAGAGGATCCAAAGCTTATCGATTTTCGAACCCAGCTTCCCAACTGTAATCAATCCAA 15226
QY 1494 TTTTCTTTTATGATATAAATAGTTAAGTATGATGTTAATAGTATGATTAATAATATAGT 1553
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QY 1554 TGTATTAATTTGTGAATAAATAATTTATATAATATATTTGTTTACATAAACAACATAGTAATG 1613
Db 15165 GACTAATTCATTTAATATAGTCAATCCATTTAGAGTTAATAAATACACATGATTTAT 15106
QY 1614 TAAAAAATATGACAGTGTGTAAGACGAGAGAGATAAAGTTGAGAGTAATAT 1673
Db 15105 TTAGAAATTAATAAGAAATGTTGATTGAAATAATACTATATAAATGATAGATCTTGGC 15046
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Db 15045 TTTGTTATATAGCAATGATATGTTTGTGTTACATTAGATTTACTGTTTCTATTAGTTG 14986
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QY 1794 AAAAAATAGATAAATAAATAAATAATTTTTTATGATTAATAGTTTATTAATAA 1853
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QY 2094 AATTTCTAAATAATCTTGTAGTTTATTAATCTTAAATGGAATGACTATTAATAAT 2153
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Db 14505 AAAGGAAAAAGAAATAATTTTCCCTTACCAGCTGGGTACCGAATTTCTCAGACC 14446
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QY 2330 TAGATTTTCAATAAACAAGACTACATAATCTGTAAACAACATATCCAGTCACTA 2389
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QY 2570 GATCGGATTTTCAACAACCTTATATCTTTTCTCTCAAGTCTGTTGGCTTCATCTGGATT 2629
Db 14145 GATCGG-----CACTACCCGAAGTATGTCAAAAAGAGTGTCTATGAAGACGCTATTAC 14090
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Db 14029 GGTCTGTGTAAAGCAACAACCATGCAGAAATGAAGCCCGTCTGTCGCTGCC---GAACGCTGG 13973
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QY 2801 AACGAGACCGGCACATCGTGCTGATCATGTCGCCAGCTTTTCATCCCGAT 2860
Db 13912 TTTGCTGACGAGAACAGG-----ACTGTGMAATGCAGTTTAAAGTTTACACUTATA 13859
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QY 2981 ACGATAACCGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTGCAATTTCAACC-----AGT 3034
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QY 3095 CTTCTGATTTTCCGCTTTCCAGCGGTTT---GGCAGCAGACGCGGCTTCATTCTGCA 3151
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QY 3152 TGG---TTGTGCTTACAGACCGGAGATATTGACATCATATATATGCTTTGACAACTGATA 3208
Db 13558 CAGCCAGTCTCAGTCTGATACAGTAGAAAATACAGAAACTTTTATCAGCTTTAGTAAGTA 13499
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QY 3269 CTTCTGTTTGTATGACAGATGATTTTTCAGGACTATGACACTAGCGGTATATGAATAGGTAG 3328
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QY 3329 ATGTTTTTATTTTGCACAAAAAGAGGCTCGCACTCTTTTCTTTTCTTTTCTTTTAT 3388
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Db 13438 AAAATGTTCTTGATGCGAGATGATTTTCAGGACTATGACACATAGCTATATGAATAGGTAG 13379
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RESULT 9
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 28.7%; Score 1277.8; DB 15; Length 17476;
Best Local Similarity 62.4%; Pred. No. 4e-183;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;

Qy 21 CTCGACAGAGTTTGTACAAAAAGCTGAAACGAGAAACGTTAAATGATATATCAAT 80
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Db 16524 CCAATGTTCTTGGGTGATGCTGCCAACTTAGTCGACGACAGCCCTTCCAAATGTTCTT 16465
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Db 15045 TTTGTTATATTAGCATTTAGATTTATGTTTGTATACATTTAGATTTACTGTTTCTTATTAGTTTG 14986
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QY 1794 AAAAAATAAGATAAATAAATAAATAATTTTTTTATGATTAATAGTATTTATTAATAA 1853
Db 14925 ATTGGAATTTCTAACAAAAATATTTATTAACCTTTTAACTAAAAATATTTAGTAATCGGTATA 14866
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QY 2570 GATCGGATTTTCAACAACCTTTATCTTTTCTTACAAGTCTGTCGGCTTCACTCTGGATTT 2629
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Db 14029 GGTCTGTAAGCACAAACATGCAAGTGAAGCCGCTGTCTGCGTGC--GAACGCTGG 13973
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QY 2921 GGGGATCAACCATCGTCGCCCGCGGTGTCATAATAATCACTCTGTACATCCACAACAG 2980
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QY 2981 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTCAACC-----AGT 3034
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QY 3152 TGG---TTGTGCTTACCAGACCGGAGATATTTGACATCATATATGCTTTGACCAACTGATA 3208
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QY 1928 TGTAAATTTTCAATAAACAATAATTAATAACAAGCTAAAGTAAACAATAAATCAAAAC 1987
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QY 1988 TAATAGAAACAGTATCTAATGTTAAACAAACATATCTAATGCTAATATATAACAAAGCCCA 2047
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18401 GATTCCTTTGAAGTTGAGTATGGCGCTCGCTCTACCGAAAGTTTACGGGCGCAATTCAC 18460
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18641 TCCAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTCAATCTGC 18691

RESULT 7

US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 29.3%; Score 1305; DB 15; Length 17458;
Best Local Similarity 62.4%; Pred. No. 3.1e-187;
Matches 2308; Conservative 0; Mismatches 1325; Indels 68; Gaps 14;

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QY 2267 A ----- 2267
Db 16301 AGAGCTGCAGCTGGATGGCAAAATATGATTTTATTTTGTAGTGTAGCTGTTCTGTTG 16360
QY 2268 ----- CCACCTTTGTACAGAAAGCTGAACGA 2293
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QY 2294 GAAACGTAATAATGATTAATAATCAATTAATAATTAATTTAGATTTTGGATTAATAACAGACT 2353
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QY 2826 TCGGTGGTGCATCAGCGCCAGCTTTCATCCCGATATGCAACCGGTAAGTTTCACGG 2885
Db 16961 TCGGTGGTGCATCAGCGCCAGCTTTCATCCCGATATGCAACCGGTAAGTTTCACGG 17020
QY 2886 GAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGGGATCACCATCCGTCGCCCGGC 2945
Db 17021 GAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGGGATCACCATCCGTCGCCCGGC 17080
QY 2946 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 3005
Db 17081 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 17140
QY 3006 GTGTAAACCTTAAATCTGATTTCCAGCTTCCCTGTCGTCAGCAAAAGAGCGTTCAT 3065
Db 17141 GTGTAAACCTTAAATCTGATTTCCAGCTTCCCTGTCGTCAGCAAAAGAGCGTTCAT 17200
QY 3066 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGCC 3125
Db 17201 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGCC 17260
QY 3126 AGCGAGACGAGCGGCTTCACTCTGTATGCTGTGCTTACCAGACCGGAGATTTGACATC 3185
Db 17261 AGCGAGACGAGCGGCTTCACTCTGTATGCTGTGCTTACCAGACCGGAGATTTGACATC 17320
QY 3186 ATATATGCTTTCAGCAACTGATGCTGCTGCTCAACTGTCACGTGATTAATAGCTGCTTC 3245
Db 17321 ATATATGCTTTCAGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17380
QY 3246 ATAGCACACCTCTTTTTCACATCTTCTGTTCTTCAATGACATGATTTTCAGGACTATGA 3305
Db 17381 ATAGCACACCTCTTTTTCACATCTTCTGTTCTTCAATGACATGATTTTCAGGACTATGA 17440
QY 3306 CACTAGCGTATATGATAGTAGTAGTGTATTTTATTTTGTTCACAAAGAGCGCTCGCAC 3365
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QY 3366 CTCTTTTCTTATTTCTTTTATGATTTTAAATACGGCATTGAGGACAAATAGCGAGTAGGCT 3425
Db 17501 CTCTTTTCTTATTTCTTTTATGATTTTAAATACGGCATTGAGGACAAATAGCGAGTAGGCT 17560
QY 3426 GGATACGAGCTTCGGTTTGAAGAACATTTGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 3485
Db 17561 GGATACGAGCTTCGGTTTGAAGAACATTTGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 17620
QY 3486 GCATACCGGAGAACATTTGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3545
Db 17621 GCATACCGGAGAACATTTGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17680
QY 3546 AGTAGTTGATTCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3605
Db 17681 AGTAGTTGATTCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17740
QY 3606 TATGCAAAATCTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3665
Db 17741 TATGCAAAATCTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17800
QY 3666 TTTTGTACAAACTTG----- 3680

Db	13421	AGAAATAGAAAAAGAGGTGGAGCCTCTTTTGTGTGACAAATAAAAAATCACTACCT	13480	Db	14501	ATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTACAAAAGTTGGCATTAAGAAGCAT	14560
Qy	386	ATTCTATACGCTAGTGTCACTAGTCTGAAATCATCTGCAATCAGAACAAATTTCAAC	445	Qy	1449	-----	1448
Db	13481	ATTCTATACGCTAGTGTCACTAGTCTGAAATCATCTGCAATCAGAACAAATTTCAAC	13540	Db	14561	TGCTTATCAATTTGTTTGCACGAACAGGTCACTATCAGTCAAAATAAAATCAATTTATTC	14620
Qy	446	TCCTTATACCTTTCTCTTACAAGTGTCTGGCTTTCATCTGGATTTTTCAGCCTCTTAC	505	Qy	1449	-----TCTCGAGGAATTCGGTACC--AACTGTAAAGGAATAATTAATTTT	1490
Db	13541	TCTTATACCTTTCTCTTACAAGTGTCTGGCTTTCATCTGGATTTTTCAGCCTCTTAC	13600	Db	14621	CATCCAGCTGCAGCTCTCGAGGAATTCGGTACCCCAATTTGGTAAGGAATAATTTAT	14680
Qy	506	CTAAACGTGATAAAGTTCTGTAATTTCTGTAATTCGACCTGCGAGCTGGCTGTGTA	565	Qy	1491	CTTTTTCCTTTTCTTAAATAAATAGTTAAAGTGTAAATTTAGTATGATTAATAATAT	1550
Db	13601	CTAAACGTGATAAAGTTCTGTAATTTCTGTAATTCGACCTGCGAGCTGGCTGTGTA	13660	Db	14681	CTTTTTCCTTTTCTTAAATAAATAGTTAAAGTGTAAATTTAGTATGATTAATAATAT	14740
Qy	566	AGGAGCTGATCAATTTATATTCCTGATACACATCAGGTTAAATGCGCTTTTGTATG	625	Qy	1551	AGTTGTTTATATTCGTGAAAAAATAATTTAATAATATTTGTTTACATAAACAATAGTA	1610
Db	13661	AGGAGCTGATCAATTTATATTCCTGATACACATCAGGTTAAATGCGCTTTTGTATG	13720	Db	14741	AGTTGTTTATATTCGTGAAAAAATAATTTAATAATATTTGTTTACATAAACAATAGTA	14800
Qy	626	TGCGGTGCTGATGATCAGCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA	685	Qy	1611	ATGTAATAAATAATGACAGGTGATGTAAGACCAAGAGATAAAAGTTGAGAGTAAGTA	1670
Db	13721	TGCGGTGCTGATGATCAGCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA	13780	Db	14801	ATGTAATAAATAATGACAGGTGATGTAAGACCAAGAGATAAAAGTTGAGAGTAAGTA	14860
Qy	686	TGCGGTGCTGATGATGCGGCTTCTTCCCGATTAATGCAATGCAATGCAATGCAAT	745	Qy	1671	TATTTATTTTAAATGAAATTTGATCGAAATGTAAGATGATATACATGCAATTA	1722
Db	13781	TGCGGTGCTGATGATGCGGCTTCTTCCCGATTAATGCAATGCAATGCAATGCAAT	13840	Db	14861	TATTTATTTTAAATGAAATTTGATCGAAATGTAAGATGATATACATGCAATTA	14920
Qy	746	GAGACTTTATCTGACAGCAGAGTGACCTGGCCAGGGGATCACCATCGTCGCCGGGC	805	Qy	1723	-----	1722
Db	13841	GAGACTTTATCTGACAGCAGAGTGACCTGGCCAGGGGATCACCATCGTCGCCGGGC	13900	Db	14921	AACTTTCACCATATGAAATAAGATCACTACCGGCGTATTTTGTGATTAATCGAGATT	14980
Qy	806	GTGCTCAATATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG	865	Qy	1723	-----	1722
Db	13901	GTGCTCAATATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG	13960	Db	14981	TCAGGAGCTAAGGAAGCTTAAATGGAGAAAAAATCCTGGATATACCACCGTTGATATA	15040
Qy	866	GTGTAACCTTAACTGCAATTTACAGCTCCCTGTTCTGTCAGCAAAAGGCGCTTCAT	925	Qy	1723	-----	1722
Db	13961	GTGTAACCTTAACTGCAATTTACAGCTCCCTGTTCTGTCAGCAAAAGGCGCTTCAT	14020	Db	15041	TCCCAATGCGATCGTAAAGAACATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACTAT	15100
Qy	926	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC	985	Qy	1723	-----	1722
Db	14021	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC	14080	Db	15101	AACAGACCGTTTACGCTGGATATTAACGGCTTTTAAAGACCGTAAGAAAAAATAGCAC	15160
Qy	986	ACGACAGACGAGGCTTCAATTTGCAATGTTGCTTTACAGACCGGAGATATTGACATC	1045	Qy	1723	-----	1722
Db	14081	ACGACAGACGAGGCTTCAATTTGCAATGTTGCTTTACAGACCGGAGATATTGACATC	14140	Db	15161	AACTTTATCCGGCTTTTATTCACATTTCTTGCCCGCTGATGAATGCTCATCCGGAATTC	15220
Qy	1046	ATATATGCTTGGACCACTGATAGCTGCTGCTGCTCACTGATGATGATGATGATGAT	1105	Qy	1723	-----	1722
Db	14141	ATATATGCTTGGACCACTGATAGCTGCTGCTGCTCACTGATGATGATGATGATGAT	14200	Db	15221	CGTATGGCAATGAAAGACCGGTGAGCTGGTATATGGGATAGTGTTCACCCCTTTTACACC	15280
Qy	1106	ATAGCACACCTCTTTTTCATATCTTCCGGTAGTGGCGATCAACGCTCTCATTTTCGCCAA	1165	Qy	1723	-----	1722
Db	14201	ATAGCACACCTCTTTTTCATATCTTCCGGTAGTGGCGATCAACGCTCTCATTTTCGCCAA	14260	Db	15281	GTTTTTCATGAGCAAACTGAAACGTTTTCATCGCTCGAGTGAATACACACGATTTTC	15340
Qy	1166	AACTTGGCCAGGCTTCCCGGTATCAACAGGAGACACCGATTTTATTTCTGCGAAG	1225	Qy	1723	-----	1722
Db	14261	AACTTGGCCAGGCTTCCCGGTATCAACAGGAGACACCGATTTTATTTCTGCGAAG	14320	Db	15341	CGGAGTTTCTACACATATATTCGCAAGATGCGGTGTTCACGGTGAATAAATCCTGGCCTAT	15400
Qy	1226	TGATCTTCCGTCACAGGATTTTATTCGCGCAAGTGGCTGGGTGATGCTGCCAACTTA	1285	Qy	1723	-----	1722
Db	14321	TGATCTTCCGTCACAGGATTTTATTCGCGCAAGTGGCTGGGTGATGCTGCCAACTTA	14380	Db	15401	TTCCCTTAAAGGGTTTATTCAGAAATATGTTTTCGCTCTCAGCCAAATCCCTGGGTGATTTTC	15460
Qy	1286	GTCGACTACAGGTCACATAACCACTAAGTAGTTGATCATATGATGATGATGATGATGAT	1345	Qy	1723	-----	1722
Db	14381	GTCGACTACAGGTCACATAACCACTAAGTAGTTGATCATATGATGATGATGATGATGAT	14440	Db	15461	ACCAGTTTGAATTTAAACGTCGCAATATGAGCAAACTTCTTCCGCCCTGTTTTCACCATG	15520
Qy	1346	GTTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTATATATATGATTTT	1405	Qy	1723	-----	1722
Db	14441	GTTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTATATATATGATTTT	14500	Db	15521	GGCAATATATACGACGACGACGAGGTGCTGATCCGCTGGCGATTTCAGGTTTCATCAT	15580
Qy	1406	ATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTACAAAAGTG-----	1448	Qy	1723	-----	1722
				Db	15581	GCGCTCTGTGATGGCTTCCATGTCCGAGATGCTTAAATGAATTAACAAGTACTCGAT	15640


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QY 4038 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGCGGCTAGTATCTAC 4097
Db |||||
Db 17441 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGCGGCTAGTATCTAC 17500
QY 4098 GACACACCGAGCGCGGAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCCGCGG 4157
Db |||||
Db 17501 GACACACCGAGCGCGGAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCCGCGG 17560
QY 4158 CGCATGGGTGATGATTCCTTGAAGTTGAGTATGGCCGCTCCCTCTACGAAAGTTACGGG 4217
Db |||||
Db 17561 CGCATGGGTGATGATTCCTTGAAGTTGAGTATGGCCGCTCCCTCTACGAAAGTTACGGG 17620
QY 4218 CACCAATCAACCCGCTCCAGACGCGCGGCTAAACGACTTGTCTGCCCGCAGAAATAT 4277
Db |||||
Db 17621 CACCAATCAACCCGCTCCAGACGCGCGGCTAAACGACTTGTCTGCCCGCAGAAATAT 17680
QY 4278 GCAGCATTTTTTTGGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACCTTGACAGTGA 4337
Db |||||
Db 17681 GCAGCATTTTTTTGGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACCTTGACAGTGA 17740
QY 4338 CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGGGACAACTGTCGAGGCTCAGCAGG 4397
Db |||||
Db 17741 CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGGGACAACTGTCGAGGCTCAGCAGG 17800
QY 4398 ACCTGAGGATCGCAAGCTAGCTTACTAGTGTATGATGATCATATTCTATAGTGTCACTAAATCT 4457
Db |||||
Db 17801 ACCTGAGGATCGCAAGCTAGCTTACTAGTGTATGATGATCATATTCTATAGTGTCACTAAATCT 17860
QY 4458 GC 4459
Db ||
Db 17861 GC 17862
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RESULT 6
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector PHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17850)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13049)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13
Query Match 71.4%; Score 3182.2; DB 15; Length 18691;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 4406; Conservative 0; Mismatches 28; Indels 1137; Gaps 7;
QY 26 GACAAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTTAAATGATATAATATCAATATATT 85
Db |||||
Db 13121 GCCAACTTTGTACAAAAAAGCTGAAACGAGAAACGTTAAATGATATAATATCAATATATT 13180
QY 86 AAATTAGATTTTGCATAAAAAACAACACTACATAACTGTAAACACACACATATCCAGTC 145
Db |||||
Db 13181 AAATTAGATTTTGCATAAAAAACAACACTACATAACTGTAAACACACACATATCCAGTC 13240
QY 146 ACTATGATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACGAGCCTTCCAAA 205
Db |||||
Db 13241 ACTATGATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACGAGCCTTCCAAA 13300
QY 206 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAGCCTTCCAAATGTTCTCTCAA 265
Db |||||
Db 13301 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAGCCTTCCAAATGTTCTCTCAA 13360
QY 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATCCGCTATTAAATCATAAA 325
Db |||||
Db 13361 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATCCGCTATTAAATCATAAA 13420
QY 326 AGBAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 385
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Db	15221	CTAATAAACAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATCTCT	15280
Qy	2090	TATTAATTTCTAAATAATACCTGTAGTTGTTTATTAACCTCTAAATCGGATGACTATTAAT	2149
Db	15281	TATTAATTTCTAAATAATACCTGTAGTTGTTTATTAACCTCTAAATCGGATGACTATTAAT	15340
Qy	2150	AAATGAATTAGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTCTCATTTGTTAT	2209
Db	15341	AAATGAATTAGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTCTCATTTGTTAT	15400
Qy	2210	CATTGATCTTACATTTGGATTGATTACAGTTTACTTACCT-----TAAGCTTT	2255
Db	15401	CATTGATCTTACATTTGGATTGATTACAGTTTGGGAAGCTGGGTTCGAAATCGATAAGCTTT	15460
Qy	2256	GGATCCTCTAGA-----	2267
Db	15461	GGATCCTCTAGAGAGCTGCAGCTGGATGCAAAATATGATGTTTATTTTGACTGATAGTGA	15520
Qy	2268	-----CCATTTGTACAAGA	2282
Db	15521	CTGTTCGTGTCAAACAAATTTGTAAGCAATGCTTCTTATAATAGCCAACTTTGTACAAGA	15580
Qy	2283	AAGCTGAACGAGAAACGTAAAATGATATAAATCAATATATAATTAATAGATTTTGCATA	2342
Db	15581	AAGCTGAACGAGAAACGTAAAATGATATAAATCAATATATAATTAATAGATTTTGCATA	15640
Qy	2343	AAAAACAGACTACATAATTAAGTTAAACACACATATCCAGTCACATGAATCAACTACT	2402
Db	15641	AAAAACAGACTACATAATTAAGTTAAACACACATATCCAGTCACATGAATCAACTACT	15700
Qy	2403	TAGATGGTATTAGTCAGCTGTAGTGAAGTTGTCAGCATCACC CGACGCACTTTGCG	2462
Db	15701	TAGATGGTATTAGTCAGCTGTAGTGAAGTTGTCAGCATCACC CGACGCACTTTGCG	15760
Qy	2463	CGAATAAATACCTGTGACGGAAGTCACTTCGAGAAATAAATAAATCTGTTGTCCTTG	2522
Db	15761	CGAATAAATACCTGTGACGGAAGTCACTTCGAGAAATAAATAAATCTGTTGTCCTTG	15820
Qy	2523	TTGATACCGGGAAGCCCTGGGCCAACTTTGGCGAAATAGACGTTGATCGG	2575
Db	15821	TTGATACCGGGAAGCCCTGGGCCAACTTTGGCGAAATAGACGTTGATCGG	15880
Qy	2576	-ATTTTCAACAACCTTTATATCTTTTCTCTTCAAGTCGTTGGCTTCATCTGGATTTTCAGC	2634
Db	15881	CAATTCACAACCTTTATATCTTTTCTCTTCAAGTCGTTGGCTTCATCTGGATTTTCAGC	15940
Qy	2635	CTCTATACCTTAACAGGTGATTAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGACT	2694
Db	15941	CTCTATACCTTAACAGGTGATTAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGACT	16000
Qy	2695	GGCTGTGATTAAGGGAGCTTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTT	2754
Db	16001	GGCTGTGATTAAGGGAGCTTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTT	16060
Qy	2755	TGATGTCATTTTCGCGGTGCTGAGATCAGCCTTCTTCCCGATTAACCGAGACC GGCA	2814
Db	16061	TGATGTCATTTTCGCGGTGCTGAGATCAGCCTTCTTCCCGATTAACCGAGACC GGCA	16120
Qy	2815	CATCGCCCATATCGGTGGTTCATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGT	2874
Db	16121	CATCGCCCATATCGGTGGTTCATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGT	16180
Qy	2875	AAAGTTCAACGGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGCGGGATACCAATCC	2934
Db	16181	AAAGTTCAACGGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGCGGGATACCAATCC	16240
Qy	2935	GTGCGCGGGCGTGTCAATATATCATCTGTACATCCACAAACAGACGATAACGGCTCT	2994
Db	16241	GTGCGCGGGCGTGTCAATATATCATCTGTACATCCACAAACAGACGATAACGGCTCT	16300
Qy	2995	CTCTTTTATAGGTGTAACACCTTAAACTGCATTTTCCACAGTCCCTGTTCTCGCTAGCAAAA	3054

Query Match		90.6%;	Score 4042;	DB 15;	Length 17862;	
Best Local Similarity		93.2%;	Pred. No. 0;			
Matches 4419;		Conservative	0;	Mismatches 15;	Indels 308;	Gaps 6;
Qy	26	GACAAAGTTTGTACAAAAAGCTGACGAGAAACGTAATAATGATATAATATCAATATATT	85			
Db	13121	GCCAACTTTGTACAAAAAGCTGACGAGAAACGTAATAATGATATAATATCAATATATT	13180			
Qy	86	AAATTAGATTGTCATTAATAAACAGACTACATAATACCTGTAATAACACACACATATCCAGTC	145			
Db	13181	AAATTAGATTGTCATTAATAAACAGACTACATAATACCTGTAATAACACACACATATCCAGTC	13240			
Qy	146	ACTATGAATCAACTACTTTAGATGTTATTAGTACCTGTAGTCGACGAGCCCTTCCAAA	205			
Db	13241	ACTATGAATCAACTACTTTAGATGTTATTAGTACCTGTAGTCGACGAGCCCTTCCAAA	13300			
Qy	206	TGTTCTTCGGGTGATGCTGCCAACTTAGTGCACCGACAGCCCTTCCAAATGTTCTTCTCAA	265			
Db	13301	TGTTCTTCGGGTGATGCTGCCAACTTAGTGCACCGACAGCCCTTCCAAATGTTCTTCTCAA	13360			
Qy	266	ACGGAATCGTGTATCCAGCCCTACTCGCTATTGCTCCTCAATGCCGTATTAAATCATAAAA	325			
Db	13361	ACGGAATCGTGTATCCAGCCCTACTCGCTATTGCTCCTCAATGCCGTATTAAATCATAAAA	13420			
Qy	326	AGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAAATAAAAAATCACTACCT	385			
Db	13421	AGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAAATAAAAAATCACTACCT	13480			
Qy	386	ATTCATATACGCTAGTGTATAGTCTCAATCATCTGCATCAGACAAATTTTCAACAC	445			
Db	13481	ATTCATATACGCTAGTGTATAGTCTCAATCATCTGCATCAGACAAATTTTCAACAC	13540			
Qy	446	TCTTATACCTTTCTCTTACAAAGTCGTTGGCTTCTCATCTGGAATTTTTCAGCCCTCTATCTTA	505			
Db	13541	TCTTATACCTTTCTCTTACAAAGTCGTTGGCTTCTCATCTGGAATTTTTCAGCCCTCTATCTTA	13600			
Qy	506	CTAAACGTGATAAAGTTTCTGTAATTTCTATGTAATCGACCTGCGAGATGCGGTGATATA	565			
Db	13601	CTAAACGTGATAAAGTTTCTGTAATTTCTATGTAATCGACCTGCGAGATGCGGTGATATA	13660			
Qy	566	AGGGAGCCCTGACATTTATATCCCCAGACACATCAGTTTAATGGCGTTTGTGATGTCATTT	625			
Db	13661	AGGGAGCCCTGACATTTATATCCCCAGACACATCAGTTTAATGGCGTTTGTGATGTCATTT	13720			
Qy	626	TGCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCCAT	685			
Db	13721	TGCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCCAT	13780			
Qy	686	TGCGTGGTCATCATGCGCGAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG	745			
Db	13781	TGCGTGGTCATCATGCGCGAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG	13840			
Qy	746	GAGACTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCCGTCGCGCCGGC	805			
Db	13841	GAGACTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCCGTCGCGCCGGC	13900			
Qy	806	GTGTCAATAATATCACTCTGTATCCCAACACAGACGATACGGCTCTCTCTTTTATAG	865			
Db	13901	GTGTCAATAATATCACTCTGTATCCCAACACAGACGATACGGCTCTCTCTTTTATAG	13960			
Qy	866	GTGTAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAAGACCGGTTCTAT	925			
Db	13961	GTGTAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAAGACCGGTTCTAT	14020			
Qy	926	TTCAATAAACCCGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCGGC	985			
Db	14021	TTCAATAAACCCGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCGGC	14080			
Qy	986	ACGACAGACCGGCTTCAATTTCTGCAATGTTGTGCTTACCAGACCGGAGATATTGACATC	1045			
Db	14081	ACGACAGACCGGCTTCAATTTCTGCAATGTTGTGCTTACCAGACCGGAGATATTGACATC	14140			

Qy	1046	ATATATGCTTGAGCAACTGATAGCTGTCTGTCACACTGTCATGTAATAACGCTGCTTC	1105
Db	14141	ATATATGCTTGAGCAACTGATAGCTGTCTGTCACACTGTCATGTAATAACGCTGCTTC	14200
Qy	1106	ATAGCACACCTCTTTTGTACATATCTCGGTAGTGCAGATCAACGCTCTCATTTTGGCAA	1165
Db	14201	ATAGCACACCTCTTTTGTACATATCTCGGTAGTGCAGATCAACGCTCTCATTTTGGCAA	14260
Qy	1166	AAAGTTGGCCCGAGGCTTCCGGTATCAACAGGGACACAGGATTTATTTTCTGCGAAG	1225
Db	14261	AAAGTTGGCCCGAGGCTTCCGGTATCAACAGGGACACAGGATTTATTTTCTGCGAAG	14320
Qy	1226	TGATCTTCCGTCACAGGTATTTATTCGGCGAAAGTCGTCGGGTGATGTCGCCAATTA	1285
Db	14321	TGATCTTCCGTCACAGGTATTTATTCGGCGAAAGTCGTCGGGTGATGTCGCCAATTA	14380
Qy	1286	GTGCACTACAGGTACATTAATACCATCTAAAGTAGTTGATTCATAGTACTCGATATGTTGT	1345
Db	14381	GTGCACTACAGGTACATTAATACCATCTAAAGTAGTTGATTCATAGTACTCGATATGTTGT	14440
Qy	1346	GTTTTACAGTATTTATGTAGTCTGTTTATGCAAAATCTAAATTAATATATTCATATTT	1405
Db	14441	GTTTTACAGTATTTATGTAGTCTGTTTATGCAAAATCTAAATTAATATATTCATATTT	14500
Qy	1406	ATATCATTTTACGTTTCTGTTTACGCTTTCTTTGTACAAAGTGG-----	1448
Db	14501	ATATCATTTTACGTTTCTGTTTACGCTTTCTTTGTACAAAGTGG-----	14560
Qy	1449	-----	1448
Db	14561	TGCTTATCAATTTGTTGCAACGACAGCTCACTATCAGTCAAAATAAAATCATTTATTTGC	14620
Qy	1449	-----TCTCGAGGAATTCGGTACC-----AACTGTAAGGAAATAATATTTT	1489
Db	14621	CATCCAGCTGCGCTCTCGAGGAATTCGGTACCAGCTTGGTAAAGGAAATAATATTTT	14680
Qy	1490	TCCTTTTTCCTTTTACGATATAAAATAGTTAAGTGTGATGTTAATAGTATGATTAATAA	1549
Db	14681	TCCTTTTTCCTTTTACGATATAAAATAGTTAAGTGTGATGTTAATAGTATGATTAATAA	14740
Qy	1550	TAGTTGTTTATTAATTTGTAAGAAAAATAATTTATAAATAATCTTTTACATAAAACAATAGT	1609
Db	14741	TAGTTGTTTATTAATTTGTAAGAAAAATAATTTATAAATAATCTTTTACATAAAACAATAGT	14800
Qy	1610	AATGTAAAAAATAATGACAGTGTGTAAGACGAAAGATAAAAGTTGAGAGTAAAGT	1669
Db	14801	AATGTAAAAAATAATGACAGTGTGTAAGACGAAAGATAAAAGTTGAGAGTAAAGT	14860
Qy	1670	ATATTTATTTTAAATGATTTGATCGAACATGTAAGATGATATCTAGCATTAATATTTTGT	1729
Db	14861	ATATTTATTTTAAATGATTTGATCGAACATGTAAGATGATATCTAGCATTAATATTTTGT	14920
Qy	1730	TTTAAATCAATATAGTAAATTTCTAGCTGGTTTGAATGAAATTAATAATCAATGATAAATACTA	1789
Db	14921	TTTAAATCAATATAGTAAATTTCTAGCTGGTTTGAATGAAATTAATAATCAATGATAAATACTA	14980
Qy	1790	TAGTAAAAAATAAGATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATTTAT	1849
Db	14981	TAGTAAAAAATAAGATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATTTAT	15040
Qy	1850	ATAATTAATAATCTATACCATTTACTTAATATTTTATGTTTAAAGGTTAATAATAATTTTGT	1909
Db	15041	ATAATTAATAATCTATACCATTTACTTAATATTTTATGTTTAAAGGTTAATAATAATTTTGT	15100
Qy	1910	TAGAAATTTCCAAATCTGCTTGTAAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAG	1969
Db	15101	TAGAAATTTCCAAATCTGCTTGTAAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAG	15160
Qy	1970	TAACAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATTAATCTAATG	2029
Db	15161	TAACAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATTAATCTAATG	15220
Qy	2030	CTAATATTAACAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCT	2089

15980 AAGTTTCGTAAATTTCTACTGTATCGACCTGCGACTGGGTGTGTAAGAGGAGCGTAC 15939
 2718 ATTATATATCCCGAAGACATCAGGTAAATGGCGTTTTTGTATGTCATTTTTTGGCGTGGCTG 2777
 15940 ATTATATATCCCGAAGACATCAGGTAAATGGCGTTTTTGTATGTCATTTTTTGGCGTGGCTG 15999
 2778 AGATCAGCAGCTTCTTCCCGGATTAACGAGACCGGCACACTGGCCATATCGGTGGTCAATC 2837
 16000 AGATCAGCAGCTTCTTCCCGGATTAACGAGACCGGCACACTGGCCATATCGGTGGTCAATC 16059
 2838 ATGCGCCAGCTTTTCAATCCCGGATTAACGAGACCGGCACACTGGCCATATCGGTGGTCAATC 2897
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 16120 GACAGCAGCTGCACTGGCGGAGGATCAACATCGGTCCCGGGCGTGTCAATAATA 16179
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 16300 GCGACCTCAGCAGCTTCTCTGATTTTCCGCTTCCAGGTTCCGCGACGACGACG 16359
 3138 GCGCTTCATTCGATGGTGTGTTTACGAGACCGGAGATATGACATCATATATGCTTGT 3197
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 16420 AGCACTGATAGCTCGCTGTCACAGTGTCACTGTAATACGCTGCTTCATGACACCTC 16479
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 3498 GAACTTTGGAAGGCTCGGTGCACTAAGTTGCACTAATACCTAAGTGTGATTC 3557
 16720 GAACTTTGGAAGGCTCGGTGCACTAAGTTGCACTAATACCTAAGTGTGATTC 16779
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 3618 AATTTAATATATGAT 3677
 16840 AATTTAATATATGAT 16899
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 16900 TTGCTAGAGTCTGCTTATATGATATATGAGATATGCGAGAGCTTATGATGATGATGATGAT 16959
 3738 TTCAATTTCTGTCAGCTGTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 3797

16960 TTCAATTTCTGTTGTGCACTGTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 17019
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 17020 CGGTTTCGGTTTCATTTCTAATGAATATATCAACCGTTTACTATCGTATTTTATGAATTAATA 17079
 3858 TTCTCGGTTCAATTTACTGATTTGTACCTACTACTACTACTACTACTACTACTACTACTACTACT 3917
 17080 TTCTCGGTTCAATTTACTGATTTGTACCTACTACTACTACTACTACTACTACTACTACTACTACT 17139
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 17140 CAATATATTTGCTGATAGTTTATAGGACATCTATGATAGAGCGCCACATAACAA 17199
 3978 CAATTCGGTTTATTTATTAACAAATTTTAAAAAGCGGCGAGAACCGGTCAACCT 4037
 17200 CAATTCGGTTTATTTATTAACAAATTTTAAAAAGCGGCGAGAACCGGTCAACCT 17259
 4038 AAAAGACTGATTAACATAAATCTTTTCAAAATTTTCAAAAGSCCCAGGGCTAGTATCTAC 4097
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 17320 GACACACCGAGCGCGAACTAATAACGTTTCACTGAGGGAACCTCCGTTTCCCGCCGCGC 17379
 4158 CGATGCGGTGAGATTCCTTGAAGTTGATGATTTGGCGCTCGCTTACCGAAAGTTACGGG 4217
 17380 CGATGCGGTGAGATTCCTTGAAGTTGATGATTTGGCGCTCGCTTACCGAAAGTTACGGG 17439
 4218 CACCAATTCACCGGTCCAGCAGCGCGCGGTAAACCGACTTGTCTCCCGCGAGAAATAT 4277
 17440 CACCAATTCACCGGTCCAGCAGCGCGCGGTAAACCGACTTGTCTCCCGCGAGAAATAT 17499
 4278 GCAGCATTTTGTGTTGTATGTTGGGCCCCAAATGAAGTGCAGGTCAAACTTGAAGTGA 4337
 17500 GCAGCATTTTGTGTTGTATGTTGGGCCCCAAATGAAGTGCAGGTCAAACTTGAAGTGA 17559
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 4398 ACCTGCGAGGATCAAGCTAGCTTACTAGTGTATGATCATATTTCTATAGTGTCACTTAAATCT 4457
 17620 ACCTGCGAGGATCAAGCTAGCTTACTAGTGTATGATCATATTTCTATAGTGTCACTTAAATCT 17679
 4458 GC 4459
 17680 GC 17681

RESULT 5
 US-10-055-001A-23
 ; Sequence 23, Application US/10055001A
 ; Publication No. US20030049835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wesley, Susan V.
 ; APPLICANT: Waterhouse, Peter
 ; APPLICANT: Hellwell, Christopher A.
 ; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
 ; FILE REFERENCE: HELIGA
 ; CURRENT APPLICATION NUMBER: US/10/055,001A
 ; CURRENT FILING DATE: 2002-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 17862
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: acceptor vector pHELLSGATE4
 US-10-055-001A-23

QY	721	ATGCA	CCACGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG	780
Db	13720	ATGCAC	CAACGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG	13779
QY	781	GGGGAT	CACCATCCGTCGCGCCCGGGGGTGTCAATAATATACACTCTGTACATCCACAAACAG	840
Db	13780	GGGGAT	CACTCCGTCGCGCCCGGGGGTGTCAATAATATACACTCTGTACATCCACAAACAG	13839
QY	841	ACGATA	ACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTCACAGTCCCTGT	900
Db	13840	ACGATA	ACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTCACAGTCCCTGT	13899
QY	901	TCTCGT	CAGCAAAAGACGGTTCATTTCAATAAACGGGGCAGCCTCAGCCATCCCTTCCT	960
Db	13900	TCTCGT	CAGCAAAAGACGGTTCATTTCAATAAACGGGGCAGCCTCAGCCATCCCTTCCT	13959
QY	961	GATTTT	CCGCTTTCACGCGTTCGGCACGACGACGGGCTTCATTTGCAATGTTGTGC	1020
Db	13960	GATTTT	CCGCTTTCACGCGTTCGGCACGACGACGGGCTTCATTTGCAATGTTGTGC	14019
QY	1021	TTACCA	GACGGAGATTTGACATCATATATGCTTGGACCACTGATAGCTGTGCTGTGC	1080
Db	14020	TTACCA	GACGGAGATTTGACATCATATATGCTTGGACCACTGATAGCTGTGCTGTGC	14079
QY	1081	AACTGT	CACGTAAATACGCTGCTTCATAGCACACCTCTTTTGCACATACTTCGGGTAGTG	1140
Db	14080	AACTGT	CACGTAAATACGCTGCTTCATAGCACACCTCTTTTGCACATACTTCGGGTAGTG	14139
QY	1141	CGGAT	CAACGTCTCATTTTGGCCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC	1200
Db	14140	CGGAT	CAACGTCTCATTTTGGCCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC	14199
QY	1201	ACCAGA	TATTTATTTCTGCGAAGTGATCTTCCTGTCAAGGTATTTATTCGGCGCAAG	1260
Db	14200	ACCAGA	TATTTATTTCTGCGAAGTGATCTTCCTGTCAAGGTATTTATTCGGCGCAAG	14259
QY	1261	TGCGT	CGGTGATGTGTCGCACTTAGTCGACTACAGGTCACTAATACCATTAAAGTAGTT	1320
Db	14260	TGCGT	CGGTGATGTGTCGCACTTAGTCGACTACAGGTCACTAATACCATTAAAGTAGTT	14319
QY	1321	GATTC	ATAGTGATGTTGTTTTTACAGTATATGTAGTCGCTGTTTTTTTATGCAA	1380
Db	14320	GATTC	ATAGTGATGTTGTTTTTACAGTATATGTAGTCGCTGTTTTTTTATGCAA	14379
QY	1381	AAFTCA	TAAATATATGATATTTATATFCAATTTACGTTTCTCGTTCCAGCTTCTTGTA	1440
Db	14380	AAFTCA	TAAATATATGATATTTATATFCAATTTACGTTTCTCGTTCCAGCTTCTTGTA	14439
QY	1441	CAAAGT	GGTCTCGAGAAATTCGGTACCAAC---TGTAAGGAATAATATTTCTTTTT	1496
Db	14440	CAAAGT	GGTCTCGAGAAATTCGGTACCCACGCTCGTAAGGAATAATATTTCTTTTT	14499
QY	1497	TCCTTT	TAGTATAAAATAGTTAAGTGATGTTAAATAGTATGATATAATAATATAGTTGT	1556
Db	14500	TCCTTT	TAGTATAAAATAGTTAAGTGATGTTAAATAGTATGATATAATAATATAGTTGT	14559
QY	1557	TATAAT	TGTGAAAAATAATTTATAATATATGTTTACATAAACAAACATAGTAATGTAA	1616
Db	14560	TATAAT	TGTGAAAAATAATTTATAATATATGTTTACATAAACAAACATAGTAATGTAA	14619
QY	1617	AAAAAT	GACAGTGATGTGTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGTATATTTAT	1676
Db	14620	AAAAAT	GACAGTGATGTGTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGTATATTTAT	14679
QY	1677	TTTTTA	TGAAATTTGATCGAACATGTAAAGATATATCTAGCATTAATATTTGTTTTAATC	1736
Db	14680	TTTTTA	TGAAATTTGATCGAACATGTAAAGATATATCTAGCATTAATATTTGTTTTAATC	14739
QY	1737	ATAAT	AGTAATCTAGCTGTTTTGATGAATTAATAATCAATGATAAAATACCTAGTAAA	1796
Db	14740	ATAAT	AGTAATCTAGCTGTTTTGATGAATTAATAATCAATGATAAAATACCTAGTAAA	14799

QY	1797	AATTAAGAAATAAATAAATAAATAAATATTTTTTTATGATTAATAGTTTATTAATAATAATA	1856
Db	14800	AATTAAGAAATAAATAAATAAATAAATAAATTTTTTTATGATAAATAAGTTTATTAATAATAATA	14859
QY	1857	AATATCTATACCAATCTACAAATATTTTTAGTTTAAAAAGTTAAATAAATATTTCTGTAGAAT	1916
Db	14860	AATATCTATACCAATCTACAAATATTTTTAGTTTAAAAAGTTTAAATAAATTTTTCTGTAGAAT	14919
QY	1917	TCCAATCTGCTTGTAATTTTATCAATAAACAATAATTTAAATAACAAGCTTAAAGTAAACAAA	1976
Db	14920	TCCAATCTGCTTGTAATTTTATCAATAAACAATAATTTAAATAACAAGCTTAAAGTAAACAAA	14979
QY	1977	TAATATCAAACTAATAGAAAACAGTAATCTAAATGCTAACAAAAACATATCTAAATCTAATAT	2036
Db	14980	TAATATCAAACTAATAGAAAACAGTAATCTAAATGCTAACAAAAACATATCTAATGCTAATAT	15039
QY	2037	AACAAAGCGAAGATCTATCATTTTTATATAGTATTAATTTTCAATCAACATCTTTATTAAT	2096
Db	15040	AACAAAGCGAAGATCTATCATTTTTATATAGTATTAATTTTCAATCAACATCTTTATTAAT	15099
QY	2097	TTCTAAATATATCTGCTAGTTTTTAACTCTCTAAATGAGATGACATTAATAATTAATGAA	2156
Db	15100	TTCTAAATATATCTGCTAGTTTTTAACTCTCTAAATGAGATGACATTAATAATTAATGAA	15159
QY	2157	TTAGTCCAAATGAATAAATAACAAGGTAAACATGATAGATCATGTCAATTCGTTTCAATTCAT	2216
Db	15160	TTAGTCCAAATGAATAAATAACAAGGTAAACATGATAGATCATGTCAATTCGTTTCAATTCAT	15219
QY	2217	CTTACATTTGGATTTGATTAAGTTTACAGTTTACCTT-----	2248
Db	15220	CTTACATTTGGATTTGATTAAGTTTACAGTTTGGGAAGCTGGGTTCGAAATCGATAGCTTGGCTGC	15279
QY	2249	-----	2248
Db	15280	AGTTATCATCATCATATAGACACACAGAAATAAAGTAAATCAGATTATCAGTTAAAGCTAT	15339
QY	2249	-----	2248
Db	15340	GTAATATTTGGCCTAATACCAATCAATTTAAAAAATAGATCAGTTTAAAGAAAGATCAAAG	15399
QY	2249	-----	2248
Db	15400	CTCAAAAAATAAAGAGAAAAAGGTCTCTAACCAAGAAAAATGAAGAGAGAAAACTAGAA	15459
QY	2249	-----	2248
Db	15460	ATTACCTGCACAAAGCTTGGATCCTCTAGACCACCTTTGACAAAGAAAGCTGAACGAGAAA	15519
QY	2298	CGTAAATGATTAATATCAATATATTAATTTAGATTTTGCATATAAANAACAGACTCAT	2357
Db	15520	CGTAAATGATTAATATCAATATATTAATTTAGATTTTGCATATAAANAACAGACTCAT	15579
QY	2358	AATACTGTAAAAACAACATATCCAGTCACTATGAACTCAACTACTTAGATGCTATTAGTG	2417
Db	15580	AATACTGTAAAAACAACATATCCAGTCACTATGAACTCAACTACTTAGATGCTATTAGTG	15639
QY	2418	ACCTGTAGTGCATTAAGTTGGAGATCATCCCGACGCACTTTTGGCCGCGAATAAATACCTG	2477
Db	15640	ACCTGTAGTGCATTAAGTTGGAGATCATCCCGACGCACTTTTGGCCGCGAATAAATACCTG	15699
QY	2478	TGACGGAAGATCACTTCGACAGATAATAAATCCTGCTGCTCTGTTGATACCGGAAGC	2537
Db	15700	TGACGGAAGATCACTTCGACAGATAATAAATCCTGCTGCTCTGTTGATACCGGAAGC	15759
QY	2538	CCTGGGCCAATTTTGGCGAAAAATGAGACGTTGATCGGATTTTCAAACTCTTTATCTTTT	2597
Db	15760	CCTGGGCCAATTTTGGCGAAAAATGAGACGTTGATCGGATTTTCAAACTCTTTATCTTTT	15819
QY	2598	CTCTTACAAGTCGTTGGCTTTCATCTTGGATTTTTCAGCCTCTATCTTACTTAAACGCTGATA	2657
Db	15820	CTCTTACAAGTCGTTGGCTTTCATCTTGGATTTTTCAGCCTCTATCTTACTTAAACGCTGATA	15879
QY	2658	AAGTTTCTGTAATTTTCTACTGTATCGACCTGCAGACTGCGCTGTGTATAGGAGGCTGCAC	2717

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Db 16420 TTGAGGACAAATAGCGAGTAGGCTGATACGACGATTCGTTTGAGAGAAACATTTGGAG 16479
QY 3463 GCTGTCGGTCGACTAAGTTGGCAGCATCACCGAAGAACATTTGGAAGCGTCTGGTGA 3522
Db 16480 GCTGTCGGTCGACTAAGTTGGCAGCATCACCGAAGAACATTTGGAAGCGTCTGGTGA 16539
QY 3523 CTACAGGTCACATAACCACTAAGTAGTGTGATTCATAGTGAAGTATGATGTTGTTT 3582
Db 16540 CTACAGGTCACATAACCACTAAGTAGTGTGATTCATAGTGAAGTATGATGTTT 16599
QY 3583 ACAGTATATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATATGATTAATC 3642
Db 16600 ACAGTATATAGTAGTCTGTTTTTATGCAAAATCTAAATTAATATATATGATTAATC 16659
QY 3643 AATTTACGTTTCTCGTTACGCTTTTGTACAACTTGTCTAGAGTCTCGCTTTAATGAG 3702
Db 16660 AATTTACGTTTCTCGTTACGCTTTTGTACAACTTGTCTAGAGTCTCGCTTTAATGAG 16719
QY 3703 ATATGCGAGACGCTATGATCGCATGATTTGCTTTCAATTCCTGTTGTCACGTTGTA 3762
Db 16720 ATATGCGAGACGCTATGATCGCATGATTTGCTTTCAATTCCTGTTGTCACGTTGTA 16779
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QY 3823 TATCACCGTTACTATCTGATTTTATGAATATATTTCCGTTCAATTTACTGATTTGA 3882
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Db 16900 CCTACTACTATATGATACAAATATAAATGAAAAAATAATATGCTGCTGAATAGTTTA 16959
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Db 16960 TAGCGACATCTATGATAGAGCGCCACAAATACAAACAAATGCGTTTATATACAAATC 17019
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QY 4063 TCAATTTTAAAAAGGCGGAGAACCGGCTCAAACTTAAAAAGCTGATTAACATAAATCTTAT 4122
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Db 17440 CTAGTGTGCAATTTCTATAGTGTACCTAATCTGC 17476
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US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26
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Query Match 94.2%; Score 4200; DB 15; Length 17681;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;

QY 1 TTTTCATTTGGAGAGACACGCTCGAGACAAAGTTTGTACAAAAAGCTGAAACGAGAAACGTT 60
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QY 241 ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGCTGATCGCTGATCGCTCAACTAGTCGCTATTGTC 300
Db 13240 ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGCTGATCGCTGATCGCTCAACTAGTCGCTATTGTC 13299
QY 301 CTCAATGCGGTATTAATCATAAAAAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTTTTTG 360
Db 13300 CTCAATGCGGTATTAATCATAAAAAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTTTTTG 13359
QY 361 TGTGACAAATTAACATCTACCTATTTCATATACGCTAGTGTCTAGTCTCCTGAAATCA 420
Db 13360 TGTGACAAATTAACATCTACCTATTTCATATACGCTAGTGTCTAGTCTCCTGAAATCA 13419
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QY 481 TCTGGATTTTCAGCCTCTATATCTTAAACGTAATAAGTTTCTGTAATTTCTACTGTA 540
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
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		Match	Length							
1	4459	100.0	17458	15	US-10-055-001A-25		Sequence 25,	Appl		
2	4406.6	98.8	17476	15	US-10-055-001A-24		Sequence 24,	Appl		
3	4406.6	98.8	17476	15	US-10-385-546-7		Sequence 7,	Appl		
4	4200	94.2	17681	15	US-10-055-001A-26		Sequence 26,	Appl		
5	4042	90.6	17862	15	US-10-055-001A-23		Sequence 23,	Appl		
C	3182.2	71.4	18691	15	US-10-055-001A-13		Sequence 13,	Appl		
	7	1305	29.3	17458	15	US-10-055-001A-25		Sequence 25,	Appl	
C	8	1277.8	28.7	17476	15	US-10-055-001A-24		Sequence 24,	Appl	
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C	10	1108.8	24.9	4470	15	US-10-151-690-21		Sequence 21,	Appl	
	11	1108.8	24.9	4892	16	US-10-357-268-1		Sequence 1,	Appl	
C	12	1108.8	24.9	5584	15	US-10-151-690-61		Sequence 61,	Appl	
13	1102.4	24.7	4428	15	US-10-151-690-62		Sequence 62,	Appl		
14	1102.4	24.7	4627	15	US-10-151-690-63		Sequence 63,	Appl		

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C	18	769	17.2	786	15	US-10-385-521-9	Sequence 9, Appl
	19	737	16.5	3002	15	US-10-353-454-57	Sequence 57, Appl
C	20	736	16.5	2116	12	US-10-644-335-3	Sequence 3, Appl
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C	35	597	13.4	10463	16	US-10-389-120-1	Sequence 1, Appl
C	36	597	13.4	12789	13	US-10-666-778-9	Sequence 9, Appl
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C	44	400.4	9.0	4627	15	US-10-151-690-64	Sequence 64, Appl
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ALIGNMENTS

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; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
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Job time : 195.557 secs

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; SOFTWARE: FastSEQ Version 1.5
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; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
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; OTHER INFORMATION:
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; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMA10.001CP1
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; CURRENT APPLICATION NUMBER: US/09/225,152A
; CURRENT FILING DATE: 1998-01-04
; PRIOR APPLICATION NUMBER: 08/379614
; PRIOR FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(378)
; OTHER INFORMATION: ccdB gene of pKIL 18.
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; US-09-225-152A-2
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Best Local Similarity 99.7%; Pred. No. 7.9e-59;
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; Patent No. 5910438
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; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
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; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-108;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3689 CCTGCTTTAATGAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTCAATTCGT 3748
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Db 14094 TATTATTACAAATCCAAATTTTAAAAAGCGGACGAGTCTGAT 14035
QY 4049 TACATAAATCTTATTCAAATTTTAAAAAGCGGACGAGTCTGAT 4108
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QY 4169 GATTCCTTGAAGTTGAGTATTTGGCGTCTTACCGAAAGTTTACGGGACCAATTCAC 4228
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US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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US-08-673-768-1			
; Sequence 1, Application US/08673768			
; Patent No. 5952546			
; GENERAL INFORMATION:			
; APPLICANT: Bedbrook, John R.			
; APPLICANT: Dunsmuir, Pamela			
; APPLICANT: Howie, William J.			
; APPLICANT: Joe, Lawrence K.			
; APPLICANT: Lee, Kathleen Y.			
; TITLE OF INVENTION: Delayed Ripening Tomato Plants			
; NUMBER OF SEQUENCES: 1			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/673,768			
; FILING DATE: 27-JUN-1996			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/000,721			
; FILING DATE: 30-JUN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bastian, Kevin L.			
; REGISTRATION NUMBER: 34,774			
; REFERENCE/DOCKET NUMBER: 012176-005010US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 576-0200			
; TELEFAX: (415) 576-0300			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 15397 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA			
US-08-673-768-1			
Query Match 12.7%; Score 566.4; DB 2; Length 15397;			
Best Local Similarity 99.8%; Pred. No. 1.8e-108;			
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Db	12001	CGGTCCAGCACGGCGCGGGTAAACGACTTGCTGCCCGAGAAATATACGACATTTTTT	11942
QY	4290	TGGTGTATGTGGGCCCCCAATGAAGTCGAGTCAAACTTGACAGTGACGACAAATTCGTT	4349
Db	11941	TGGTGTATGTGGGCCCCCAATGAAGTCGAGTCAAACTTGACAGTGACGACAAATTCGTT	11862
QY	4350	GGCGGGGTCCAGGGCGGAATTTTCGACACACATGTCAGGCTCAGCAG	4396
Db	11881	GGCGGGGTCCAGGGCGGAATTTTCGACACACATGTCAGGCTCAGCAG	11835
RESULT 11			
US-08-673-768-1			
; Sequence 1, Application US/08673768			
; Patent No. 5952546			
; GENERAL INFORMATION:			
; APPLICANT: Bedbrook, John R.			
; APPLICANT: Dunsmuir, Pamela			
; APPLICANT: Howie, William J.			
; APPLICANT: Joe, Lawrence K.			
; APPLICANT: Lee, Kathleen Y.			
; TITLE OF INVENTION: Delayed Ripening Tomato Plants			
; NUMBER OF SEQUENCES: 1			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/673,768			
; FILING DATE: 27-JUN-1996			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/000,721			
; FILING DATE: 30-JUN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bastian, Kevin L.			
; REGISTRATION NUMBER: 34,774			
; REFERENCE/DOCKET NUMBER: 012176-005010US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 576-0200			
; TELEFAX: (415) 576-0300			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 15397 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA			
US-08-673-768-1			
Query Match 12.7%; Score 566.4; DB 2; Length 15397;			
Best Local Similarity 99.8%; Pred. No. 1.8e-108;			
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	3689	CTGCTTTTAATGAGATATGCGAGACGCGCTATGCGATGATATTCGTTCAATTCGTT	3748
Db	7110	CTGCTTTTAATGAGATATGCGAGACGCGCTATGCGATGATATTCGTTCAATTCGTT	7169
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NAME/KEY: - 2441..3256
LOCATION: 2441..3256
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NAME/KEY: - 3257..4315
LOCATION: 3257..4315
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OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: - 4316..6555
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
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US-09-025-583-2
Query Match 15.9%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3689 CTTGCTTTAATGAGATATGCGAGACGCTATGATGCGCATGATATTTGCTTTCAATTCGT 3748
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Qy 4289 TTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTCAACAGTACGACAAATCGT 4348
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RESULT 9

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US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3
Query Match 15.9%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 2.5e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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/ OTHER INFORMATION: /label= 3'ocs
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA octopine synthase gene"
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/ NAME/KEY: -
/ LOCATION: 4316...6555
/ OTHER INFORMATION: /label= pUC18
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US-08-351-413-2

Query Match 15.9%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3689 CTTGCTTTTATGAGATATGGAGACCGCTATGATCGCATGATATTTGCTTCAATTCCT 3748
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QY 3749 TGTGCACTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3808
DB 3489 TGTGCACTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3548
QY 3809 CATTCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 3868
DB 3549 CATTCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 3608
QY 3869 ATTACTGATTTGACCTTACTTATCTATGATATTAATTAATTAATTAATTAATTTGT 3928
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US-09-025-583-2

; Sequence 2, Application US/09025583

; Patent No. 597433

; GENERAL INFORMATION:

; APPLICANT: Williams, Mark

; APPLICANT: Leemans, Jan

; TITLE OF INVENTION: Maintenance of male-sterile plants

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/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
/ STREET: 8110 Gatehouse Road, Suite 500 East
/ CITY: Falls Church
/ STATE: Virginia
/ COUNTRY: U.S.A.
/ ZIP: 2046
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025.583
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/351.413
/ FILING DATE:
/ APPLICATION NUMBER: US 07/899,072
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/970,849
/ FILING DATE: 03-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svensson, Leonard R.
/ REGISTRATION NUMBER: 30,330
/ REFERENCE/DOCKET NUMBER: 2121-102PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6555 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: plasmid pVE144 (replicable in E.coli)
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Best Local Similarity 99.7%; Pred. No. 1.9e-138;
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RESULT 7
US-08-351-413-2
; Sequence 2, Application US/08351413
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; City: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
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; OTHER INFORMATION: /label= NPRTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
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; US-08-475-975-1
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; Query Match 15.9%; Score 709.8; DB 3; Length 5399;
; Best Local Similarity 99.7%; Pred. No. 1.9e-138;
; Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; QY 3689 CCTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATTTGCTTCAATTCGT 3748
; DB |||||
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; DB |||||
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; QY 2333 TGTGACGCTGTGTAACAACTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 2392
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; QY 3809 CATTCATGAATATATACCGGTTACTATGCTATTTTATGAATAATATTCCTCGTTCA 3868
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; QY 2393 CATTCATGAATATATACCGGTTACTATGCTATTTTATGAATAATATTCCTCGTTCA 2452
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; QY 3869 ATTTACTGATTCCTACTACTTATGTAACAATATTAATGAAAAACAATATTTGT 3928
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; QY 4109 CGGCGAATTAATACGTTCACTGAGGAACTTCGGTTCCCGCGCGCGGATCGGTGA 4168
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; US-09-084-889-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALUIN, Kathleen
; APPLICANT: Gobel, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDB108
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; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
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; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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; OTHER INFORMATION: /label= NPRTII
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; OTHER INFORMATION: phosphotransferase gene"
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; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; NAME/KEY: -
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OTHER INFORMATION:	/label= pUC18
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Query Match	15.9%; Score 709.8; DB 1; Length 5399;
Best local Similarity	99.7%; Pred. No. 1.9e-138; Indels 0; Gaps 0;
Matches 711; Conservative 0; Mismatches 2;	
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QY	3749 TGTGACGTTGTAAAAACCTGAGCATGTGTAGCTGATCCTTACCGCGGTTTCGGTT 3808
DB	2333 TGTGACGTTGTAAAAACCTGAGCATGTGTAGCTGATCCTTACCGCGGTTTCGGTT 2392
QY	3809 CATTTCAATGAATATATACACCGTTACTATCGTATTTTATGAATATATTCCTCGGTCA 3868
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DB	2453 ATTACTGATGTACCTTACTATCTTATATGTACATATTAATAATGAAAAAATATATGT 2512
QY	3929 GCTCAATAGGTTTATAGCGCATCTATGATAGAGCGGCACAAATAACAAACAAATTCGCTTT 3988
DB	2513 GCTCAATAGGTTTATAGCGCATCTATGATAGAGCGGCACAAATAACAAACAAATTCGCTTT 2572
QY	3989 TATTATTACAAATCCAAATTTTAAAAAAGCGGCGAAGCCGGTCAAACTTAAAGACTGAT 4048
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DB	2633 TACATTAATCTTATTCAAAATTTTCAAAAGGCCCGGCTAGTATCTACGACACACCGAG 2692
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; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
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; OTHER INFORMATION: Cauliflower mosaic virus isolate Cabb8-J1"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1285..2100
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycinase"
; OTHER INFORMATION: phosphotransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; US-08-064-121-1
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; Query Match 15.9%; Score 709.8; DB 1; Length 5399;
; Best Local Similarity 99.7%; Pred. No. 1.9e-138;
; Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 3689 CTGCTTTTATGATGATGCGAGCGCTATGATGCGATGATTTGCTTTCAATTCGT 3748
Db 2273 CTGCTTTTATGATGATGCGAGCGCTATGATGCGATGATTTGCTTTCAATTCGT 2332
QY 3749 TGTGCGAGTTGTAATAAACTGAGCATGCTAGCTAGATCCTTACGCGGTTTCGGTT 3808
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QY 3809 CATTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATATATTCCTCGTTCA 3868
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QY 3869 ATTTACTGATGTACCTACTATCTATGATGATGATGATGATGATGATGATGATGATGAT 3928
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RESULT 4

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US-08-478-015-1
; Sequence 1, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,015
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451

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QY 4169 GATTCCTTTGAAGTTGAGTATTGGCCGTCCTACCGAAAGTTACCGGCGACCAATCAAC 4228
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QY 4229 CCGGTCCAGCACGCGCGCGGTTAACCGACTTGTGCGCCGAGAAATATGCGACATTTT 4288
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QY 4289 TTGGTGTATGTGGGCCCCCAATGAATGCGAGTCAAAACCTTTGACAGTACGACAAATCGT 4348
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STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
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 ORGANISM: plasmid DNA designated as pJD884
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 NAME/KEY: CDS
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 OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884 gene
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1877..2110 /note= "3' regulatory sequence
 OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
 OTHER INFORMATION: T-DNA gene 7."
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 NAME/KEY: misc_feature
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 LOCATION: 5684..6541 /note= "Sequence complementary to
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 Patent No. 5952547
 OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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 LOCATION: 7155..7639 /note= "Trl' and Tr2' promoter
 OTHER INFORMATION: derived from Agrobacterium T-DNA."
 OTHER INFORMATION:

US-08-232-016-22

Query Match 16.3%; Score 728.8; DB 2; Length 7639;
 Best Local Similarity 99.7%; Pred. No. 2.3e-142;
 Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 3740 CAATTCGTTGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3799
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 3800 GTTTCGGTTTCATTCTAATGAATATATACCGGTTTACTATCGTATTTTATGAATAATTT 3859
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 3980 ATTGCGTTTATTTATTAACAAATCAATTTTAAAAAAGCGGACGAAACCGGTCAAACTAA 4039
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QY 4040 AAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAGCA 4099
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 ; Sequence 1, Application US/08064121
 ; Patent No. 5641664
 ; GENERAL INFORMATION:
 ; APPLICANT: D'HALLUIN, Kathleen
 ; APPLICANT: GOBEL, Elke
 ; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
 ; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: George Mason Bldg., Washington & Prince Sts.
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/064,121
 ; FILING DATE: 24-MAY-1993
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90403332.1
 ; FILING DATE: 23-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 91401888.2
 ; FILING DATE: 08-JUL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crane-Feury, Sharon E
 ; REGISTRATION NUMBER: 36,113
 ; REFERENCE/DOCKET NUMBER: 010830-043
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5399 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double

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ORGANISM: plasmid DNA designated as pPS0212
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LOCATION: 1..1785
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OTHER INFORMATION:
US-08-232-016-23

Query Match 16.3%; Score 728.8; DB 2; Length 7566;
Best Local Similarity 99.7%; Pred. No. 2.3e-142;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 3692 GTCTAGAGTCCTGCTTTAATGAGATATGCCAGAGCCCTATGATCGCATGATATTTGCTTT 3751
QY 3740 CAATTCCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGTAGTCAGATCCTTACGCCCG 3799
DB 3752 CAATTCCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGTAGTCAGATCCTTACGCCCG 3811
QY 3800 GTTTTCGGTTCATCTTAATGATATATCACCGTTACTATCGTATTTTATGAAATAATTT 3859
DB 3812 GTTTTCGGTTCATCTTAATGATATATCACCGTTACTATCGTATTTTATGAAATAATTT 3871
QY 3860 CTCGGTTCAAATTTACTGATTGTACCCCTACTATTATGTACAAATATTTAAATGAAAAACA 3919
DB 3872 CTCGGTTCAAATTTACTGATTGTACCCCTACTATTATGTACAAATATTTAAATGAAAAACA 3931
QY 3920 ATATATTGCTGTAATAGCTTTATAGCCACATCTATGATAGAGCGCCACATATAACAACA 3979
DB 3932 ATATATTGCTGTAATAGCTTTATAGCCACATCTATGATAGAGCGCCACATATAACAACA 3991
QY 3980 ATTGCGTTTTTATTATTACAAATPCCAAATTTTAAAAAAGCGGCAGAACCGGTCAACCTAA 4039
DB 3992 ATTGCGTTTTTATTATTACAAATCBAATTTTAAAAAAGCGGCAGAACCGGTCAACCTAA 4051
QY 4040 AAGACTGATTACATAAATCTTTATTCAATTTTCAAAAGGCCCGGCGGTAGTATCTACGA 4099

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 192.557 Seconds
(without alignments)

12850.857 Million cell updates/sec

Title: US-10-055-001B-25_COPY_13000_17458

Perfect score: 4459

Sequence: 1 ttctattggagagacacg.....atagtgcaacataatgc 4459

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	728.8	16.3	7566	2	US-08-232-016-23
2	728.8	16.3	7839	2	US-08-232-016-22
3	709.8	15.9	5399	1	US-08-064-121-1
4	709.8	15.9	5399	1	US-08-478-015-1
5	709.8	15.9	5399	3	US-08-475-975-1
6	709.8	15.9	5399	3	US-09-084-889-1
7	709.8	15.9	6555	1	US-08-351-413-2
8	709.8	15.9	6555	2	US-09-025-583-2
9	709.8	15.9	14194	4	US-09-577-424-3
10	707	15.9	24595	6	5428147-1
11	566.4	12.7	15397	2	US-08-673-768-1
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13	325.4	7.3	420	2	US-08-379-614-2
14	325.4	7.3	420	3	US-09-225-152A-2
15	323.2	7.2	416	2	US-08-379-614-3
16	323.2	7.2	416	3	US-09-225-152A-3
17	304.4	6.8	306	2	US-08-379-614-1
18	304.4	6.8	306	3	US-09-225-152A-1
19	289.2	6.5	13188	4	US-08-961-527-70
20	151	4.3	134	1	US-07-792-466-6
21	182.8	4.1	13188	4	US-08-961-527-70
22	152.8	3.4	4909	3	US-08-556-978B-78
23	152.8	3.4	4909	3	US-08-556-978B-78
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25	152.8	3.4	6043	4	US-09-630-929-4
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28	148.4	3.3	231	4	US-09-489-039A-4117	Sequence 4117, Ap
29	148.4	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
30	148.4	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
31	148.4	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
32	148.4	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
33	148.4	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
34	148.4	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
35	148.4	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
36	148.4	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli
37	146.2	3.3	231	4	US-09-489-039A-4117	Sequence 4117, Ap
38	146.2	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
39	146.2	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
40	146.2	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
41	146.2	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
42	146.2	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
43	146.2	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
44	146.2	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
45	146.2	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-232-016-23
; Sequence 23, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAEET, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

us-10-055-001b-25_copy_13000_17458.rng

Wed May 12 08:21:03 2004

Search completed: May 7, 2004, 18:29:07
Job time : 1060.16 secs

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986 ACGCAGACGACGGGCTTCATTTCTGCTAGTGTGCTTACCAGACGGGAGATATTGACATC 1045
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1046 ATATATGCTTGTAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTGAATAACGCTGCTTC 1105
1110 ATATATGCTTGTAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTGAATAACGCTGCTTC 1169
1106 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
1170 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1201

RESULT 15
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX ABZ58770;
XX
XX
XX 01-MAY-2003 (first entry)
XX
XX Destination plasmid pDONR212(R) nucleotide sequence.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
XX
XX Nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX OS
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US015947.
XX
XX 21-MAY-2001; 2001US-0291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule for
XX selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid.
XX
XX Disclosure; Fig 29B-C; 273pp; English.
XX
XX The invention relates to inserting a population of nucleic acids into a
XX second target molecule. The method involves (a) mixing a first population
XX of nucleic acid comprising one or more recombination sites with a target
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX the first population to recombine with the first target nucleic acid
XX molecules to form a second population; (c) mixing the second population
XX of nucleic acid with a second target nucleic acid; and (d) causing some
XX or all of the nucleic acid molecules of the second population to
XX recombine with some or all of the second target nucleic acid molecules to
XX form a third population of nucleic acid. The method is useful for
XX selecting and isolating nucleic acid molecules. The present sequence
XX represents the destination plasmid pDONR212(R) nucleotide sequence
XX
XX Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;
XX
XX Query Match 24.7%; Score 1102.4; DB 7; Length 4627;
XX Best Local Similarity 99.5%; Pred. No. 8.9e-148;
XX Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX 26 GACAAAGTTGTACAAAAAGCTGGAACGAGAAACGTAATAATGATATAATATATATATT 85
XX 90 GCCAACTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAATATATATATT 149

86 AAATTAGATTTTCCATATAAAAAACAGACTACATAANTACTGTAAACACAAACATATCCAGTC 145
150 AAATTAGATTTTGCATATAAAAAACAGACTACATAANTACTGTAAACACAAACATATCCAGTC 209
146 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 205
210 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 269
206 TGTTCCTTCGGGTGAGTGTGCGAACTTAGTCGACCGACAGCCTTCCAAATGCTTCTCTCAA 265
270 TGTTCCTTCGGGTGATGTGCGAACTTAGTCGACCGACAGCCTTCCAAATGCTTCTCTCAA 329
266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAAA 325
330 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAAA 389
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386 ATTCAATATACGCTAGTGTATAGTCTTGAAATCATCTGCATCAAGAACAAATTTTCAACAC 445
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506 CTAAACGTGATAAAGTTTCTGTAAATTTCTATGTATGACCTGACAGACTGGCTGTGTATA 565
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566 AGGAGCCTGTACATTTATATTTCCCGACAGACATCAGGTTAAATGGCGCTTTTGTATGTCAATT 625
630 AGGAGCCTGTACATTTATATTTCCCGACAGACATCAGGTTAAATGGCGCTTTTGTATGTCAATT 689
626 TCGCGTGTGCTGAGATCAGACCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA 685
690 TCGCGTGTGCTGAGATCAGACCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA 749
686 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCAACCGCGGTAAAGTTTCAACGG 745
750 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCAACCGCGGTAAAGTTTCAACGG 809
746 GAGACTTTATCTGACAGACAGAGTGCATCTGGCCAGGGGATCAACCATCGCTCGCCGGGC 805
810 GAGACTTTATCTGACAGACAGAGTGCATCTGGCCAGGGGATCAACCATCGCTCGCCGGGC 869
806 GTGTCAATAATATCACTCTGTATATCCAAACAGACAGATAACGGCTCTCTCTTTTATAG 865
870 GTGTCAATAATATCACTCTGTATATCCAAACAGACAGATAACGGCTCTCTCTTTTATAG 929
866 GTGTAAACCTTAAACTGTGATTTTCAACAGTCCCTGTCTCGTCAGAGAAAAGAGCGGTTTCA 925
930 GTGTAAACCTTAAACTGTGATTTTCAACAGTCCCTGTCTCGTCAGAGAAAAGAGCGGTTTCA 989
926 TTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTTCGGC 985
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986 ACGCAGACGACGGGCTTCATTTCTGATGTTGTGTATTCAGACCGGAGATATTGACATC 1045
1050 ACGCAGACGACGGGCTTCATTTCTGATGTTGTGTATTCAGACCGGAGATATTGACATC 1109
1046 ATATATGCTTGTAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTATATACCTGCTTC 1105
1110 ATATATGCTTGTAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTATATACCTGCTTC 1169
1106 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
1170 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1201

746 GAGACTTTATCTGACGACGAGCTGACCTGGCCAGGGGATCACCATCGCTCGCCCGGC 805
DB |||||
1659 GAGACTTTATCTGACGACGAGCTGACCTGGCCAGGGGATCACCATCGCTCGCCCGGC 1718
QY |||||
806 GTGTCAATATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTATAG 865
DB |||||
1719 GTGTCAATATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTATAG 1778
QY |||||
866 GTGTAAACCTTAACTGCACTTCCACAGTCCCTGTTCTGTGACGAAAGAGCGCTTCAT 925
DB |||||
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QY |||||
926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTCCGCTTTCCAGCGTTCCGC 985
DB |||||
1839 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTCCGCTTTCCAGCGTTCCGC 1898
QY |||||
986 ACGCAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
DB |||||
1899 ACGCAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1958
QY |||||
1046 ATATATGCTTGTGACCACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTCTTC 1105
DB |||||
1959 ATATATGCTTGTGACCACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTCTTC 2018
QY |||||
1106 ATAGCACACTCTTTTGTGACATCTTCGGGTA 1137
DB |||||
2019 ATAGCACACTCTTTTGTGACATCTTCGGGTA 2050

RESULT 14

ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.

AC ABZ58769;

DT 01-MAY-2003 (first entry)

DE Destination plasmid pDONR212(F) nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;
XX Nucleic acid isolation; ds.

OS Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INVI-) INVITROGEN CORP.

XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.

PS Disclosure; Fig 28B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to

CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.7%; Score 1102.4; DB 7; Length 4627;

Best Local Similarity 99.5%; Pred. No. 8.9e-148;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAAGTTGTACAAAAGAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 90 GCCAACTTTGTACAAAAGAGCTGATATCGAAACGTAATAATGATATAAATATCAATATAT 149
QY 86 AAATTAGATTTTGCATATAAAAACAGACTACATAACTGTGTAACACACACATATCCAGTC 145
DB 150 AAATTAGATTTTGCATATAAAAACAGACTACATAACTGTGTAACACACACATATCCAGTC 209
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTCACCTGTAGTCGACGAGCGCTTCCAAA 205
DB 210 ACTATGAATCAACTACTTAGATGGTATTAGTCACCTGTAGTCGACGAGCGCTTCCAAA 269
QY 206 TGTCTTCGGGTGATGTCGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 265
DB 270 TGTCTTCGGGTGATGTCGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 329
QY 266 ACGGAATCGTGTATCCAGCGCTTCTGCTTATGTCCTCAATGCGCTTATTAATCATATAA 325
DB 330 ACGGAATCGTGTATCCAGCGCTTCTGCTTATGTCCTCAATGCGCTTATTAATCATATAA 389
QY 326 AGAAATAAGAAAAGAGGTGCGAGCGCTCTTTTGTGTGACAAAATAFAAAAATCTTACCT 385
DB 390 AGAAATAAGAAAAGAGGTGCGAGCGCTCTTTTGTGTGACAAAATAFAAAAATCTTACCT 449
QY 386 ATTCAATACGCTAGTGTCACTAGTCCTGAAATCATCTGCTCAGAGAAACATTTTCAACAC 445
DB 450 ATTCAATACGCTAGTGTCACTAGTCCTGAAATCATCTGCTCAGAGAAACATTTTCAACAC 509
QY 446 TCTTATACCTTTCTCTTCAAGCTCGTTCGGCTTCATCTGATTTTTCAGCGCTCTTACTATTA 505
DB 510 TCTTATACCTTTCTCTTCAAGCTCGTTCGGCTTCATCTGATTTTTCAGCGCTCTTACTATTA 569
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTA 565
DB 570 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTA 629
QY 566 AGGAGCGCTGACATTTATATTTCCCGCAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 625
DB 630 AGGAGCGCTGACATTTATATTTCCCGCAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 689
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGAGACCGGACACCTGGCCATA 685
DB 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGAGACCGGACACCTGGCCATA 749
QY 686 TCGGTGGCTCATCATCGCCAGCGCTTTCATCCCGATATGCAACACCGGTTAAAGTTTCAAGG 745
DB 750 TCGGTGGCTCATCATCGCCAGCGCTTTCATCCCGATATGCAACACCGGTTAAAGTTTCAAGG 809
QY 746 GAGACTTTTATCTGACGACGAGCTGCTGCGCCAGGGGATCACCATCGCTCGCCCGGC 805
DB 810 GAGACTTTTATCTGACGACGAGCTGCTGCGCCAGGGGATCACCATCGCTCGCCCGGC 869
QY 806 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 865
DB 870 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 929
QY 866 GTGTAAACCTTAACTGCACTTCCACAGTCCCTGTTCTGTGACGAAAGAGCGCTTCAT 925
DB 930 GTGTAAACCTTAACTGCACTTCCACAGTCCCTGTTCTGTGACGAAAGAGCGCTTCAT 989
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGC 985

QY 506 CTAACGTCGATAAAGTTCTGTAAATTTCTAATCTGATCGACCTCGACAGCTGGCTGTGTATA 565
Db |||||
QY 5003 CTAACGTCGATAAAGTTCTGTAAATTTCTAATCTGATCGACCTCGACAGCTGGCTGTGTATA 4944
Db |||||
QY 566 AGGGAGCCTGACATATATATATCCCGACAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db |||||
QY 4943 AGGGAGCCTGACATATATATATCCCGACAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 4884
Db |||||
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACCTGGCCCATTA 685
Db |||||
QY 4883 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACCTGGCCCATTA 4824
Db |||||
QY 686 TCGGTGGCTCATCATGCGCCAGCTTTCATCCCGATATGACACCGCGGTAAGTTTCACGG 745
Db |||||
QY 4823 TCGGTGGCTCATCATGCGCCAGCTTTCATCCCGATATGACACCGCGGTAAGTTTCACGG 4764
Db |||||
QY 746 GAGACTTTATCTGACAGACAGTGCACCTGGCCAGGGGATCACCATCGTCCGCGCGGC 805
Db |||||
QY 4763 GAGACTTTATCTGACAGACAGTGCACCTGGCCAGGGGATCACCATCGTCCGCGCGGC 4704
Db |||||
QY 806 GTGTCAATTAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTCTTTATAG 865
Db |||||
QY 4703 GTGTCAATTAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTCTTTATAG 4644
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Db |||||
QY 4643 GTGTAAACCTTAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGACCGCTTCAT 4584
Db |||||
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGGC 985
Db |||||
QY 4583 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGGC 4524
Db |||||
QY 986 AGCAGACGACGGGCTTCAATTCGCAATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
Db |||||
QY 4523 AGCAGACGACGGGCTTCAATTCGCAATGTTGTGCTTACAGACCGGAGATATTGACATC 4464
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QY 1046 ATATATGCTTGTAGCAACTGATAGCTGTCGCTGCACTGCACTGATATACGCTGCTTC 1105
Db |||||
QY 4463 ATATATGCTTGTAGCAACTGATAGCTGTCGCTGCACTGCACTGATATACGCTGCTTC 4404
Db |||||
QY 1106 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1137
Db |||||
QY 4403 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 4372
Db |||||

RESULT 13

ABZ58768

ID ABZ58768 standard; DNA; 4428 BP.

XX AC ABZ58768;

XX DT 01-MAY-2003 (first entry)

XX DE Destination plasmid pDONR212 nucleotide sequence.

XX DX Nucleic acid insertion; recombination; nucleic acid selection;

XX KW Nucleic acid isolation; ds.

XX OS Synthetic.

XX PN WO200295055-A2.

XX PD 28-NOV-2002.

XX PF 21-MAY-2002; 2002WO-US015947.

XX PR 21-MAY-2001; 2001US-0291973P.

XX PA (INVI-) INVITROGEN CORP.

XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DR;

XX DR WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX Disclosure; Fig 27B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence

XX SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 24.7%; Score 1102.4; DB 7; Length 4428;
Best Local Similarity 99.5%; Pred. No. 8.9e-148;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 85
Db |||||
QY 939 GCCAACTTTGTACAAAAAAGCTGATATCGAAACGTAATAATGATATAAATATCAATATATT 998
Db |||||
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATATATCTGTAATAACACAGATATCCAGTC 145
Db |||||
QY 999 AAATTAGATTTTGCATAAAAACAGACTACATATATCTGTAATAACACAGATATCCAGTC 1058
Db |||||
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACTGCTAGTCGACCGCAGCGCTTCCAAA 205
Db |||||
QY 1059 ACTATGAATCAACTACTTAGATGGTATTAGTACTGCTAGTCGACCGCAGCGCTTCCAAA 1118
Db |||||
QY 206 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGACAGCCTTCCAAATGTTCTCTCAA 265
Db |||||
QY 1119 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGACAGCCTTCCAAATGTTCTCTCAA 1178
Db |||||
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGCTCAATGCGCTATTAATCATATAAA 325
Db |||||
QY 1179 ACGGAATCGTGTATCCAGCCTACTCGCTATTGCTCAATGCGCTATTAATCATATAAA 1238
Db |||||
QY 326 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAATCATCTACT 385
Db |||||
QY 1239 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAATCATCTACT 1298
Db |||||
QY 386 ATTCAATACGCTAGTGTCTAGTCTGAAAATCATCTGCAATCAAGAAACAATTTCAACAAC 445
Db |||||
QY 1239 ATTCAATACGCTAGTGTCTAGTCTGAAAATCATCTGCAATCAAGAAACAATTTCAACAAC 1358
Db |||||
QY 446 TCTTATCTTTTCTCTTACAAAGTGGTGGCTTCACTGGAATTTTTCAGCCTCTTACTACTTA 505
Db |||||
QY 1359 TCTTATCTTTTCTCTTACAAAGTGGTGGCTTCACTGGAATTTTTCAGCCTCTTACTACTTA 1418
Db |||||
QY 506 CTAACGTCGATAAAGTTCTGTAAATTTCTAATCTGATCGACCTCGACAGCTGGCTGTGTATA 565
Db |||||
QY 1419 CTAACGTCGATAAAGTTCTGTAAATTTCTAATCTGATCGACCTCGACAGCTGGCTGTGTATA 1478
Db |||||
QY 566 AGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db |||||
QY 1479 AGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 1538
Db |||||
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACCTGGCCCATTA 685
Db |||||
QY 1539 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACCTGGCCCATTA 1598
Db |||||
QY 686 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGACACCGGTAAGTTTCACGG 745
Db |||||
QY 1599 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGACACCGGTAAGTTTCACGG 1658
Db |||||

Db 5243 ACCGAATCGTCGATCAGCGCTACTCGCTATTGCTCTCAATGCGCTATTAAATCATAAA 5184
QY 326 AGAAATAAGAAAAAGAGTCGCGAGCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT 385
Db 5183 AGAAATPAGAAAAGAGTCGCGAGCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT 5124
QY 386 ATTATATACGCTAGTGTCTATAGTCCTGTAATAATCATCTGCATCAAGAACAAATTTTCAAC 445
Db 5123 ATTATATACGCTAGTGTCTATAGTCCTGTAATAATCATCTGCATCAAGAACAAATTTTCAAC 5064
QY 446 TCTTATACCTTTCTCTTACAGTCGTCGCTCTCATCTGGAATTTTCAAGCTCTATCTTA 505
Db 5063 TCTTATACCTTTCTCTTACAGTCGTCGCTCTCATCTGGAATTTTCAAGCTCTATCTTA 5004
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTACTGTATCTGACCTGCAGCTGGCTGTATA 565
Db 5003 CTAAACGCTGATAAAGTTTCTGTAAATTTACTGTATCTGACCTGCAGCTGGCTGTATA 4944
QY 566 AGGAGCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 625
Db 4943 AGGAGCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 4884
QY 626 TCGCGTGGTGTAGATCAGCCACTTCTCCCGATACCGAGACCGGCACACTGGCCATA 585
Db 4883 TCGCGTGGTGTAGATCAGCCACTTCTCCCGATACCGAGACCGGCACACTGGCCATA 4824
QY 686 TCGGTGGTTCATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG 745
Db 4823 TCGGTGGTTCATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG 4764
QY 746 GAGACTTTATCTGACAGACAGTCGACCTGGCCAGGGGATCATCATCGTGGCCGGGC 805
Db 4763 GAGACTTTATCTGACAGACAGTCGACCTGGCCAGGGGATCATCATCGTGGCCGGGC 4704
QY 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATACCGGCTCTCTTTTATAG 865
Db 4703 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATACCGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGTGATTTTCAACGTCCTGTTCTCGTACGAAAAGACCGTTTCAAT 925
Db 4643 GTGTAAACCTTAACTGTGATTTTCAACGTCCTGTTCTCGTACGAAAAGACCGTTTCAAT 4584
QY 926 TTCAATAACCGGCGACCTCAGCCATCTCTGATTTTCCGCTTTCCAGGTTTCGCG 985
Db 4583 TTCAATAACCGGCGACCTCAGCCATCTCTGATTTTCCGCTTTCCAGGTTTCGCG 4524
QY 986 ACGCAGACGCGGCTTTCATTTCTGCAATGGTTGTGCTTACGACCGGAGATTTGACATC 1045
Db 4523 ACGCAGACGCGGCTTTCATTTCTGCAATGGTTGTGCTTACGACCGGAGATTTGACATC 4464
QY 1046 ATATATGCTTGTAGCAACTGTAGTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC 1105
Db 4463 ATATATGCTTGTAGCAACTGTAGTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC 4404
QY 1106 ATAGCACACCTCTTTTGTACATCTTCGGGTA 1137
Db 4403 ATAGCACACCTCTTTTGTACATCTTCGGGTA 4372

RESULT 12

ABZ58766/c

ID ABZ58766 standard; DNA; 5584 BP.

XX AC ABZ58766;

XX 01-MAY-2003 (first entry)

XX Donor plasmid pDONR207 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;

XX Nucleic acid isolation; ds.

XX

XX

XX

XX

XX

XX

OS

XX Synthetic.

PN WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INVI-) INVITROGEN CORP.

XX Brach MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for

XX selecting and isolating nucleic acid molecules by mixing the second

XX population of nucleic acid with a second target nucleic acid.

XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a

XX second target molecule. The method involves (a) mixing a first population

XX of nucleic acid comprising one or more recombination sites with a target

XX nucleic acid; (b) causing some or all of the nucleic acid molecules of

XX the first population to recombine with the first target nucleic acid

XX molecules to form a second population; (c) mixing the second population

XX of nucleic acid with a second target nucleic acid; and (d) causing some

XX or all of the nucleic acid molecules of the second population to

XX recombine with some or all of the second target nucleic acid molecules to

XX form a third population of nucleic acid. The method is useful for

XX selecting and isolating nucleic acid molecules. The present sequence

XX represents the donor plasmid pDONR207 nucleotide sequence

XX

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.9%; Score 1108.8; DB 7; Length 5584;

Best Local Similarity 99.8%; Pred. No. 1.1e-148;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATATATATATT 85

Db 5483 GCCAATCTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATATATATT 5424

QY 86 AAATTAGATTTTGCATATAAAAAACAGACTACATATACTGTAAACACAACTATCCAGTC 145

Db 5423 AAATTAGATTTTGCATATAAAAAACAGACTACATATACTGTAAACACAACTATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACCGACAGCTTTCCAAA 205

Db 5363 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACCGACAGCTTTCCAAA 5304

QY 206 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAGCTTCCAAATGTTCTTCTCAA 265

Db 5303 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAGCTTCCAAATGTTCTTCTCAA 5244

QY 266 ACGGAATCGTGTATCCAGCGCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 325

Db 5243 ACGGAATCGTGTATCCAGCGCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 5184

QY 326 AGAATAAGAAAAAGAGTCGCGAGCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT 385

Db 5183 AGAATAAGAAAAAGAGTCGCGAGCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT 5124

QY 386 ATTATATACGCTAGTGTCTATAGTCCTGAAAATCATCTGCAATCAAGAACAAATTTTCAAC 445

Db 5123 ATTATATACGCTAGTGTCTATAGTCCTGAAAATCATCTGCAATCAAGAACAAATTTTCAAC 5064

QY 446 TCTTATACCTTTCTCTTACAAAGTCGTCGCTTTCATCTGGAATTTTCAAGCTCTATCTTA 505

Db 5063 TCTTATACCTTTCTCTTACAAAGTCGTCGCTTTCATCTGGAATTTTCAAGCTCTATCTTA 5004

QY 266 ACGGAATCGTCTGATCCAGCTACTCGCTATTGTCTCAATGCCGTTATTAATCATATAA 325
DB |||||
3876 ACGGAATCGTCTGATCCAGCTACTCGCTATTGTCTCAATGCCGTTATTAATCATATAA 3935
QY 326 AGAAATTAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAAACATCTACCT 385
DB |||||
3936 AGAAATTAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAAACATCTACCT 3995
QY 386 ATTATATACGCTAGTGTCTAGTCTGAAATCATCTGCATCAAGAAACAATTTTCAAC 445
DB |||||
3996 ATTATATACGCTAGTGTCTAGTCTGAAATCATCTGCATCAAGAAACAATTTTCAAC 4055
QY 446 TCTTATACCTTCTCTTAAGTCGTTTCGCTTCATCTCGAATTTTTCAGCCTCTTATCTTA 505
DB |||||
4056 TCTTATACCTTCTCTTAAGTCGTTTCGCTTCATCTCGAATTTTTCAGCCTCTTATCTTA 4115
QY 506 CTAACCGTGTATTAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGCTGGTGTATTA 565
DB |||||
4116 CTAACCGTGTATTAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGCTGGTGTATTA 4175
QY 566 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGCTTTTGTGATCTCATTT 625
DB |||||
4176 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGCTTTTGTGATCTCATTT 4235
QY 626 TCGCGTGTGATGATCAGCACTTCTTCCCGATTAACGGAGACCGGACACTGGCCATA 685
DB |||||
4236 TCGCGTGTGATGATCAGCACTTCTTCCCGATTAACGGAGACCGGACACTGGCCATA 4295
QY 686 TCGGTGTGATCATATGCGGACGCTTTCATCCCGATATGCACACCGGTAAGTTTCAACGG 745
DB |||||
4296 TCGGTGTGATCATATGCGGACGCTTTCATCCCGATATGCACACCGGTAAGTTTCAACGG 4355
QY 746 GAGACTTTATCTGACAGAGAGTGCACTGGCCAGGGGATCACCATCGTCCCGCGGC 805
DB |||||
4356 GAGACTTTATCTGACAGAGAGTGCACTGGCCAGGGGATCACCATCGTCCCGCGGC 4415
QY 806 GTGTCAATATATCACTGTATCATCCACAGAGAGATTAACGGCTCTCTCTTTTATAG 865
DB |||||
4416 GTGTCAATATATCACTGTATCATCCACAGAGAGATTAACGGCTCTCTCTTTTATAG 4475
QY 866 GTGTAACCTTAACTGCACTTTTCAACAGTCCCTGTTCTGTGACAAAAGAGCGCTTCAT 925
DB |||||
4476 GTGTAACCTTAACTGCACTTTTCAACAGTCCCTGTTCTGTGACAAAAGAGCGCTTCAT 4535
QY 926 TTCATTAACCGGGGACCTGACGATTCCTGCTTCTGATTTTCGCTTTTCCAGGTTTCGGC 985
DB |||||
4536 TTCATTAACCGGGGACCTGACGATTCCTGCTTCTGATTTTTCGCTTTTCCAGGTTTCGGC 4595
QY 986 ACGCAGACGACGGGCTTCTATCTGCAATGTTGTGCTTACAGACCGGAGATTTGACATC 1045
DB |||||
4596 ACGCAGACGACGGGCTTCTATCTGCAATGTTGTGCTTACAGACCGGAGATTTGACATC 4655
QY 1046 ATATATGCTTGTAGCACTGATAGCTGTGCTGTGCTCAACTGTCACTGTAATAGCTGCTTC 1105
DB |||||
4656 ATATATGCTTGTAGCACTGATAGCTGTGCTGTGCTCAACTGTCACTGTAATAGCTGCTTC 4715
QY 1106 ATAGCACACCTCTTTTGTACATCTTCGGGTA 1137
DB |||||
4716 ATAGCACACCTCTTTTGTACATCTTCGGGTA 4747

RESULT 11

AAC55632/c

ID AAC55632 standard; DNA; 5584 BP.

XX AC AAC55632;

XX AC AAC55632;

XX 11-JAN-2001 (first entry)

XX Donor plasmid pDONR207 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attL;
KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

PN 08-SEP-2000.

PD 02-MAR-2000; 2000WO-US005432.

PF 02-MAR-1999; 99US-0122389P.

XX 23-MAR-1999; 99US-0126049P.

PR 28-MAY-1999; 99US-0136744P.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides.

XX Disclosure; Fig 97; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is used
in the exemplification of the present invention

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match

Best Local Similarity 24.9%; Score 1108.8; DB 3; Length 5584;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAATTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAAATATATATT 85

DB 5483 GCCAACTTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAAATATATATT 5424

QY 86 AAATTAGATTTTGCATAAABACAGACTACATATACCTGTAAACACACATATCCAGTC 145

DB 5423 AAATTAGATTTTGCATAAABACAGACTACATATACCTGTAAACACACATATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCCAAA 205

DB 5363 ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCCAAA 5304

QY 206 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 265

DB 5303 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 5244

QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGCTATTAAATCATATAA 325

QY 266 ACGGAATCGTCGATCCAGCTACTCGCTATTGTCCTCAATGCGTATTAAATCAATAAAA 325
DB |||||
QY 342 ACGGAATCGTCGATCCAGCTACTCGCTATTGTCCTCAATGCGTATTAAATCAATAAAA 401
DB |||||
QY 326 AGAATTAAGAAAAGAGGTGGAGCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
DB |||||
QY 402 AGAATTAAGAAAAGAGGTGGAGCTCTTTTGTGTGACAAAATAAAACATCTACCT 461
DB |||||
QY 386 ATTCAATACGCTAGTCTCATAGTCTCTGAAATCATCTGATCAAGAACAAATTTCAAC 445
DB |||||
QY 462 ATTCAATACGCTAGTCTCATAGTCTCTGAAATCATCTGATCAAGAACAAATTTCAAC 521
DB |||||
QY 446 TCTTATACCTTTCTCTTACAGTCTGTTTCTGCTTTCATCTGATTTTTCAGCTCTTATCTTA 505
DB |||||
QY 522 TCTTATACCTTTCTCTTACAGTCTGTTTCTGCTTTCATCTGATTTTTCAGCTCTTATCTTA 581
DB |||||
QY 506 CTAACGCTGATAAGTTTCTGTAATTTCTACTGTATCGACTGAGCTGGCTGTGTATA 565
DB |||||
QY 582 CTAACGCTGATAAGTTTCTGTAATTTCTACTGTATCGACTGAGCTGGCTGTGTATA 641
DB |||||
QY 566 AGGAGCTGACATTTATATTCCTCCAGAACATCAGGTTTATGGCTTTTGTGATTCATTT 625
DB |||||
QY 642 AGGAGCTGACATTTATATTCCTCCAGAACATCAGGTTTATGGCTTTTGTGATTCATTT 701
DB |||||
QY 626 TCGCGGTGGCTGAGTACAGCACTTCTTCCCGATTAACGGAGACCGGACACTGGCCATA 685
DB |||||
QY 702 TCGCGGTGGCTGAGTACAGCACTTCTTCCCGATTAACGGAGACCGGACACTGGCCATA 761
DB |||||
QY 686 TCGGTGGTCAATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTACCG 745
DB |||||
QY 762 TCGGTGGTCAATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTACCG 821
DB |||||
QY 746 GAGACTTTATCTGACAGAGCTGACCTGGCCAGGGGATCACCATCGTCCGCCGGC 805
DB |||||
QY 822 GAGACTTTATCTGACAGAGCTGACCTGGCCAGGGGATCACCATCGTCCGCCGGC 881
DB |||||
QY 806 GTGTCAATATATCATCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 865
DB |||||
QY 882 GTGTCAATATATCATCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 941
DB |||||
QY 866 GTGTAAACCTTAACTGCACTTTTCAACAGTCCCTGTTCTGTCAGCAAAAGACCGTTTAT 925
DB |||||
QY 942 GTGTAAACCTTAACTGCACTTTTCAACAGTCCCTGTTCTGTCAGCAAAAGACCGTTTAT 1001
DB |||||
QY 926 TTCAATAAACCGGGGACCTGACCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 985
DB |||||
QY 1002 TTCAATAAACCGGGGACCTGACCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 1061
DB |||||
QY 986 ACGCAGACGACGGCTTCAATTCGATGCTTGTGCTTACAGACCGGATATTGACATC 1045
DB |||||
QY 1062 ACGCAGACGACGGCTTCAATTCGATGCTTGTGCTTACAGACCGGATATTGACATC 1121
DB |||||
QY 1046 ATATATGCTTTCAGCAACTGATAGCTGTCGCTGTCACCTGTCACTGTAATACGCTGCTC 1105
DB |||||
QY 1122 ATATATGCTTTCAGCAACTGATAGCTGTCGCTGTCACCTGTAATACGCTGCTC 1181
DB |||||
QY 1106 ATAGCACACCTCTTTTGTACATCTTTCGGGTA 1137
DB |||||
QY 1182 ATAGCACACCTCTTTTGTACATCTTTCGGGTA 1213
DB |||||

RESULT 10

AAC55525

ID AAC55525 standard; DNA; 4939 BP.

XX AC

XX AAC55525;

DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;
KM gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
XX WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US005432.
XX PR 02-MAR-1999; 99US-0122389P.
XX PR 23-MAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX PT recombinational cloning of polypeptides.
XX PS Example 10; Fig 53; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), (IV), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;

Query Match 24.9%; Score 1108.8; DB 3; Length 4939;
Best Local Similarity 99.8%; Pred. NO. 1.1e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAACCTGTAATATGATTAATATCAATATT 85
DB 3636 GCCAACTTTGTACAAAAAGCTGAACGAGAACCTGTAATATGATTAATATCAATATT 3695
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAACTATCCAGTC 145
DB 3696 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAACTATCCAGTC 3755
QY 146 ACTAATGAATCAACTACTTAGATGTTATAGTACTGTAGTCGACCGACGCTTCCAAA 205
DB 3756 ACTAATGAATCAACTACTTAGATGTTATAGTACTGTAGTCGACCGACGCTTCCAAA 3815
QY 206 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCAA 265
DB 3816 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCAA 3875

Best Local Similarity 99.8%; Pred. No. 1.1e-148; Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 26	GACAAAGTTGTACAAAAAGCTCAACGAGAAACGTAATAATGATATAATAATCAATATATT 85
Db 102	GCCAACTTTGTACAAAAAGCTCAACGAGAAACGTAATAATGATATAATAATCAATATATT 161
QY 86	AAATTAGATTTCATAAAAAAGAGACTACATAATACTGTAAAAACAACATATCCAGTC 145
Db 162	AAATTAGATTTCATAAAAAAGAGACTACATAATACTGTAAAAACAACATATCCAGTC 221
QY 146	ACTATGAATCACTACTAGATGGTATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 205
Db 222	ACTATGAATCACTACTAGATGGTATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 281
QY 206	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTTCCAAATGTTCTCTCAA 265
Db 282	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTTCCAAATGTTCTCTCAA 341
QY 266	ACGGAATCGGTGATCCAGCCTACTCGCTATTGCTCTCAATGCCGATTAAATCATAAAA 325
Db 342	ACGGAATCGGTGATCCAGCCTACTCGCTATTGCTCTCAATGCCGATTAAATCATAAAA 401
QY 326	AGAAATGAAGAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAACAATCACTACCT 385
Db 402	AGAAATGAAGAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAACAATCACTACCT 461
QY 386	ATTCAATATAGCTAGTGTCTATAGTCTGAAATCATCTGATCAAGAAACAATTTCAAAAC 445
Db 462	ATTCAATATAGCTAGTGTCTATAGTCTGAAATCATCTGATCAAGAAACAATTTCAAAAC 521
QY 446	TCATTATCTTTCTTTAAGTCTGTTGGCTTCATCTGATTTTCAGGCTCTATATCTTA 505
Db 522	TCATTATCTTTCTTTAAGTCTGTTGGCTTCATCTGATTTTCAGGCTCTATATCTTA 581
QY 506	CTAAACGTGATAAGTTCTGTAATTTCTACTGTCTGACCTGACAGTGGCTGTGTATA 565
Db 582	CTAAACGTGATAAGTTCTGTAATTTCTACTGTATCGACCTGACAGTGGCTGTGTATA 641
QY 566	AGGAGCCTGACATTTATATTCGCCAGAAATCAGAGTTAATGGCTTTTGTATGTCAATT 625
Db 642	AGGAGCCTGACATTTATATTCGCCAGAAATCAGAGTTAATGGCTTTTGTATGTCAATT 701
QY 626	TCGCGTGGCTGATGACAGCACTCTTCCCGATTAACGAGACCGGACACTGGCCATA 685
Db 702	TCGCGTGGCTGATGACAGCACTCTTCCCGATTAACGAGACCGGACACTGGCCATA 761
QY 686	TCGCTGTCTCATCTGCGCCAGCTTTTATCCCGATATGACACCGGCTAAAGTTCAACGG 745
Db 762	TCGCTGTCTCATCTGCGCCAGCTTTTATCCCGATATGACACCGGCTAAAGTTCAACGG 821
QY 746	GAGACTTTTATCTGACAGCAGAGTGTGCTGGCCAGGGGATCAACATCCGTCGCCGGGC 805
Db 822	GAGACTTTTATCTGACAGCAGAGTGTGCTGGCCAGGGGATCAACATCCGTCGCCGGGC 881
QY 806	GTGTCAATATATACCTCTGTATATCCACAAACAGAGATTAACGGCTCTCTTTTATAG 865
Db 882	GTGTCAATATATACCTCTGTATATCCACAAACAGAGATTAACGGCTCTCTTTTATAG 941
QY 866	GTGTAAACCTTAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 925
Db 942	GTGTAAACCTTAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 1001
QY 926	TTCAATAAACCGGCGACCTCAGGCATCCCTTCTGATTTTCGCTTTCCAGGTTCCGGC 985
Db 1002	TTCAATAAACCGGCGACCTCAGGCATCCCTTCTGATTTTCGCTTTCCAGGTTCCGGC 1061
QY 986	ACGAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACCAGACCGGAGATATGACATC 1045
Db 1062	ACGAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACCAGACCGGAGATATGACATC 1121
QY 1046	ATATATGCTTGAACCACTGATAGCTGTGCTGTCACTGTCACTGTAAATACGCTGCTTC 1105
Db 1122	ATATATGCTTGAACCACTGATAGCTGTGCTGTCACTGTCACTGTAAATACGCTGCTTC 1181
QY 1106	ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
Db 1182	ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1213
RESULT 9	
ADA50329	
ID	ADA50329 standard; DNA; 4892 BP.
XX	ADA50329;
XX	20-NOV-2003 (first entry)
XX	Plasmid vector pMK2010 DNA sequence.
XX	site-specific recombination; array construction; reporter gene fusion;
KW	mutagenesis; protein production; protein characterisation;
KW	plasmid pMK2010; ds.
XX	Synthetic.
OS	WO2003064623-A2.
PN	07-AUG-2003.
XX	31-JAN-2003; 2003WO-US003176.
XX	31-JAN-2002; 2002US-0354063P.
PR	(UNIW) UNIV WASHINGTON STATE RES FOUND.
PA	Kahn ML, House BL, Mortimer MW;
XX	WPI; 2003-679497/64.
DR	Moving an insert nucleic acid between vectors using site-specific
XX	recombination in vivo, useful for studying the biology of the organism,
PT	including array construction, reporter gene fusions, mutagenesis and
PT	protein production.
XX	Claim 41; Page 47-51; 52pp; English.
PS	The invention comprises a method for moving an insert nucleic acid
CC	molecule between vectors, the method involves moving an insert nucleic
CC	acid from one vector to another using site-specific recombination. The
CC	method of the invention is useful for studying the biology of an
CC	organism, including array construction, reporter gene fusions,
CC	mutagenesis, protein production and characterisation. The present DNA
CC	sequence represents the plasmid vector pMK2010 of the invention.
XX	Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
SQ	Query Match 24.9%; Score 1108.8; DB 8; Length 4892;
Best Local Similarity 99.8%; Pred. No. 1.1e-148; Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 26	GACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATATT 85
Db 102	GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATATT 161
QY 86	AAATTAGATTTCATAAAAAAGAGACTACATAATACTGTAAAAACAACATATCCAGTC 145
Db 162	AAATTAGATTTCATAAAAAAGAGACTACATAATACTGTAAAAACAACATATCCAGTC 221
QY 146	ACTATGAATCACTACTAGATGGTATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 205
Db 222	ACTATGAATCACTACTAGATGGTATAGTACCTGTAGTCGACGAGAGCCCTCCAAA 281
QY 206	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTTCCAAATGTTCTCTCAA 265
Db 282	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTTCCAAATGTTCTCTCAA 341

comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into plasmids and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.9%; Score 1108.8; DB 3; Length 4470;

Best Local Similarity 99.8%; Pred. No. 1.1e-148;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAGTTTGTACAAAAAGCTGAACGAGAAACGTTAAATGATATAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTTAAATGATATAATATCAATATATT 161
QY 86 AAATTAGATTTTGCATAAAAAAGACTACATAAATCTGTAACACACACATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAAAGACTACATAAATCTGTAACACACACATATCCAGTC 221
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCGACGAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCGACGAGCCTTCCAAA 281
QY 206 TCTTCTTCGGGTGATGTCGCCAAGTACTAGTCGACGAGCCTTCCAAATGTTCTCTCAA 265
DB 282 TCTTCTTCGGGTGATGTCGCCAAGTACTAGTCGACGAGCCTTCCAAATGTTCTCTCAA 341
QY 266 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAA 325
DB 342 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAA 401
QY 326 AGAATATAGAAAAAGAGGTGGAGCCTCTTTTGTGACAAAAATAAAACATCTACT 385
DB 402 AGAATATAGAAAAAGAGGTGGAGCCTCTTTTGTGACAAAAATAAAACATCTACT 461
QY 386 ATTCAATACGCTAGTGTATGATGCTGAATATCATCTGCATCAAGAAATTTCAACAC 445
DB 462 ATTCAATACGCTAGTGTATGATGCTGAATATCATCTGCATCAAGAAATTTCAACAC 521
QY 446 TCTTATACCTTTCTCTTACAGCTGTCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 505
DB 522 TCTTATACCTTTCTCTTACAGCTGTCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 581
QY 506 CTAAACGTTGATTAAGTTTCTGTAATTTCTGTAATCGACCTGACAGCTGGCTGTATTA 565
DB 582 CTAAACGTTGATTAAGTTTCTGTAATTTCTGTAATCGACCTGACAGCTGGCTGTATTA 641
QY 566 AGGAGCTCTGACATTTATATATCCAGAACATCAAGTTTAAAGGCTTTTGTGATGATTT 625
DB 642 AGGAGCTCTGACATTTATATATCCAGAACATCAAGTTTAAAGGCTTTTGTGATGATTT 701
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGACACCTGGCCATA 685
DB 702 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGACACCTGGCCATA 761
QY 686 TCGGTGGCTCATATCGGCAGCTTTTCAATCCCGATATGACACCGGGTAAAGTTCAAGG 745
DB 762 TCGGTGGCTCATATCGGCAGCTTTTCAATCCCGATATGACACCGGGTAAAGTTCAAGG 821
QY 746 GAGACTTTATCTGACAGAGCTGCTACTGGCCAGGGGATCACCATCGCTCGCCGGGC 805
DB 822 GAGACTTTATCTGACAGAGCTGCTACTGGCCAGGGGATCACCATCGCTCGCCGGGC 881
QY 806 GTGTCAATAATATCACTCTGTATATCCCAACAGACGATACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATCACTCTGTATATCCCAACAGACGATACGGCTCTCTCTTTTATAG 941

QY 866 GTGTAACCTTAAACTGATTTTCCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 925
DB 942 GTGTAACCTTAAACTGATTTTCCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 1001
QY 926 TTCAATAAACCGGGGAGCTTCCAGCCATCCCTTCTCTGATTTTCCGCTTCCAGCGTTCGGC 985
DB 1002 TTCAATAAACCGGGGAGCTTCCAGCCATCCCTTCTCTGATTTTCCGCTTCCAGCGTTCGGC 1061
QY 986 ACGCAGACGAGCGGCTTCAATTTCTGATGTTGCTGTACCAAGACCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGAGCGGCTTCAATTTCTGATGTTGCTGTACCAAGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATAGCGTGTTC 1105
DB 1122 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATAGCGTGTTC 1181
QY 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1213

RESULT 8

ABZ58767

ID ABZ58767 standard; DNA; 4470 BP.

XX AC ABZ58767;

XX AC ABZ58767;

DT 01-MAY-2003 (first entry)

XX XX

DE Destination plasmid pDONR201 nucleotide sequence.

XX XX

KW Nucleic acid insertion; recombination; nucleic acid selection;

XX XX

KW nucleic acid isolation; ds.

XX XX

OS Synthetic.

XX XX

PN WO200295055-A2.

XX XX

PD 28-NOV-2002.

XX XX

PF 21-MAY-2002; 2002WO-US015947.

XX XX

PR 21-MAY-2001; 2001US-0291973P.

XX XX

PA (INVI-) INVITROGEN CORP.

XX XX

PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX XX

DR WPI; 2003-129436/12.

XX XX

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

XX XX

PS Disclosure; Fig 26B-C; 273pp; English.

XX XX

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

XX XX

SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

XX XX

Query Match 24.9%; Score 1108.8; DB 7; Length 4470;

2648 AAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGG-----CT 2698
14071 CAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGTTCTGTAAGCACAACT 14012
2699 GTGTATAAGGAGCCCTGAATTTATATATCCCGAGAACATCAGGTTAATGGCGTTTGTAT 2758
14011 ATGCAGATGAAGCCGCTGCTGCTGCGTGC--GAACGCTGGAAGCGGAAATCAGGAA 13955
2759 GTCAATTTCCGCGTGGCTGAGATCAGCACTCTCTCCCGATAAAGGAGACCGGACACT 2818
13954 GGGATGGCTGAGTGCCTGCGGTTTATGAAATGAACGGCTCTTTGCTGACGAGAACAGG 13895
2819 GGCCATATCGGTGGTGCATATCGCGCAGCTTTTATCCCGATATGACCAACCGGGTAAG 2878
13894 GA-----CTGGTGAATGCAGTTTAAAGTTTACACCTATAAAGAGAGACGGTTATCG 13841
2879 TTCGGGAGACTTTATCTGACAGAGAGCTGCTGGCCAGGGGATCACCATCGGTGG 2938
13840 TCTGTTTGTGGATGTCAGAGTGATATTTATGACAGCCCGGGCGACGGATGGTGATCCC 13781
2939 CCGGGCGTGTCAATAATATCACTCTGTATATCACTCAACAAACAGACGATAACGGCTCTCTCT 2998
13780 CTGGCCAGTGCAGCTGCTGTCAGATAAAGTCTCCGCTGAACCTTACCCGGTGTGCA 13721
2999 TTATAGGTGTAAACCTTAACTTAACTGCAATTTCAAC-----AGTCCCTGTTTCTCGTCAAGCA 3052
13720 TATCGGGATGAAGCTGGCGCATGATGACCAACCGATATGGCAGTGTGCGGCTCTCCGT 13661
3053 AAGAGCGTTCATTTCAATAAACCAGCGGACCTCAGCCATCCCTTCTGATTTTCGCTT 3112
13660 TATCGGGAGAGTGGTGTATCTGACCAACCGGAAATGATCAAAAGCCCATTTAA 13601
3113 TCAGAGGTTTC---GGCAGCAGACGAGCGGCTTCACTCTGCATGG---TTGTGCTTTACCA 3166
13600 CCTGATGTTCTGGGAATAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGTGG 13541
3167 GACCGAGATATGACATCATATATGCTTGAGCAACTGATAGCTGCTGCTCAACTGT 3226
13540 ATACAGTGAATAATACAGAACTTTATCAGTTTAGTAAAGTATAGAGGCTGAAATCCAG 13481
3227 CACTGTAATACGCTGCTTCATACACACCTCTTTTGGACATCTCTGTTTGTATGTCAG 3286
13480 ATGAACCGAGACACTGTGTAAGAGAAAGTATGAAGTGTGGAATGTTCTTGTATGTCAG 13421
3287 ATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGTATGTTTATTTTGTCTAC 3346
13420 ATGATTTTCAGGACTATGACACTAGCGTATATGATAGGTAGTATGTTTATTTTGTCTAC 13361
3347 ACAGAAAGAGGCTCGCAGCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTCGA 3406
13360 ACAGAAAGAGGCTCGCAGCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTCGA 13301
3407 GGACATAGCGAGTGGCTGGATACGACAGTTCGGTTTGAAGAGAACATTTGGAAGGCTG 3466
13300 GGACATAGCGAGTGGCTGGATACGACAGTTCGGTTTGAAGAGAACATTTGGAAGGCTG 13241
3467 TCGGTGCACTAAGTTGCGACGATCAACCGAAGAACATTTGGAAGGCTGCTGCTGACTAC 3526
13240 TCGGTGCACTAAGTTGCGACGATCAACCGAAGAACATTTGGAAGGCTGCTGCTGACTAC 13181
3527 AGGTCACTATACATCTAAGTATGTTGATTCATAGTACGATGATGTTGTTTACAG 3586
13180 AGGTCACTATACATCTAAGTATGTTGATTCATAGTACGATGATGTTGTTTACAG 13121
3587 TATTATAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATTAATTTATATCATTT 3646
13120 TATTATAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATTAATTTATATCATTT 13061
3647 TACGTTTCTGTTGAGCTTTTGTACAAACTGCTGAGAG 3687
13060 TACGTTTCTGTTGAGCTTTTGTACAAACTGCTGAGAG 13020

RESULT 6

ABQ82141/c
ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ds.
XX Synthetic.
XX WO200259294-A1.
XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU000073.
XX 26-JAN-2001; 2001US-0264067P.
XX 29-NOV-2001; 2001US-0333743P.
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
XX replication, a selectable marker and a chimeric DNA construct, useful for
XX silencing target nucleic acids and for producing large amounts of double-
XX stranded RNA.
XX
XX Claim 15; Page 74-83; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
XX DNA fragments having: (a) origin of replication allowing replication in a
XX recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
XX selectable marker region capable of being expressed in the recipient cell
XX ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
XX region capable of being recognized by RNA polymerases of a eukaryotic
XX cell or by prokaryotic RNA polymerase; (ii) first, second, third and
XX fourth recombination sites; (iii) 3' transcription terminating and
XX polyadenylation region functional in the eukaryotic cell. The first and
XX fourth recombination sites, or the second and third recombination sites
XX are capable of reacting with a same recombination site, and preferably
XX are identical. The first and second recombination sites, or the third and
XX fourth recombination sites, do not recombine with each other or with a
XX same recombination site. The vector is useful for producing large amounts
XX of double-stranded RNA which can be used for silencing target nucleic
XX acid sequences. The vectors can also be used to convert a DNA fragment
XX into an inverted repeat structure. Plants transformed with a vector from
XX the present invention can be used in a conventional breeding scheme to
XX produce more plants with the same characteristics or to introduce a
XX chimeric gene for reduction of the phenotypic expression of nucleic
XX acids. The present sequence represents an acceptor vector nucleotide
XX sequence from the present invention
XX
XX Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
Query Match 28.7%; Score 1277.8; DB 6; Length 17476;
Best Local Similarity 62.4%; Pred. No. 1.1e-172;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;
21 CTCGACAGCAAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 80
16704 CTCGACAGCAAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 16645
81 ATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 140
16644 ATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 16585

16266 ATGTCAAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGACA 16210
Db
501 ACTTACTAAACGTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTCGAGACTCGCTGT 560
Qy
16209 GCTATCAGTTGCTCAGGCGATATATGATGCAATATCTCCGCTGTGGTAAGCACAAACCAT 16150
Db
561 GTATAAGGAGGCTGACATTTATATCCCGCAAAACATCAGGTTAATGCGGTTTTTGATGT 620
Qy
16149 GCAGATGAAGCCGCTGCTCGGTGCC---GAAAGCTGGAAGCGGAAATCAGGAAGG 16093
Db
621 CATTTTCCGGTGGTGAATCAGCGACCTTTCTTCCCGGATTAACGAGAGCCGCGACACTGG 680
Qy
16092 GATGGCTGAGTGGCCCGGTTTTATTGAAATGAACCGCTCTTTTGTCTGACGAAACAGGG- 16034
Db
681 CCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCGCGGTAAAGTT 740
Qy
16033 -----ACTGGTGAATGCGAGTTTAAAGTTTACCTATTAAGAGAGAGCCGTTATCGTC 15979
Db
741 CAGGGAGACTTTATCTGACAGCAGCGTGCATCTGGCCAGGGGGATCACCATCCGTCGCC 800
Qy
15978 TGTGTTGTGATGTACAGAGTGATATTATTGACAGCGCCGCGCGACGGATGGTGTATCCGCC 15919
Db
801 CCGGCGTGTCAATATATCATCTGTGTACATCCAAACAGACGATRAACGGCTCTCTCTTT 860
Qy
15918 TGGCCAGTGCAGCTGTGCTGTGATGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCTATA 15859
Db
861 TATAGGTGTAACCTTAAACTGCAATTTACCC-----AGTCCTGTCTCTCGTCAGCAAAA 914
Qy
15858 TCGGGGATGAAGCTGGCGCATGATGACCAACCGATATGCCAGTGTGCGGTCTCGGTTA 15799
Db
915 GAGCGGTTTCAATTAATAACCGGGCGAGCTCAGCCATCCCTTCTGTATTTCCGCTTTTC 974
Qy
15798 TCGGGGAAGAGTGGCTGTCTCAGCCACCGCGAATAATGACATCAAAAACGCCATTTAAAC 15739
Db
975 CAGCGTTC---GGCAGCGAGAGCGGGCTTCATCTGCTGATGTTGCTTACCGACCG 1031
Qy
15738 TGATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACAG-----CCAGTCTG 15688
Db
1032 GAGATATTGACATCATATATGCTTCAGCAACTGATAGTGTGCTGTCAACTGTCACTG 1091
Qy
15687 CAGGTGATACAGTAGAATACAGAACTTTATACGTTTAGTAGTATAGAGGCTGAA 15628
Db
1092 TAATACGCTGTTTCAAGCACACCTCTTTTGTACATCTCTCGGTTAGT-----CCGATCA 1147
Qy
15627 AATCCAGATGAAGCCGAAACGACTGTGAAGAGAAAGTATAAAGAGTTGTGAAATCCGATCA 15568
Db
1148 ACCTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGCGACACCGAGA 1207
Qy
15567 ACCTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGCGACACCGAGA 15508
Db
1208 TTTATTTATTTCTCGAAGTGANCTTCGCTCAGAGTATTATTATTCGGCGCAAAAGTGGCTCG 1267
Qy
15507 TTTATTTATTTCTCGAAGTGANCTTCGCTCAGAGTATTATTATTCGGCGCAAAAGTGGCTCG 15448
Db
1268 GGTGATGCTCCCACTTAGTCTGACAGTACAGTCACTATACCATCTAAGTAGTTGATTCAT 1327
Qy
15447 GGTGATGCTCCCACTTAGTCTGACAGTACAGTCACTAATACCATCTAAGTAGTTGATTCAT 15388
Db
1328 AGTGACTGGATATGTTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAA 1387
Qy
15387 AGTGACTGGATATGTTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAA 15328
Db
1388 TTTAATATATTTGATATTTATATCATTTTACGTTTCTCGTTTACGCTTTCTTTGTACAAAGTG 1447
Qy
15327 TTTAATATATTTGATATTTATATCATTTTACGTTTCTCGTTTACGCTTTCTTTGTACAAAGTG 15268
Db
1448 GTCTCGAGGAATTCGGTACCACTGTAAAGGAATAATATTTCTTTTCTTTTCTTTTGTAT 1507
Qy
15267 GTCTAGAGGAATCCAGGCTTAAGGTAAGTAACTGTGAATCAATCCAAATGTAAAGTCAATGA 15208
Db
1508 TAAAAATAGTTAAGTGATTTAATTTAGTATGATTATATATATATATAGTTGTTTATATTTGTGA 1567
Qy
15207 TAACACATGACATGATCTATCATGTTACCTTGTATTATTCATGTTGCGACTTAATTCATTTA 15148
Db

1568 AAAATAATTTTATAATATATATTTGTTTACATAAAACAAATAGTAATGTAAAAAATATGAC 1627
Qy
15147 ATTAATAGTCAATCCATTTTAGAAGTTAATAAAACCTACAGTATTATTATTGAAATTAATA 15088
Db
1628 AAGTGATGTGTAAGCAGGAAGATAAAAGTTGAGAGTAAGTATATATTTTAAATGAAT 1687
Qy
15087 GAATGTTGATTGAAATTAATCTATATATAATGATAGATCTTGCGCTTTGTTATATTAGC 15028
Db
1688 TTGATCGAACATGTAAGATGATATACAGCAATTAATTTGTTTAAATCATAAATAGTAAAT 1747
Qy
15027 ATTAGATTATGTTTGTGTTACATTAGATTACTGTTTCTATTAGTTGATATTATTGTTTAC 14968
Db
1748 TCTAGCTGTTTGTAGTAATTAATAATCAATGATAAAATACATATATAAATAAAGATAA 1807
Qy
14967 TTTAGCTTGTATTAAATATTGTTTATTGATAAATACAAAGCAGATTGGAAATTTCTAA 14908
Db
1808 ATAAATTAATAATATTTTATGATTAATAGTTTATATAAATTAATAATCTATATAC 1867
Qy
14907 CAAAATATTATTAACTTTTAAACTTAAATATTTAGTAATGGTATAGATATTAAATTATA 14848
Db
1868 CATTAATAATATTGTTTAAAGTTAAATAATTTTGTAGAAATTCCTCAATCTGCT 1927
Qy
14847 TAATAAATCTTAATCATAAATAAATAATTTTAATTTATTTTCTTATTCTTTTACTAT 14788
Db
1928 TGTAAATTTTATCAATAAACAATAATTAATAAACAGCTAAAGTAAACAATAATATCAAA 1987
Qy
14787 AGTATTTTATCATGATATTAAATTTTCAAAACAGCTAGAAATTAATATGATTAAAA 14728
Db
1988 TAATAAGAACAGTAACTAATGTAAACAAACATAATCTAATGCTAATTAATAACAAAGCGA 2047
Qy
14727 CAAATATTAAATGCTAGTATATCATCTTACATGTTGCGATCAAAATTCATTTAAAAAATA 14668
Db
2048 AGATCTATCATTTTATATAGTATTATTTTCAATCAACATCTCTTATTAATTTCTAATAAT 2107
Qy
14667 CTTACTCTCAACTTTTATCTTCTGCTTACATGATCACTGTGATATTTTTCATATTA 14608
Db
2108 ACTTGTAGTTTATTAATCTTCTAAATGGATTGACTATTAAATTAATGAATTTAGTCCGAACA 2167
Qy
14607 CTTATGTTGTTATGTAACAATAATATTATAAATTTTATTAATTTTTCACAAATTTATAACA 14548
Db
2168 TGAATAAACAAGGTAACATGATAGATCAATGTCATTTGTTTATCATTTGATTTTACATTTGG 2227
Qy
14547 ATTATTATAATCATACTAATTAACATCACTTAACATTTTATATACATAAAGGAAAAAGAA 14488
Db
2228 ATTGATTACAGTTACTTACCTTAAAGTTGGATCCCTCTAGACCACTTTGTACAGAAAGCT 2287
Qy
14487 AATAATTTTCTTACAGTTGTTACCGAATTTCTCGAGACCACTTTGTACAGAAAGCT 14428
Db
2288 GAACGAGAAAACGTAAAAATGATATAATATCAATATTAATAATTAAGATTGTTGATAAAAA 2347
Qy
14427 GAACGAGAAAACGTAAAAATGATATAATATCAATATTAATAATTAAGATTGTTGATAAAAA 14368
Db
2348 CAGACTACATAATCTGTAAAAACACATATCCAGTCACTATGAATCAACTACTTAGAT 2407
Qy
14367 CAGACTACATAATCTGTAAAAACACATATCCAGTCACTATGAATCAACTACTTAGAT 14308
Db
2408 GGTATTAGTGACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGAGCGCACTTTGCGCCGAA 2467
Qy
14307 GGTATTAGTGACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGAGCGCACTTTGCGCCGAA 14248
Db
2468 TAAATACCTGTGACGGAAGATCACTTCGAGAAATAATAAATCTCTGGTGTCCCTGTTGAT 2527
Qy
14247 TAAATACCTGTGACGGAAGATCACTTCGAGAAATAATAAATCTCTGGTGTCCCTGTTGAT 14188
Db
2528 ACCGGGAACCTCGGCCAACTTTTGGGAAATGAGAGTTGATCGGATTTTCAACAATC 2587
Qy
14187 ACCGGGAACCTCGGCCAACTTTTGGGAAATGAGAGTTGATCGG-----CACTACCC 14132
Db
2588 TTATATCTTTTCTTACAAAGTCTGGCTTCATCTGGATTTTTCAGCCCTCTTACTTACT 2647
Qy
14131 GAAGTATGTCAAAAGAGGTTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGA 14072
Db

Qy	3798	CGGTTCCGGTTCATTCTAATGAATATATACCCGGTACTATCGTATTTTATGAATATTA	3857
Db	17020	CGGTTTCCGGTTCATTCTAATGAATATATACCCGGTACTATCGTATTTTATGAATATTA	17079
Qy	3858	TTCTCCGGTTCAAATTTACTGATTTGACCTCTACTACTTATATGTCACAAATTTAAAATGAAAA	3917
Db	17080	TTCTCCGGTTCAAATTTACTGATTTGACCTCTACTACTTATATGTCACAAATTTAAAATGAAAA	17139
Qy	3918	CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGCGGCACAATACAAA	3977
Db	17140	CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGCGGCACAATACAAA	17199
Qy	3978	CAATCCGGTTTTATTATTACAAATCCAAATTTTAAAAAGCGGCAGAACCGGTCAAAACCT	4037
Db	17200	CAATCCGGTTTTATTATTACAAATCCAAATTTTAAAAAGCGGCAGAACCGGTCAAAACCT	17259
Qy	4038	AAAAGACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAC	4097
Db	17260	AAAAGACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAC	17319
Qy	4098	GACACACCGAGCGCGAACTAATAAGCTTCACATGAAGGAACTCCGGTTCCCGCGCGCG	4157
Db	17320	GACACACCGAGCGCGAACTAATAAGCTTCACATGAAGGAACTCCGGTTCCCGCGCGCG	17379
Qy	4158	CGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCTACCGAAAAGTTACGGG	4217
Db	17380	CGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCTACCGAAAAGTTACGGG	17439
Qy	4218	CACATTCAAACCCGGTCCAGACACGGCGCGGGTAAACCGACTTGTCTGCCCGAGAAATTAT	4277
Db	17440	CACATTCAAACCCGGTCCAGACACGGCGCGGGTAAACCGACTTGTCTGCCCGAGAAATTAT	17499
Qy	4278	GCAGCATTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGA	4337
Db	17500	GCAGCATTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGA	17559
Qy	4338	CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGCACAAACATGTCGAGGCTCAGCAGG	4397
Db	17560	CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGCACAAACATGTCGAGGCTCAGCAGG	17619
Qy	4398	ACCTGCAGGCATGCAGCTAGCTTACTGATGTCATATTTCTATAGTGTCACTTAAATCT	4457
Db	17620	ACCTGCAGGCATGCAGCTAGCTTACTGATGTCATATTTCTATAGTGTCACTTAAATCT	17679
Qy	4458	GC 4459	
Db	17680	GC 17681	
RESULT 4			
ABQ82130	ID	ABQ82130 standard; DNA; 18691 BP.	
XX	AC	ABQ82130;	
XX	DT	11-DEC-2002 (first entry)	
XX	DE	Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.	
XX	DE	Chimeric nucleic acid construct; recombinational cloning; silencing;	
XX	KW	recombination site; double stranded RNA; plant; ds.	
XX	OS	Synthetic.	
XX	PN	WC200259294-A1.	
XX	PD	01-AUG-2002.	
XX	XX	24-JAN-2002; 2002WO-AU000073.	
XX	XX	26-JAN-2001; 2001US-0264067P.	
XX	XX	29-NOV-2001; 2001US-0333743P.	

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Wesley S, Waterhouse P, Helliwell C;

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 13; Page 62-72; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

XX	SQ	Sequence	18691 BP;	4837 A;	4621 C;	4607 G;	4626 T;	0 U;	0 Other;	
		Query Match	71.4%;	Score	3182.2;	DB	6;	Length	18691;	
		Best Local Similarity	79.1%;	Pred. No.	0;					
		Matches	4406;	Conservative	0;	Mismatches	28;	Indels	1137;	Gaps 7;
QY	26	GACAGCTTTGTACAAAAAGCTGGAACGAGAGAACGTAATAATGATATAAATATCAATATATT	85							
DB	13121	GCCAACTTTTGTAACAAAAAGCTGGAACGAGAGAACGTAATAATGATATAAATATCAATATATT	13180							
QY	86	AAATTAGATTTTGCATATAAAAAACAGCATACATATACTGTGTAAAAACAAACATATCCAGTC	145							
DB	13181	AAATTAGATTTTGCATATAAAAAACAGCATACATATACTGTGTAAAAACAAACATATCCAGTC	13240							
QY	146	ACTATCAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA	205							
DB	13241	ACTATGAAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA	13300							
QY	206	TGTTCTTCGGGTGAAGTCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA	265							
DB	13301	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA	13360							
QY	266	ACGGAATCGTCGATCCAGCCTACTCGCTATGTGCTCAATGCGGTATTAATCATATAAA	325							
DB	13361	ACGGAATCGTCGATCCAGCCTACTCGCTATGTGCTCAATGCGGTATTAATCATATAAA	13420							
QY	326	AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAACATCTACCT	385							
DB	13421	AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAACATCTACCT	13480							
QY	386	ATTCAATATACGCTAGTGTGCATAGTCCTGAAAATCATCTGCATCAAGAACAAATTTCAACAAC	445							
DB	13481	ATTCAATATACGCTAGTGTGCATAGTCCTGAAAATCATCTGCATCAAGAACAAATTTCAACAAC	13540							
QY	446	TCTTATATCTTTTCTCTTACAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACHTTA	505							
DB	13541	TCTTATATCTTTTCTCTTACAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACHTTA	13600							

Db	14800	AA	TAAAGAAATAAATAAAATTTAAATAATATATTTTTATGATTAATAATAGTTTATATATATAATTA	14859
Qy	14857	AA	TATCTATACCATTTACTTAATATATTTTAGTTTAAAGTTAAATAATATTTTGTGTAGAAAT	1916
Db	14860	AA	TATCTATACCATTTACTTAATATATTTTAGTTTAAAGTTAAATAATATTTTGTGTAGAAAT	14919
Qy	1917	TC	CAATCTGCTTGTAATTTTATCAATATAACAAAAATTTAAATTAACAAGCTAAAGTAACAAA	1976
Db	14920	TC	CAATCTGCTTGTAATTTTATCAATATAACAAAAATTTAAATTAACAAGCTAAAGTAACAAA	14979
Qy	1977	TA	ATATCAAACTAATAGAAAAAGTAATCTAATATGTATAACAAACATAATCTAATGCTAATAT	2036
Db	14980	TA	ATATCAAACTAATAGAAAAAGTAATCTAATATGTATAACAAACATAATCTAATGCTAATAT	15039
Qy	2037	BA	CAAGCGCAAGATCTATCATTTTATATAGTATATTTTCAATCAACATCTTATTAAT	2096
Db	15040	BA	CAAGCGCAAGATCTATCATTTTATATAGTATATTTTCAATCAACATCTTATTAAT	15099
Qy	2097	TT	CTAAAAATAACTTTGTAGTTTTTATTAACCTCTAAATGGATGACTATTAATTAATAATGAA	2156
Db	15100	TT	CTAAAAATAACTTTGTAGTTTTTATTAACCTCTAAATGGATGACTATTAATTAATAATGAA	15159
Qy	2157	TT	AGTCGAACATGAATATAACAGAGTAACATGATAGATCATGTCAATTTGTCTTATCATTTGAT	2216
Db	15160	TT	AGTCGAACATGAATATAACAGAGTAACATGATAGATCATGTCAATTTGTCTTATCATTTGAT	15219
Qy	2217	CT	TACATTTGGGATTGATTACAGTTACGTTACCT-----	2248
Db	15220	CT	TACATTTGGATTGATTACAGTTGGGAGCTGGGTTCGAAATCGATAAGCTTGCGCTGC	15279
Qy	2249	---	-----	2248
Db	15280	AG	TTATCATCATCATAGACACACAGAAATAAGTAATCAGATTATCAGTTTAAAGCTAT	15339
Qy	2249	---	-----	2248
Db	15340	GT	AATATTTGCGCCATAACCAATCAATATAAAATATAGATCAGTTTAAAGAAAGATCAAAG	15399
Qy	2249	---	-----	2248
Db	15400	CT	CAAAAAATAAAGAGAAAAGGGTCTTAACCAAGAAAAATGAAGAGAGAAAACTAGAA	15459
Qy	2249	---	-----	2248
Db	15460	AT	TACCTGCACAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAAACGAGAAA	15519
Qy	2298	CG	TAAATGATATAATATCAATATATATAATATAGATTTTGCATMAAAAAACAGACTACAT	2357
Db	15520	CG	TAAATGATATAATATCAATATATATAATATAGATTTTGCATMAAAAAACAGACTACAT	15579
Qy	2358	AA	TACTGTAAAAACAACATATCCAGTCACATGAATCAACTACTTATAGATGGTATTAGTG	2417
Db	15580	AA	TCTGTAAAAACACACATATCCAGTCACATGAATCAACTACTTATAGATGGTATTAGTG	15639
Qy	2418	AC	CTGTAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGGAATAATACCTG	2477
Db	15640	AC	CTGTAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGGAATAATACCTG	15699
Qy	2478	TG	ACGGAAGATCACTTCGCAGAAATAATAATCTGGTGCTCCCTGTTGATACCCGGGAAGC	2537
Db	15700	TG	ACGGAAGATCACTTCGCAGAAATAATAATCTGGTGCTCCCTGTTGATACCCGGGAAGC	15759
Qy	2538	CT	TGGGCGAAATGAGACGTTGATCGGATTTCAAACTCTTATACCTTTT	2597
Db	15760	CT	TGGGCGAAATGAGACGTTGATCGGATTTCAAACTCTTATACCTTTT	15819
Qy	2598	CT	TCTTACAAGTCGTTCCGCTTCATCTGGATTTTTCAGCCTCTATACCTTACTTAAACGTGATA	2657
Db	15820	CT	TCTTACAAGTCGTTCCGCTTCATCTGGATTTTTCAGCCTCTATACCTTACTTAAACGTGATA	15879
Qy	2658	AA	GTTCGTGTAATTTCTACTGTATCGACTGCAGCTGCTGTGTATTAAGGAGCCTGCAC	2717
Db	15880	AA	GTTCGTGTAATTTCTACTGTATCGACTGCAGCTGCTGTGTATTAAGGAGCCTGCAC	15939

QY	2718	ATTATATATCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTTTCGCGTGGCTG	2777
DB	15940	ATTATATATCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTTTCGCGTGGCTG	15999
QY	2778	AGATCAGCCACTTCTTCCCGATTAACGGAGACGGGCACTGGGCCATATCGTGCTCATC	2837
DB	16000	AGATCAGCCACTTCTTCCCGATTAACGGAGACGGGCACTGGGCCATATCGTGCTCATC	16059
QY	2838	ATGGCGAGCTTTCATCCCGATATGACACACCGGTTAAAGTTTCACGGAGACTTTATCT	2897
DB	16060	ATGGCGAGCTTTCATCCCGATATGACACACCGGTTAAAGTTTCACGGAGACTTTATCT	16119
QY	2898	GACAGCAGCTGCACCTGGCCAGGGGGATACACATCCGTCGCCCGGGCGTGTCAATAATA	2957
DB	16120	GACAGCAGCTGCACCTGGCCAGGGGGATACACATCCGTCGCCCGGGCGTGTCAATAATA	16179
QY	2958	TCACCTCTGTACATCCACAAAACAGACGATPAAACGGCTCTCTCTTTATAGGTGTAAACCTTA	3017
DB	16180	TCACCTCTGTACATCCACAAAACAGACGATPAAACGGCTCTCTCTTTATAGGTGTAAACCTTA	16239
QY	3018	AATCGCATTTACACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTCATAAACC	3077
DB	16240	AATCGCATTTACACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTCATAAACC	16299
QY	3078	GGCGACCTCAGCATCCCTCTCTGATTTTTCCGCTTTCAGCGTTCCGGACGACGACG	3137
DB	16300	GGCGACCTCAGCATCCCTCTCTGATTTTTCCGCTTTCAGCGTTCCGGACGACGACG	16359
QY	3138	GGCTTCATTTCTGCATGGTTGTGCTTACAGACCGGAGATATTGACATCATATATGCCCTG	3197
DB	16360	GGCTTCATTTCTGCATGGTTGTGCTTACAGACCGGAGATATTGACATCATATATGCCCTG	16419
QY	3198	AGCAACTGATGCTGTCGCTGTCACCTGTCACTGTAACTACGCTGCTTCATAGCACACCTC	3257
DB	16420	AGCAACTGATGCTGTCGCTGTCACCTGTCACTGTAACTACGCTGCTTCATAGCACACCTC	16479
QY	3258	TTTTTGACATCTCTGTTCTTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATA	3317
DB	16480	TTTTTGACATCTCTGTTCTTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATA	16539
QY	3318	TGAATAGGTAGATGTTTTTATTTTTGTCAACAAAAAGGGTCGCACCTCTTTTCTTATA	3377
DB	16540	TGAATAGGTAGATGTTTTTATTTTTGTCAACAAAAAGGGTCGCACCTCTTTTCTTATA	16599
QY	3378	TTTTCTTTTATGATTTAATACGGCATGTAGGACAAATAGCAGTAGGCTGGATACGACAT	3437
DB	16600	TTTTCTTTTATGATTTAATACGGCATGTAGGACAAATAGCAGTAGGCTGGATACGACAT	16659
QY	3438	TCGGTTTGAGAGAAACATTTGGAAAGCTGTCCGTCGACTAAGTTGGCAGCATACCCGAA	3497
DB	16660	TCGGTTTGAGAGAAACATTTGGAAAGCTGTCCGTCGACTAAGTTGGCAGCATACCCGAA	16719
QY	3498	GAAATTTTGAAGGCTGTCCGTCGACTAATACCATCTAAGTAGTTGATTC	3557
DB	16720	GAAATTTTGAAGGCTGTCCGTCGACTAATACCATCTAAGTAGTTGATTC	16779
QY	3558	ATAGTGACTGGATATGTTGTTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCT	3617
DB	16780	ATAGTGACTGGATATGTTGTTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCT	16839
QY	3618	AAATTAATATATGATATTTATATCAATTTACGTTTTCTCGTTCAGCTTTTTGTGACAAAC	3677
DB	16840	AAATTAATATATGATATTTATATCAATTTACGTTTTCTCGTTCAGCTTTTTGTGACAAAC	16899
QY	3678	TTGTCTAGGCTCTGCTTTTAATGAGATATGGAGACGCTATGATCCGATGATTTGCT	3737
DB	16900	TTGTCTAGGCTCTGCTTTTAATGAGATATGGAGACGCTATGATCCGATGATTTGCT	16959
QY	3738	TTCAATTTCTGTTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATTCCTACCGC	3797
DB	16960	TTCAATTTCTGTTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATTCCTACCGC	17019

region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

XX
SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

Query Match 94.2%; Score 4200; DB 6; Length 17681;
Best Local Similarity 95.0%; Pred No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;

QY 1 TTTCATTTGGAGAGACACGCTCGAGACAAGTTTCTACAAAAAGCTGAAACGAGAAAGCT 60
DB 13000 TTTCATTTGGAGAGACACGCTCGAGACAAGTTTCTACAAAAAGCTGAAACGAGAAAGCT 13059

QY 61 AAAATGATATAAATATCAATATTAATTAATAGATTTTGCATAAAAAAGACATACATAAT 120
DB 13060 AAAATGATATAAATATCAATATTAATTAATAGATTTTGCATAAAAAAGACATACATAAT 13119

QY 121 ACTGTAAAAACAAACATATCCAGTCACTATGATCAACTACTTAGATGATTAAGTGACC 180
DB 13120 ACTGTAAAAACAAACATATCCAGTCACTATGATCAACTACTTAGATGATTAAGTGACC 13179

QY 181 TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTGCGCAACTTAGTCGACGG 240
DB 13180 TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTGCGCAACTTAGTCGACGG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCGCAACGAATCGTGTATCCAGCTACTCGCTATTGTC 300
DB 13240 ACAGCCTTCCAAATGTTCTTCGCAACGAATCGTGTATCCAGCTACTCGCTATTGTC 13299

QY 301 CTCATATGCGGTATTAATCATAAAAAGAAATGAAGAAAGAGGTGCGACCTCTTTTGG 360
DB 13300 CTCATATGCGGTATTAATCATAAAAAGAAATGAAGAAAGAGGTGCGACCTCTTTTGG 13359

QY 361 TGTGACAAAATAAAAACATCTACCTATTTCATATACGCTAGTGTCAATGTCCTGAAAAATCA 420
DB 13360 TGTGACAAAATAAAAACATCTACCTATTTCATATACGCTAGTGTCAATGTCCTGAAAAATCA 13419

QY 421 TCTGATCAAGAACAAATTTCAACATCTTATATCTTTCTTACAGTGTGTTCCGGCTTCA 480
DB 13420 TCTGATCAAGAACAAATTTCAACATCTTATATCTTTCTTACAGTGTGTTCCGGCTTCA 13479

QY 481 TCTGGATTTTCAGCCTCTTACTACTTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTA 540
DB 13480 TCTGGATTTTCAGCCTCTTACTACTTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTA 13539

QY 541 TCGACTCGACAGTGGCTGTATTAAGGAGGCTTGACATTTATTTATTTCCCCAGAACATCAG 600
DB 13540 TCGACTCGACAGTGGCTGTATTAAGGAGGCTTGACATTTATTTATTTCCCCAGAACATCAG 13599

QY 601 GTTAATGGGGTTTTTTCATGTCATTTTTCGGGTGCTGAGATCAGCACCTTCTTCCCGGAT 660
DB 13600 GTTAATGGGGTTTTTTCATGTCATTTTTCGGGTGCTGAGATCAGCACCTTCTTCCCGGAT 13659

QY 661 AACGGAGACCGGACATCGGCCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGGAT 720
DB 13660 AACGGAGACCGGACATCGGCCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGGAT 13719

QY 721 ATGCACACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGGTGCATCGGCCAG 780

DB 13720 ATGCACACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAG 13779

QY 781 GGGGATCACCACATCGTCGCCCGCGCGTGTCAATAATATCACTCTGTATACATCCACAAAACAG 840

DB 13780 GGGGATCACCACATCGTCGCCCGCGCGTGTCAATAATATCACTCTGTATACATCCACAAAACAG 13839

QY 841 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGT 900

DB 13840 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGT 13899

QY 901 TCTCGTCAGCAAAAGACCGCTTCATTTCAATAAACCGGGGACCTCAGCATCCCTTCCT 960

DB 13900 TCTCGTCAGCAAAAGACCGCTTCATTTCAATAAACCGGGGACCTCAGCATCCCTTCCT 13959

QY 961 GATTTTCCGGTTTCCACGGTTCGGCACGACGACGCGGGTTCATTTCTGATGTTGTGTC 1020

DB 13960 GATTTTCCGGTTTCCACGGTTCGGCACGACGACGCGGGTTCATTTCTGATGTTGTGTC 14019

QY 1021 TTACCAGACCGGAGATATTGACATCATATATATGCTTGCCTTGAGCAACTGATAGTGTGCTGTC 1080

DB 14020 TTACCAGACCGGAGATATTGACATCATATATGCTTGCCTTGAGCAACTGATAGTGTGCTGTC 14079

QY 1081 AACTGTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGGACATACATCTTCGGGTAGTG 1140

DB 14080 AACTGTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGGACATACATCTTCGGGTAGTG 14139

QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGACGGCTTCCCGGTATCAACAGGGAC 1200

DB 14140 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGACGGCTTCCCGGTATCAACAGGGAC 14199

QY 1201 ACCAGGATTTATTTATTTCTGCGAAGTGTATCTTCGCTCACAGGTATTTATTCGGGCGAAAG 1260

DB 14200 ACCAGGATTTATTTATTTCTGCGAAGTGTATCTTCGCTCACAGGTATTTATTCGGGCGAAAG 14259

QY 1261 TGGCTCGGGTGCATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGT 1320

DB 14260 TGGCTCGGGTGCATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGT 14319

QY 1321 GATTCAATAGTCACTGGATATGTTGTTTATACAGTATTTATGATGTCTGTTTTTATGCAA 1380

DB 14320 GATTCAATAGTCACTGGATATGTTGTTTATACAGTATTTATGATGTCTGTTTTTATGCAA 14379

QY 1381 AATCTAATTTAATATTTATTTATATCAATTTTACATTTTCTGTTCCAGCTTCTTGTGA 1440

DB 14380 AATCTAATTTAATATTTATTTATATCAATTTTACATTTTCTGTTCCAGCTTCTTGTGA 14439

QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCAAC---TGTAAAGGAATAATTTATTTCTTTT 1496

DB 14440 CAAAGTGTCTCGAGGAATTCGGTACCAAC---TGTAAAGGAATAATTTATTTCTTTT 14499

QY 1497 TCCTTTTAGTATAAATAGTTAAGTGTATTAATTTAGTATGATTAATAATAATATAGTTGT 1556

DB 14500 TCCTTTTAGTATAAATAGTTAAGTGTATTAATTTAGTATGATTAATAATAATATAGTTGT 14559

QY 1557 TATAATTTGAAAAAATAATTTATTAATAATTTGTTTACATAAACAACATAGTATGTA 1616

DB 14560 TATAATTTGAAAAAATAATTTATTAATAATTTGTTTACATAAACAACATAGTATGTA 14619

QY 1617 AAAAAATATGACAAGTGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAGTATATAT 1676

DB 14620 AAAAAATATGACAAGTGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAGTATATAT 14679

QY 1677 TTTTAATGAATTTGATCGAACATGTAAGATGATATATAGCAATTAATTTGTTTAAATC 1736

DB 14680 TTTTAATGAATTTGATCGAACATGTAAGATGATATATAGCAATTAATTTGTTTAAATC 14739

QY 1737 ATAAATAGTAATTTCTAGCTGGTTTGAATTAATTAATTAATCAATGATAAATACATATAGTAA 1796

DB 14740 ATAAATAGTAATTTCTAGCTGGTTTGAATTAATTAATTAATCAATGATAAATACATATAGTAA 14799

QY 1797 AATAAGATAAATAAATAAATAATATTTTATGATTAATAGTTTATATATAAATTA 1856

Db 15940 GGATCACCATCGTCCGCGCGGTGTCAATAATATCACTCTGTACATCCCAACAGAC 15999
QY 2983 GATACGGCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACCACTCCCTGTTCC 3042
Db 16000 GATAACGGCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACCACTCCCTGTTCC 16059
QY 3043 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCTGA 3102
Db 16060 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCTGA 16119
QY 3103 TTTTCGGCTTTCAGGGTTTCGCGACGCGACGAGCGGCTTCATTTCTGCAATGTTGCTTT 3162
Db 16120 TTTTCGGCTTTCAGGGTTTCGCGACGCGACGAGCGGCTTCATTTCTGCAATGTTGCTTT 16179
QY 3163 ACCAGACCGGAGATTTGACATCATATATGCTTCAGCAACTGATAGCTGTCGCTGTCAA 3222
Db 16180 ACCAGACCGGAGATTTGACATCATATATGCTTCAGCAACTGATAGCTGTCGCTGTCAA 16239
QY 3223 CTGTCACTGTAATACGCTCTTCATAGCACACCTCTTTTGTGACATCTCTCTCTCTGAT 3282
Db 16240 CTGTCACTGTAATACGCTCTTCATAGCACACCTCTTTTGTGACATCTCTCTCTCTGAT 16299
QY 3283 GCAGATGATTTTCAGGACTATGACACTAGCTAGCTATGATAGTATGATGATGATTTT 3342
Db 16300 GCAGATGATTTTCAGGACTATGACACTAGCTAGCTATGATAGTATGATGATGATTTT 16359
QY 3343 TCACACAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAACGGCA 3402
Db 16360 TCACACAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAACGGCA 16419
QY 3403 TTGAGGACAAATAGCGAGTGGGTGGAATACGAGATTCGCTTTGAGAGAAACATTTGGAA 3462
Db 16420 TTGAGGACAAATAGCGAGTGGGTGGAATACGAGATTCGCTTTGAGAGAAACATTTGGAA 16479
QY 3463 GCTGTCGCTCGATAGTTGGGAGCATCACCGAGAAACATTTGGAAGGCTGTCGTCGA 3522
Db 16480 GCTGTCGCTCGATAGTTGGGAGCATCACCGAGAAACATTTGGAAGGCTGTCGTCGA 16539
QY 3523 CTACAGCTCACTAATACCACTAAGTAGTGTGATTCATAGTGTGATGATGATGATGATTT 3582
Db 16540 CTACAGCTCACTAATACCACTAAGTAGTGTGATTCATAGTGTGATGATGATGATGATTT 16599
QY 3583 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3642
Db 16600 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16659
QY 3643 ATTTTACGTTTCTCGTTTCAGCTTTTGTACAACTTGTCTAGAGTCTGCTTTTATGAG 3702
Db 16660 ATTTTACGTTTCTCGTTTCAGCTTTTGTACAACTTGTCTAGAGTCTGCTTTTATGAG 16719
QY 3703 ATATCGAGACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3762
Db 16720 ATATCGAGACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16779
QY 3763 AAAACCTGACATGCTAGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 3822
Db 16780 AAAACCTGACATGCTAGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 16839
QY 3823 TATCACCGTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3882
Db 16840 TATCACCGTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16899
QY 3883 CCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3942
Db 16900 CCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16959
QY 3943 TAGCGACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4002
Db 16960 TAGCGACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 17019
QY 4003 CAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAATAATCTTAT 4062

Db 17020 CAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAATAATCTTAT 17079
QY 4063 TCAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAATAATCTTAT 4122
Db 17080 TCAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAATAATCTTAT 17139
QY 4123 CGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGCATGGGTGAGATTCCTTGAAGTT 4182
Db 17140 CGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGCATGGGTGAGATTCCTTGAAGTT 17199
QY 4183 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGACCACTTCAACCGGTCACGACGG 4242
Db 17200 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGACCACTTCAACCGGTCACGACGG 17259
QY 4243 CGGCGGGTAAACCGACTTGTCTGCCCCCGAGAAATTAAGCAGCAATTTTGGTGTATGTTGG 4302
Db 17260 CGGCGGGTAAACCGACTTGTCTGCCCCCGAGAAATTAAGCAGCAATTTTGGTGTATGTTGG 17319
QY 4303 CCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAATTCGTTGGGCGGTCACG 4362
Db 17320 CCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAATTCGTTGGGCGGTCACG 17379
QY 4363 GCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGCTCAGCAGGCTGCAAGCTGCAAGCTAGCTTA 4422
Db 17380 GCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGCTCAGCAGGCTGCAAGCTGCAAGCTAGCTTA 17439
QY 4423 CTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4459
Db 17440 CTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 17476

RESULT 3
ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHEILSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX WPI; 2002-682669/73.
XX
XX
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 17; Page 93-102; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter

QY 781 GGGATCAACCCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAG 840
Db 13780 GGGATCAACCCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAG 13839
QY 841 AGGATAAGCGGCTCTCTCTTTATAGGTGTAAACCTTAACTGCAATTCACAGTCCCTGT 900
Db 13840 AGGATAAGCGGCTCTCTCTTTATAGGTGTAAACCTTAACTGCAATTCACAGTCCCTGT 13899
QY 901 TCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCC 960
Db 13900 TCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCC 13959
QY 961 GATTTTCGCTTCCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCTGCAATGCTGTGTC 1020
Db 13960 GATTTTCGCTTCCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCTGCAATGCTGTGTC 14019
QY 1021 TTACCAAGCCGAGATATGACATATATGCTTGGCAACTGATAGCTGTGCTGTC 1080
Db 14020 TTACCAAGCCGAGATATGACATATATGCTTGGCAACTGATAGCTGTGCTGTC 14079
QY 1081 AACTGTCACTGAATACGCTGCTTCATAGCACACCTCTTTTGGACATATCTCGGCTAGTG 1140
Db 14080 AACTGTCACTGAATACGCTGCTTCATAGCACACCTCTTTTGGACATATCTCGGCTAGTG 14139
QY 1141 CCGATCAAGCTCTCAATTTTCGCAAAAGTGGCCCAAGGCTTCCGGTATCAACAGGAC 1200
Db 14140 CCGATCAAGCTCTCAATTTTCGCAAAAGTGGCCCAAGGCTTCCGGTATCAACAGGAC 14199
QY 1201 ACCAGGATTTATTTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAG 1260
Db 14200 ACCAGGATTTATTTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAG 14259
QY 1261 TCGCTCGGCTGATGCTGCCAATTAAGTGCATACAGGTCACTAATACCACTCAAGTAGTT 1320
Db 14260 TCGCTCGGCTGATGCTGCCAATTAAGTGCATACAGGTCACTAATACCACTCAAGTAGTT 14319
QY 1321 GATTCATAGTACTGATAGTGTGTTTACAGTATATGTAAGTCTGTTTATGCA 1380
Db 14320 GATTCATAGTACTGATAGTGTGTTTACAGTATATGTAAGTCTGTTTATGCA 14379
QY 1381 AATCTAAATTTATATATGATATTTATATCATTTTACGTTCTCGTTCAGCTTCTTGTA 1440
Db 14380 AATCTAAATTTATATATGATATTTATATCATTTTACGTTCTCGTTCAGCTTCTTGTA 14439
QY 1441 CAAAGTGTCTCGAGGAATTCGGTACC-----AAGTGTAAAGGAAATTAATTTCTTTT 1496
Db 14440 CAAAGTGTCTCGAGGAATTCGGTACC-----AAGTGTAAAGGAAATTAATTTCTTTT 14499
QY 1497 TCGTTTATGATAAATAGTAAAGTGTAAATAGTATGATATATAATATAGTTGT 1556
Db 14500 TCGTTTATGATAAATAGTAAAGTGTAAATAGTATGATATATAATATAGTTGT 14559
QY 1557 TATAATTTGAAAAAATAATTTATAAATATATTTTACATAAAACACATAGTAATGTA 1616
Db 14560 TATAATTTGAAAAAATAATTTATAAATATATTTTACATAAAACACATAGTAATGTA 14619
QY 1617 AAAAAATGCAAGTGTGTAAAGCAGGAAGATATAAAGTTGAGGTAAATATATAT 1676
Db 14620 AAAAAATGCAAGTGTGTAAAGCAGGAAGATATAAAGTTGAGGTAAATATATAT 14679
QY 1677 TTTTAATGAATTTGATCGAAGATGTAAGATGATATAGTATGATATATTTCTGTTTATC 1736
Db 14680 TTTTAATGAATTTGATCGAAGATGTAAGATGATATAGTATGATATATTTCTGTTTATC 14739
QY 1737 ATAATAGTAATTTAGCTGGTTTGAATTAATAATCAATGATAAAATACATATAGTAA 1796
Db 14740 ATAATAGTAATTTAGCTGGTTTGAATTAATAATCAATGATAAAATACATATAGTAA 14799
QY 1797 ATAAGAATAAATAAATTAATAATTTTATGATTAATAGTTTATATATAATTA 1856
Db 14800 ATAAGAATAAATAAATTAATAATTTTATGATTAATAGTTTATATATAATTA 14859

QY 1857 AATATCTATACCAATTTACTAAATATTTTAGTTTAAAGTTAATAATATTTTGTAGAAAT 1916
Db 14860 AATATCTATACCAATTTACTAAATATTTTAGTTTAAAGTTAATAATATTTTGTAGAAAT 14919
QY 1917 TCCAAATCTGCTGTAAATTTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAA 1976
Db 14920 TCCAAATCTGCTGTAAATTTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAA 14979
QY 1977 TAAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACAATAATCTAATGCTAATAT 2036
Db 14980 TAAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACAATAATCTAATGCTAATAT 15039
QY 2037 AACAAAGCGCAAGATCTATCAATTTATATAGTATTTTCAATCAACATCTTATTAAT 2096
Db 15040 AACAAAGCGCAAGATCTATCAATTTATATAGTATTTTCAATCAACATCTTATTAAT 15099
QY 2097 TTCTAATAATACTGTGTAGTTTATTAACCTTAATAATGGAATGACTATTAATTAATGAA 2156
Db 15100 TTCTAATAATACTGTGTAGTTTATTAACCTTAATAATGGAATGACTATTAATTAATGAA 15159
QY 2157 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTATCATTTGAT 2216
Db 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTATCATTTGAT 15219
QY 2217 CTTACATTTGGATTTACAGTTACTTACCT-----TAAAGCTTGGATCCT 2262
Db 15220 CTTACATTTGGATTTACAGTTTGGGAAGCTGGGTTTCAAAATCGATAAGCTTGGATCCT 15279
QY 2263 CTAGACCACTTTTGTACAAAGAAAGCTGAACGAGAAACGTTAAATGATATAAAATATCAATAT 2322
Db 15280 CTAGACCACTTTTGTACAAAGAAAGCTGAACGAGAAACGTTAAATGATATAAAATATCAATAT 15339
QY 2323 ATTAATTTAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAACACAAACATATCCA 2382
Db 15340 ATTAATTTAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAACACAAACATATCCA 15399
QY 2383 GTCATATGATCAACTACTTTAGATGGTATTTAGTGACCTGTAGTCGACTAAGTTGGCAGC 2442
Db 15400 GTCATATGATCAACTACTTTAGATGGTATTTAGTGACCTGTAGTCGACTAAGTTGGCAGC 15459
QY 2443 ATCACCCAGCAGCTTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCGAGAATA 2502
Db 15460 ATCACCCAGCAGCTTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCGAGAATA 15519
QY 2503 AATAAATCCTGGTCCCTGTGTGATACCGGAAGCCCTGGGCCAACCTTTTGGCGAAAAATG 2562
Db 15520 AATAAATCCTGGTCCCTGTGTGATACCGGAAGCCCTGGGCCAACCTTTTGGCGAAAAATG 15579
QY 2563 AGACGTTGATCGGATTTTCAACACTCTTATACCTTTCTTACAGTCTGCTGCTTCAATC 2622
Db 15580 AGACGTTGATCGGATTTTCAACACTCTTATACCTTTCTTACAGTCTGCTGCTTCAATC 15639
QY 2623 TGGATTTTCAGCCTCTATCTACTTAAACGTAATAAGTTTCTGTAAATTTCTACTGTATC 2682
Db 15640 TGGATTTTCAGCCTCTATCTACTTAAACGTAATAAGTTTCTGTAAATTTCTACTGTATC 15699
QY 2683 GACCTGAGACATGCGCTGTGTATAGGGAGCTGACATTTATTTCCCGAGAACATCAGGT 2742
Db 15700 GACCTGAGACATGCGCTGTGTATAGGGAGCTGACATTTATTTCCCGAGAACATCAGGT 15759
QY 2743 TAAATGCGGTTTTGTATGATGTCATTTTTCGCGTGGCTGAGATCAGCCATCTTCCCGATAA 2802
Db 15760 TAAATGCGGTTTTGTATGATGTCATTTTTCGCGTGGCTGAGATCAGCCATCTTCCCGATAA 15819
QY 2803 CGGAGACCGGACACATGCGCCATATCGGTGGTCACTCATCGCGCAGCTTTTTCATCCCGATAT 2862
Db 15820 CGGAGACCGGACACATGCGCCATATCGGTGGTCACTCATCGCGCAGCTTTTTCATCCCGATAT 15879
QY 2863 GCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGG 2922
Db 15880 GCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGG 15939
QY 2923 GGATCACCATCGTCCGCGCGCGGTGTCAATAATATCACTCTGTATATCCCAACACAGAC 2982

QY 4081 CAGGGGCTAGTATCTACGACACACCGAGCGGCAACTAATAACGTTCACTGAAGGAACT 4140
DB |||||
QY 17080 CAGGGGCTAGTATCTACGACACACCGAGCGGCAACTAATAACGTTCACTGAAGGAACT 17139
DB |||||
QY 4141 CCGGTTCCCGCGCGCGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCCGCTCCGCT 4200
DB |||||
QY 17140 CCGGTTCCCGCGCGCGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCCGCTCCGCT 17199
DB |||||
QY 4201 CTACCGAAAGTTACGGGACACCAATCAACCGGTCCAGCAGCGCGCGGTTAACCGACTT 4260
DB |||||
QY 17200 CTACCGAAAGTTACGGGACACCAATCAACCGGTCCAGCAGCGCGCGGTTAACCGACTT 17259
DB |||||
QY 4261 GCTGCCCCGAGAAATATGACGATTTTTTTGTTGTTGATGTGGCCCCCAATGAAGTGCAGG 4320
DB |||||
QY 17260 GCTGCCCCGAGAAATATGACGATTTTTTTGTTGTTGATGTGGCCCCCAATGAAGTGCAGG 17319
DB |||||
QY 4321 TCAAACTTGACAGTACGACGACAAATCGTTGGCGGGTCCAGGCGCAATTTGCGACACA 4380
DB |||||
QY 17320 TCAAACTTGACAGTACGACGACAAATCGTTGGCGGGTCCAGGCGCAATTTGCGACACA 17379
DB |||||
QY 4381 TGTGAGGCTCAGCAGGACCTCAGGCATGCAAGCTAGCTTACTAGTGTGATGATATTCTA 4440
DB |||||
QY 17380 TGTGAGGCTCAGCAGGACCTCAGGCATGCAAGCTAGCTTACTAGTGTGATGATATTCTA 17439
DB |||||
QY 4441 TAGTGTCACTAAATCTGC 4459
DB |||||
QY 17440 TAGTGTCACTAAATCTGC 17458
DB |||||

RESULT 2

AB082141
ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELSSGATE 8 nucleotide sequence SEQ ID NO:24.
XX
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
XX WO200259294-A1.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU0000073.
XX
XX 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX WPI; 2002-682669/73.
DR

XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.

PS Claim 15; Page 74-83; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and

CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX

SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 98.8%; Score 4406.6; DB 6; Length 17476;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;

QY 1 TTTTCATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACGAGAAAGCT 60
DB |||||
QY 13000 TTTTCATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACGAGAAAGCT 13059
DB |||||
QY 61 AAAATGATATAATATCAATATATAATAATTAGATTTTGCATAAAAAACAGACTACATAAT 120
DB |||||
QY 13060 AAAATGATATAATATCAATATATAATAATTAGATTTTGCATAAAAAACAGACTACATAAT 13119
DB |||||
QY 121 ACTGTAAAAACAACATATCCAGTCATATGAATCAACTACTTAGATGGTATTAGTGACC 180
DB |||||
QY 13120 ACTGTAAAAACAACATATCCAGTCATATGAATCAACTACTTAGATGGTATTAGTGACC 13179
DB |||||
QY 181 TGTAGTCGACGACAGCCTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 240
DB |||||
QY 13180 TGTAGTCGACGACAGCCTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 13239
DB |||||
QY 241 ACAGCCTTCCAAATGTTCTTCAAACGGAAATCGTCGATCCAGCCTACTCGCTATTGTC 300
DB |||||
QY 13240 ACAGCCTTCCAAATGTTCTTCAAACGGAAATCGTCGATCCAGCCTACTCGCTATTGTC 13299
DB |||||
QY 301 CTCAATGCCGTATTAATCATATAAAGAAATAAAGAAAGAGGTGCGAGCCTCTTTTTCG 360
DB |||||
QY 13300 CTCAATGCCGTATTAATCATATAAAGAAATAAAGAAAGAGGTGCGAGCCTCTTTTTCG 13359
DB |||||
QY 361 TGTGACAAAAATAAAAAACATCTACCTATTATATACGCTAGTGTGATAGTCTCTGAAAAATCA 420
DB |||||
QY 13360 TGTGACAAAAATAAAAAACATCTACCTATTATATACGCTAGTGTGATAGTCTCTGAAAAATCA 13419
DB |||||
QY 421 TCTGCATCAAGAACAAATTCACAACTCTTATACCTTTCTTTTCTTACAAGTCGTTTCGCTTCA 480
DB |||||
QY 13420 TCTGCATCAAGAACAAATTCACAACTCTTATACCTTTCTTTTCTTACAAGTCGTTTCGCTTCA 13479
DB |||||
QY 481 TCTGGATTTTCAGCCTCTATACCTTACTAAAGCTGATAAAGTTCTGTAATTTCTACTGTA 540
DB |||||
QY 13480 TCTGGATTTTCAGCCTCTATACCTTACTAAAGCTGATAAAGTTCTGTAATTTCTACTGTA 13539
DB |||||
QY 541 TCGACCTTCAGACTGGCTGTGTATATAAGGAGCGCTGACATTTATATTTCCCGAGAACATCAG 600
DB |||||
QY 13540 TCGACCTTCAGACTGGCTGTGTATATAAGGAGCGCTGACATTTATATTTCCCGAGAACATCAG 13599
DB |||||
QY 601 GTTAATGCGGTTTTTGTATGTCATTTTTCGCGGTGCTGAGATCAGGCACCTTCTTCCCGAT 660
DB |||||
QY 13600 GTTAATGCGGTTTTTGTATGTCATTTTTCGCGGTGCTGAGATCAGGCACCTTCTTCCCGAT 13659
DB |||||
QY 661 AACGAGACCGGCACTGGGCCATATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGAT 720
DB |||||
QY 13660 AACGAGACCGGCACTGGGCCATATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGAT 13719
DB |||||
QY 721 ATGCACCAACCGGGTAAAGTTTACCGGAGACTTTATCTACAGCAGACAGCTGCACTGGCCAG 780
DB |||||
QY 13720 ATGCACCAACCGGGTAAAGTTTACCGGAGACTTTATCTACAGCAGACAGCTGCACTGGCCAG 13779
DB |||||

Db 14860 TCTATACCATTACTAAATATTTTAGTTTAAAGTTTAAATAATTTTGTAGAAATTCGA 14919
QY 1921 ATCTGCTGTAAATTTATCAATAAACAATAATTAATAACACAGCTAAAGTAACAAAATAAT 1980
Db 14920 ATCTGCTGTAAATTTATCAATAAACAATAATTAATAACACAGCTAAAGTAACAAAATAAT 14979
QY 1981 ATCAAACCTAAATAGAAACAGTAAATCTAAATGTAACAAAACATAATCTAAATGTAATAACA 2040
Db 14980 ATCAAACCTAAATAGAAACAGTAAATCTAAATGTAACAAAACATAATCTAAATGTAATAACA 15039
QY 2041 AAGCCAGAGCTATCATTTTATATAGTATTTTCAATCAACATCTCTATTAATTTCT 2100
Db 15040 AAGCCAGAGCTATCATTTTATATAGTATTTTCAATCAACATCTCTATTAATTTCT 15099
QY 2101 AAATAAATCTGTAGTATTTTAACTCTCTAAATGATTGACTATTAATAATGAATTTAG 2160
Db 15100 AAATAAATCTGTAGTATTTTAACTCTCTAAATGATTGACTATTAATAATGAATTTAG 15159
QY 2161 TCGAACATGAATAAACAAGGTAAACATAGATCATGTCTATGTGTATCATTTGATCTTA 2220
Db 15160 TCGAACATGAATAAACAAGGTAAACATAGATCATGTCTATGTGTATCATTTGATCTTA 15219
QY 2221 CATTTGGATTGATACAGTTACTTACCTTAAGCTTTGGATCTCTAGACCACTTTGTACAA 2280
Db 15220 CATTTGGATTGATACAGTTACTTACCTTAAGCTTTGGATCTCTAGACCACTTTGTACAA 15279
QY 2281 GAAAGCTGAAACGAGAAACGTAATAATGATATAAATCAATATATAAATTAAGATTTTGCA 2340
Db 15280 GAAAGCTGAAACGAGAAACGTAATAATGATATAAATCAATATATAAATTAAGATTTTGCA 15339
QY 2341 TAAAAACAGACTACATTAATCTGTAAACACCAACATATCAAGTCACTATGAATCAACTA 2400
Db 15340 TAAAAACAGACTACATTAATCTGTAAACACCAACATATCAAGTCACTATGAATCAACTA 15399
QY 2401 CTTAGATGGTATTAGTGACCTGTAGTCGACCTAAGTTGGCAGCATCCCGACGCACTTTG 2460
Db 15400 CTTAGATGGTATTAGTGACCTGTAGTCGACCTAAGTTGGCAGCATCCCGACGCACTTTG 15459
QY 2461 CGCCGAATAAATPACCTGTGAAGAGATCACTTCGCAGAAATAAATAAATCTCTGTGTCCC 2520
Db 15460 CGCCGAATAAATPACCTGTGAAGAGATCACTTCGCAGAAATAAATAAATCTCTGTGTCCC 15519
QY 2521 TGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTGTGATCGGATTC 2580
Db 15520 TGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTGTGATCGGATTC 15579
QY 2581 ACAACTCTTATCTTTCTCTTACAGTCGTTTCGCGCTTCATCTGGATTTTCAGCCTCTAT 2640
Db 15580 ACAACTCTTATCTTTCTCTTACAGTCGTTTCGCGCTTCATCTGGATTTTCAGCCTCTAT 15639
QY 2641 ACTTACTAAACGTGATAAAGTTTCTGTAAATTTCTATCTGTATCGACCTGCAGACTGGCTGT 2700
Db 15640 ACTTACTAAACGTGATAAAGTTTCTGTAAATTTCTATCTGTATCGACCTGCAGACTGGCTGT 15699
QY 2701 GTATAAGGAGCGCTGACATTTATTTCCCGAGAACTCAGGTAAATGGGTTTTGTATGT 2760
Db 15700 GTATAAGGAGCGCTGACATTTATTTCCCGAGAACTCAGGTAAATGGGTTTTGTATGT 15759
QY 2761 CATTTTCGGGTGGCTGAGATCAGCACCTCTCTCCCGATACCGAGACCGGCACACTGG 2820
Db 15760 CATTTTCGGGTGGCTGAGATCAGCACCTCTCTCCCGATACCGAGACCGGCACACTGG 15819
QY 2821 CCATATCGGTGTCTATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTT 2880
Db 15820 CCATATCGGTGTCTATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTT 15879
QY 2881 CACGGGAGCTTTATCTGACGACGACGTCGCTGCGCCAGGGGATCAACATCGCTGCC 2940
Db 15880 CACGGGAGCTTTATCTGACGACGACGTCGCTGCGCCAGGGGATCAACATCGCTGCC 15939
QY 2941 CGGGGTGTCAATAATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTT 3000
Db 15940 CGGGGTGTCAATAATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTT 15999

QY 3001 TATAGGTGTAAACCTTTAAATTCGATTTTCAACAGTCCCTGTCTCGTCAGCAAAAGAGCGG 3060
Db 16000 TATAGGTGTAAACCTTTAAATTCGATTTTCAACAGTCCCTGTCTCGTCAGCAAAAGAGCGG 16059
QY 3061 TTAATTTCAATAAACCAGGCGGAGCTCAGCAATCCCTTCCTGTGATTTTCGGCTTTCCAGCGT 3120
Db 16060 TTAATTTCAATAAACCAGGCGGAGCTCAGCAATCCCTTCCTGTGATTTTCGGCTTTCCAGCGT 16119
QY 3121 TCGGCACGACGACGACGGGCTTCATCTGCATGCTGTCTGCTTACCAACCGGAGATATTG 3180
Db 16120 TCGGCACGACGACGACGGGCTTCATCTGCATGCTGTCTGCTTACCAACCGGAGATATTG 16179
QY 3181 ACATCATATATGCTTCGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTATATACGCT 3240
Db 16180 ACATCATATATGCTTCGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTATATACGCT 16239
QY 3241 GCTTCATAGCACACCTCTTTTGGACATACCTTCGCTTCTTGATCGAGATGATTTTCAGGAC 3300
Db 16240 GCTTCATAGCACACCTCTTTTGGACATACCTTCGCTTCTTGATCGAGATGATTTTCAGGAC 16299
QY 3301 TATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTACACAAAAAGAGGCT 3360
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QY 3421 AGGCTGATAGCAGGATTCGTTTGGAGAAACATTTTGGAGGCTGTTCGGTTCGACTAAGT 3480
Db 16420 AGGCTGATAGCAGGATTCGTTTGGAGAAACATTTTGGAGGCTGTTCGGTTCGACTAAGT 16479
QY 3481 TGGCAGCATCACCCGAGAAACATTTGGAAGGCTGTTCGGTTCGACTACAGGTCACTAATACC 3540
Db 16480 TGGCAGCATCACCCGAGAAACATTTGGAAGGCTGTTCGGTTCGACTACAGGTCACTAATACC 16539
QY 3541 ATCTAAGTATGATTCATAGTCTCGATATGTTGTGTTTTAAGATATATAGTATGATCTG 3600
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QY 3961 AGCCCAATAAACAATAATGCTTTTATTTATTAATAATCCAAATTTTAAAAAAGCGG 4020
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QY 4021 CAGAACCGGTCAAAACCTAAAAAGACTGATTAATAATCTTATTTCAAAATTTCAAAAGGCC 4080
Db 17020 CAGAACCGGTCAAAACCTAAAAAGACTGATTAATAATCTTATTTCAAAATTTCAAAAGGCC 17079

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;

Query Match 100.0%; Score 4459; DB 6; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db AAAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13119

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Db ACTGTAAACACAAATATCCAGTCACTATGAATCACTATGAATCACTATGAATCACTATGAAT 13179

QY 181 TGTAGTCGACGACGACGCTTCCAAATGTTCTTCGGGTGATGTCGCAACTAGTCGACCG 240
Db TGTAGTCGACGACGACGCTTCCAAATGTTCTTCGGGTGATGTCGCAACTAGTCGACCG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCTCAACGAATCGTGTATCCAGCCTACTCGCTATTGTC 300
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QY 301 CTCATATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGGAGCCCTTTTGTG 360
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QY 361 TGTGACAAATATAAATCATCTACTATTCATATACGCTAGTGTCTAGTGTCTGAAATCA 420
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QY 421 TCTGCAATCAAGACAAATTTCAACACTTATCTTTCTTTACAGTGTCTTCGGCTTCA 480
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QY 481 TCTGGAATTTTACGCTCTATCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 540
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QY 541 TCGACCTGACAGATCGGTGTGTAAGAGGAGCCTGACATTTATTTCCCGACAGATCAG 600
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QY 601 GTTAATGGGGTTTTTGTATGTCATTTTCGGGTGCTGAGATCAGCCACTTCTTCCCGGAT 660
Db GTTAATGGGGTTTTTGTATGTCATTTTCGGGTGCTGAGATCAGCCACTTCTTCCCGGAT 13659

QY 661 AAGCGAGACCGGACACACTGCGCCATATCGGTGGTCACTCATCGCGCAGCTTTTCATCCCGAT 720
Db AAGCGAGACCGGACACACTGCGCCATATCGGTGGTCACTCATCGCGCAGCTTTTCATCCCGAT 13719

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Db 13780 GGGGATCACCATCCGTGCGCGGGGGTGTCAATAATATCACTCTGTATCCCAACACAG 13839

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Db 14080 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGAACATCTTCGGGTAGT 14139

QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGAC 1200

Db 14140 CCGATCAACGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGAC 14199

QY 1201 ACCAGGATTTATTTATCTCGAAAGTATCTTCGTCACAGGTATTTATTCGGCGCAAG 1260

Db 14200 ACCAGGATTTATTTATCTCGAAAGTATCTTCGTCACAGGTATTTATTCGGCGCAAG 14259

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QY 1321 GATTCATAGTCACGTGATATGTTCTGTTTACAGTATTTATGCTGTTTATTTATGCA 1380

Db 14320 GATTCATAGTCACGTGATATGTTCTGTTTACAGTATTTATGCTGTTTATTTATGCA 14379

QY 1381 AATCTAATTTAATATATTTATATATCAATTTTACGTTTCTCGTTCAGCTTCTGTGA 1440

Db 14380 AATCTAATTTAATATATTTATATATCAATTTTACGTTTCTCGTTCAGCTTCTGTGA 14439

QY 1441 CAAGTGTCTCGAGGATTCGGTACCAACGTGAAGGAAATTAATTTCTCTTTTCT 1500

Db 14440 CAAGTGTCTCGAGGATTCGGTACCAACGTGAAGGAAATTAATTTCTCTTTTCT 14499

QY 1501 TTTAGTATAAAATAGTTAAGTGTAAATTTAATTTAGTATGATTAATAATATAGTTTGTATA 1560

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QY 1621 ATATCAACAGTGTGTGTAAGCAAGAAAGTGAAGTTGAGAGTAAGTATATTTT 1680

Db 14620 ATATCAACAGTGTGTGTAAGCAAGAAAGTGAAGTTGAGAGTAAGTATATTTT 14679

QY 1681 AATGAATTTGATCGAACATGTAAAGATGATATCTAGCATTAATTTGTTTAAATCAATA 1740

Db 14680 AATGAATTTGATCGAACATGTAAAGATGATATCTAGCATTAATTTGTTTAAATCAATA 14739

QY 1741 TAGTAATTTCTAGCTGGTTTGTATGAATTAATAATCAATGATAAATACTATAGTAAAAATA 1800

Db 14740 TAGTAATTTCTAGCTGGTTTGTATGAATTAATAATCAATGATAAATACTATAGTAAAAATA 14799

QY 1801 AGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1860

Db 14800 AGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 14859

QY 1861 TCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1920

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1027.16 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4459	100.0	17458	6	ABQ82142 Acceptor
2	4406.6	98.8	17476	6	ABQ82141 Acceptor
3	4200	94.2	17681	6	ABQ82143 Acceptor
4	3182.2	71.4	18691	6	ABQ82130 Acceptor
C 5	1305	29.3	17458	6	ABQ82142 Acceptor
C 6	1277.8	28.7	17476	6	ABQ82141 Acceptor
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9	1108.8	24.9	4892	8	ADA50329 Plasmid v
10	1108.8	24.9	4939	3	AAC55525 Donor pla
C 11	1108.8	24.9	5584	3	AAC55532 Donor pla
C 12	1108.8	24.9	5584	7	ABZ58766 Donor pla
13	1102.4	24.7	4428	7	ABZ58768 Destinati
14	1102.4	24.7	4627	7	ABZ58769 Destinati
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C 16	1072.8	24.1	17681	6	ABQ82143 Acceptor
17	989.6	22.2	4165	3	AAC55524 Donor pla
C 18	947.8	21.3	4208	3	AAC55523 Donor pla
C 19	827	18.5	4204	3	AAC55522 Donor pla
C 20	823.8	18.5	5156	3	AAC55526 Donor pla
C 21	769	17.2	786	3	AAC55526 Donor pla
22	769	17.2	786	9	ADD44386 Flaveria
23	747	16.8	7050	2	AAQ40419 Sequence

24	728.8	16.3	7566	2	AAQ42160 Plasmid p
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26	713	16.0	4947	3	AAZ60627 Nucleotid
27	711.4	16.0	3435	8	ACC85049 Nucleotid
C 28	710.2	15.9	7599	4	AAF25320 Nucleotid
29	709.8	15.9	5399	2	AAQ25706
30	709.8	15.9	6555	2	AAQ53874 Plasmid p
C 31	709.8	15.9	14194	4	AAC66932 Plant sig
C 32	707	15.9	24596	1	AAN50182 Complete
C 33	703.8	15.8	24593	1	AAN50226 Sequence
34	703	15.8	2867	7	ABZ68391 Nucleotid
C 35	621.6	13.9	18691	6	ABQ82130 Acceptor
C 36	597	13.4	1846	6	AAD44626 Gateway t
C 37	597	13.4	5148	6	AAD27063 Plasmid p
C 38	597	13.4	5957	3	AAC55467 Destinati
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C 41	597	13.4	6264	3	AAC55507 Destinati
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C 43	597	13.4	6422	3	AAC55483 Destinati
C 44	597	13.4	6464	3	AAC55454 Destinati
C 45	597	13.4	6526	3	AAC55471 Destinati

ALIGNMENTS

RESULT 1
ABQ82142
ID ABQ82142 standard; DNA; 17458 BP.
XX
AC ABQ82142;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector PHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
(CSIR) COMMONWEALTH SCI & IND RES ORG.
Wesley S, Waterhouse P, Helliwell C;
WPI; 2002-682669/73.
New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
Claim 16; Page 83-93; 104pp; English.
The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell; preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

Db	4292	AGCATTTT	TTTGGTGTATGTGGGCCCAATGAAGTCAGGTCAAACCTTGACAGTGACG	4351
Qy	4340	ACAAATCGT	TGGCGGGTCCAGGGCGAAATTTTGCACAAACATGTCGAGGCTCAGCAGGAC	4399
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Qy	4400	CTGCAGGCATGC		4411
Db	4412	CTGCAGGAATTC		4423

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RESULT 13
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DEFINITION A23998
ACCESSION A23998
VERSION A23998.1 GI:833338
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 7049)
AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J.
TITLE A novel ribonuclease and its inhibitor
JOURNAL Patent: EP 0537399-A 3 21-APR-1993;
PLANT GENETIC SYSTEMS, N.V
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Query Match 16.8%; Score 747; DB 6; Length 7049;
Best Local Similarity 94.6%; Pred. No. 3.7e-98;
Matches 771; Conservative 0; Mismatched 44; Indels 0; Gaps 0;

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QY 3664 TTTTGTGACAACTGTCTAGAGTCCTGCTTAAATGAGATATGGAGAGCGCTATGATC 3723
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RESULT 14
AF187951/c
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DEFINITION Activation-tagging vector psKI015, complete sequence.
ACCESSION AF187951
VERSION AF187951.1 GI:6537289
KEYWORDS Activation-tagging vector psKI015
SOURCE Activation-tagging vector psKI015
ORGANISM Activation-tagging vector psKI015
REFERENCE 1 (bases 1 to 10138)
AUTHORS Weigel, D., Ahn, J. H., Blazquez, M. A., Borevitz, J. O.,
Christensen, S. K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharavi, E. J., Neff, M. M., Nguyen, J. T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R. A., Harrison, M. J., Lamb, C. J., Yanofsky, M. F. and
Chory, J.
TITLE Activation tagging in Arabidopsis
JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
MEDLINE 20223715
PubMed 10759496
REFERENCE 2 (bases 1 to 10138)
AUTHORS Kardailsky, I. and Weigel, D.
TITLE Direct Substitution
JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
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DEFINITION	BD194641					
ACCESSION	BD194641					
VERSION	BD194641.1	GI:33004386				
KEYWORDS	JP 2002511258-A/7.					
SOURCE	synthetic construct					
ORGANISM	artificial constructs.					
	1 (bases 1 to 786)					
REFERENCE	Waterhouse,P.M., Wang,M.B. and Graham,M.W.					
AUTHORS	Method and means of obtaining improved phenotype					
TITLE	Patent: JP 2002511258-A 7 16-APR-2002;					
JOURNAL	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION					
COMMENT	OS Artificial Sequence					
	PN JP 2002511258-A/7					
	PD 16-APR-2002					
	PF 07-APR-1999 JP 2000543598					
	PR 08-APR-1998 US 09/056767,03-AUG-1998 US 09/127735 P1					
	PETER MICHAEL WATERHOUSE, MIN BO WANG, MICHAEL WAIN GRAHAM PC					
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	Artificial Sequence: intron 2 of the Flaveria CC					
	trinervia					
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	FT Key	Location/Qualifiers				
	FT source	1..786				
	FT	/organism='Artificial Sequence'.				
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REFERENCE
1 (bases 1 to 14645)
Rosche,E., Streubel,M. and Westhoff,P.
Primary structure of the photosynthetic pyruvate orthophosphate
dikinase of the C3 plant Flaveria pringlei and expression analysis
of pyruvate orthophosphate dikinase sequences in C3, C3-C4 and C4
Flaveria species
Plant Mol. Biol. 26 (2), 763-769 (1994)
JOURNAL
MEDLINE 95036056
PUBMED 7948930
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2
Rosche,E. and Westhoff,P.
Genomic structure and expression of the pyruvate, orthophosphate
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Plant Mol. Biol. 29 (4), 663-678 (1995)
JOURNAL
MEDLINE 96128009
PUBMED 8541493
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3 (bases 1 to 14645)
Rosche,E.
Direct Submission
Submitted (03-MAY-1994) E. Rosche, Institut f. Entwicklungs- und
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  AUTHORS Waterhouse,P.M.
  TITLE Direct Submission
  JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,

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RESULT 7
BD263378/c
LOCUS BD263378
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263378
VERSION BD263378.1 GI:33073146
KEYWORDS JP 2002537790-A/156.
SOURCE synthetic construct
ORGANISM Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
REFERENCE 1 (bases 1 to 4204)
TITILE Compositions and methods for use in recombinational cloning of

nucleic acids
JOURNAL Patent: JP 2002537790-A 156 12-NOV-2002;
COMMENT INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/156
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
PI 28-MAY-1999 US 60/136744
PI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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CC ori
CC KmR
CC attP2
CC Cmr
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RESULT 4
BD263402/c
LOCUS
DEFINITION
  BD263402 5584 bp DNA linear PAT 17-JUL-2003
  Compositions and methods for use in recombinational cloning of
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ACCESSION
  BD263402.1 GI:33073170
VERSION
  JP 2002537790-A/180.
KEYWORDS
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SOURCE
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    1 (bases 1 to 5584)
    Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
    Compositions and methods for use in recombinational cloning of
    nucleic acids
    Patent: JP 2002537790-A 180 12-NOV-2002;
    INVITROGEN CORP
    OS Artificial Sequence
    PN JP 2002537790-A/180
    PD 12-NOV-2002
    PF 02-MAR-2000 JP 2000602252
    PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
    28-MAY-1999 US 60/136744
    PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
    C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
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RESULT 5
BD263380
LOCUS
DEFINITION
  BD263380 4165 bp DNA linear PAT 17-JUL-2003
  Compositions and methods for use in recombinational cloning of
  nucleic acids.
ACCESSION
  BD263380
VERSION
  JP 2002537790-A/158.
KEYWORDS
  synthetic construct
SOURCE
  ORGANISM
    1 (bases 1 to 4165)
    Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
    Compositions and methods for use in recombinational cloning of
    nucleic acids
    Patent: JP 2002537790-A 158 12-NOV-2002;
    INVITROGEN CORP
    OS Artificial Sequence
    PN JP 2002537790-A/158
    PD 12-NOV-2002
    PF 02-MAR-2000 JP 2000602252
    PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
    28-MAY-1999 US 60/136744

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RESULT 3

BD263381 4939 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION
BD263381 GI:33073149
VERSION
JP 2002537790-A/159.
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
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REFERENCE
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
AUTHORS
Compositions and methods for use in recombinational cloning of
TITLE
nucleic acids
JOURNAL
Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP

COMMENT
OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
FI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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FEATURES
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Query Match 24.9%; Score 1108.8; DB 6; Length 4939;
Best Local Similarity 99.8%; Pred. No. 3 4e-150;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 17861 TCACTATCAGTCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 17920
Qy 3689 CTTGCTTTTATGAGATATCGAGACGCTTATGATCGCATGATTTTGTCTTCAATTTCTGT 3748
Db 17921 CTTGCTTTTATGAGATATCGAGACGCTTATGATCGCATGATTTTGTCTTCAATTTCTGT 17980

QY 506 CTAACGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGACGGCTGTGTATA 565
Db |||||
13601 CTAACGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCAGACGGCTGTGTATA 13660
QY 566 AGGAGCCTGACATTTATATTCGCCGAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db |||||
13661 AGGAGCCTGACATTTATATTCGCCGAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 13720
QY 626 TCGCGGTGGCTGAGATCAGACCACTTCTTCCCGCATACGAGACCGGCACACTGGCCATA 685
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13721 TCGCGGTGGCTGAGATCAGACCACTTCTTCCCGCATACGAGACCGGCACACTGGCCATA 13780
QY 686 TCGGTGGTCAATCAGTGGCCAGCTTTTCATCCCCGATATGCACCAACCGGGTAAAGTTTCACGG 745
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13781 TCGGTGGTCAATCAGTGGCCAGCTTTTCATCCCCGATATGCACCAACCGGGTAAAGTTTCACGG 13840
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13841 GAGACTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATCACCATTCGGTCGCCGGGC 13900
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13901 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACCGGCTCTCTCTTTTATAG 13960
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Db |||||
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QY 1449 - 1448
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Db 15281 GTTTTCCATGACAAACTGAAACGTTTTTCACTGCTCTGAGTGAATACCAAGCATTTTC 15340
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Db 15461 ACCAGTTTGTATTAACGTGGCCAAATATGGACAACTTCTTTCGCCCGGTTTTCACCATG 15520
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QY 1723 - 1722
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QY 1741 TAGTAATTTCTAGCTGGTTGTGATGAATTAATAATCAATGATAAAAATCTATAGTAAAAATA 1800
Db |||||

Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
JOURNAL MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 18691)
AUTHORS Waterhouse, P.M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL Location/Qualifiers
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LVQDDLDDEHOGIAPAEFLARKAMPDGEDIAVTHGDACILNIMVENGRFSGFIDC
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Best Local Similarity 79.1%; Pred. No. 0;
Matches 4406; Conservative 0; Mismatches 28; Indels 1137; Gaps 7;
QY 26 GACAAAGTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 85
Db 13121 GCCAACTTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 13180
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACGACCTTCCAAA 205
Db 13241 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACGACCTTCCAAA 13300
QY 206 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 265
Db 13301 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 13360
QY 266 ACGGAATCGTCGATCCAGCCTACTCGCTTATGTTCCTCAATGCCGATTTAAATCATAAAA 325
Db 13361 ACGGAATCGTCGATCCAGCCTACTCGCTTATGTTCCTCAATGCCGATTTAAATCATAAAA 13420
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Db 13421 AGAAATAAGAAAAAGAGTGCAGGCTCTTTTGTGTGCAAAATAAAAAACATCTACCT 13480
QY 386 ATTCAATATACCTAGTGTCAATAGTCCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC 445
Db 13481 ATTCAATATACCTAGTGTCAATAGTCCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC 13540
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Db 13541 TCTTATATCTTTCTCTTACAGTCGTTCCGGCTTCATCTGGATTTTTCAGCCTCTATACCTTA 13600

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11095.3 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001B-25_COPY_13000_17458

Perfect score: 4459

Sequence: 1 tttcatttgaggagacacg.....atagtgtaacataatctgc 4459

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_hgt_hum.*

31: em_hgt_inv.*

32: em_hgt_other.*

33: em_hgt_mus.*

34: em_hgt_pln.*

35: em_hgt_rod.*

36: em_hgt_nam.*

37: em_hgt_vrt.*

38: em_sy.*

39: em_hgt_hum.*

40: em_hgt_mus.*

41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3182.2	71.4	18691	12	CVE311874
2	1108.8	24.9	4470	6	BD263377
3	1108.8	24.9	4939	6	BD263381
c	1108.8	24.9	5584	6	BD263402
5	989.6	22.2	4165	6	BD263380
6	947.8	21.3	4208	6	BD263379
c	827	18.5	4204	6	BD263378
c	823.8	18.5	5156	6	BD263382
9	779	17.5	5824	12	CVE311872
10	779	17.5	6063	12	CVE311873
11	769.4	17.3	14645	8	FTPDKG
12	769	17.2	786	6	BD194641
13	747	16.8	7049	6	A23998
c	735	16.5	10138	12	AF187951
15	728.8	16.3	7566	6	A24783
16	728.8	16.3	7566	6	AR074388
17	728.8	16.3	7639	6	A24782
18	728.8	16.3	7639	6	AR074387
19	722.8	16.2	11405	12	AY310901
20	719.4	16.1	22574	12	CVE18556
21	713	16.0	4947	6	BD217610
c	710.2	15.9	7599	6	AX063413
23	709.8	15.9	5399	6	AI8050
24	709.8	15.9	5399	6	AR095106
25	709.8	15.9	5399	6	AR098312
26	709.8	15.9	5399	6	I49885
27	709.8	15.9	5399	6	I82373
28	709.8	15.9	5399	6	AX012337
c	709.8	15.9	6428	12	SYN1PSPSS
30	709.8	15.9	6555	6	AR007512
31	709.8	15.9	6555	6	AR084078
32	709.8	15.9	14194	6	AX052541
33	708.8	15.9	10907	12	AY310333
c	707	15.9	24595	1	ATACH5
c	707	15.9	24595	6	E00404
c	707	15.9	24595	6	E00546
c	707	15.9	24595	6	AR364803
c	707	15.9	24595	6	BD016312
c	707	15.9	194140	1	AF242881
40	697.2	15.6	6875	12	AF433042
41	697.2	15.6	6928	12	AF433043
c	697.2	15.6	27608	12	AF184978
43	697.2	15.6	28708	12	AY218787
44	695.8	15.6	3669	12	ATU41408
45	695.8	15.6	5341	12	ATU414109

ALIGNMENTS

RESULT 1	CVE311874	18691 bp	DNA	circular SYN 09-JUL-2002
LOCUS	CVE311874			
DEFINITION	Cloning vector pHELLSGATE.			
ACCESSION	AJ311874			
VERSION	AJ311874.1	GI:15982218		
KEYWORDS	kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.			
SOURCE	Cloning vector pHELLSGATE			
ORGANISM	Cloning vector pHELLSGATE			
REFERENCE	artificial sequences; vectors.			
AUTHORS	1			
	Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q., Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 12100.6 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001B-23_COPY_13000_17862

Perfect score: 4863

Sequence: 1 ttctatttgagaggacagc.....atagtgccacataaaatctgc 4863

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
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28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
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38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
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2	1207.4	24.8	4470	6	BD263377	BD263377 Compositi	
3	1207.4	24.8	4939	6	BD263381	BD263381 Compositi	
c	4	1207.4	24.8	5584	6	BD263402	BD263402 Compositi
5	1068.2	22.0	4165	6	BD263380	BD263380 Compositi	
6	1046.2	21.5	4208	6	BD263379	BD263379 Compositi	
c	7	842	17.3	18691	12	CVE311874	AJ311874 Cloning v
c	8	827	17.0	4204	6	BD263378	BD263378 Compositi
9	824.2	16.9	5824	12	CVE311872	AJ311872 Cloning v	
10	824.2	16.9	6063	12	CVE311873	AJ311873 Cloning v	
c	11	823.8	16.9	5156	6	BD263382	BD263382 Compositi
12	780	16.0	786	6	BD194641	BD194641 Method an	
13	778.6	16.0	14645	8	FTPDKG	X79095 F.trinervia	
14	738.6	15.2	7049	6	A23998	A23998 pTE4 expres	
c	15	735	15.1	10138	12	AF187951	AF187951 Activatio
16	729.6	15.0	7566	6	A24783	A24783 plasmid pPS	
17	729.6	15.0	7566	6	AR074388	AR074388 Sequence	
18	729.6	15.0	7639	6	A24782	A24782 plasmid pJD	
19	729.6	15.0	7639	6	AR074387	AR074387 Sequence	
20	723.2	14.9	11405	12	AY310901	AY310901 Binary ve	
21	719.4	14.8	22574	12	CVE18556	Y18556 Cloning vec	
22	713	14.7	4947	6	BD217610	BD217610 Method an	
c	23	710.2	14.6	7599	6	AX063413	AX063413 Sequence
24	709.8	14.6	5399	6	A18050	A18050 DNA for tra	
25	709.8	14.6	5399	6	AR095106	AR095106 Sequence	
26	709.8	14.6	5399	6	AR098312	AR098312 Sequence	
27	709.8	14.6	5399	6	I49885	I49885 Sequence 1	
28	709.8	14.6	5399	6	I82373	I82373 Sequence 1	
29	709.8	14.6	5399	6	AX012337	AX012337 Sequence	
c	30	709.8	14.6	6428	12	SYNTIPNPSS	M35007 A.tumefacie
31	709.8	14.6	6555	6	AR007512	AR007512 Sequence	
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33	709.8	14.6	14194	6	AX052541	AX052541 Sequence	
34	709.2	14.6	10907	12	AY310333	AY310333 Cloning v	
c	35	707	14.5	24595	1	ATACH5	X00493 Agrobacteri
c	36	707	14.5	24595	6	E00404	E00404 Ti plasmid
c	37	707	14.5	24595	6	E00546	E00546 DNA fragmen
c	38	707	14.5	24595	6	AR364803	AR364803 Sequence
c	39	707	14.5	24595	6	BD016312	BD016312 Method of
c	40	707	14.5	194140	1	AF242881	AF242881 Agrobacte
41	697.2	14.3	6875	12	AF433042	AF433042 Cloning v	
42	697.2	14.3	6928	12	AF433043	AF433043 Cloning v	
c	43	697.2	14.3	27608	12	AF184978	AF184978 Binary ve
44	697.2	14.3	28708	12	AY218787	AY218787 Cloning v	
45	695.8	14.3	3669	12	ATU414108	AY414108 Binary ve	

ALIGNMENTS

RESULT 1
CVE311874
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

CVE311874
Cloning vector pHELLSGATE.
AJ311874
AJ311874.1 GI:15982218
kanamycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; Spec Gene; spectinomycin resistance protein;
transposon Tn7.
Cloning vector pHELLSGATE
artificial sequences; vectors.
1
Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,

circular SYN 09-JUL-2002

Pred. No. is the number of results predicted by chance to have a

Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
JOURNAL MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 18691)
Waterhouse, P.M.
Direct Submission
TITLE Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL
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RESULT 2
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VERSION
  BD263377.1 GI:33073145
KEYWORDS
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  Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
  Compositions and methods for use in recombinational cloning of
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PN JP 2002537790-A/155
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC
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 ORGANISM artificial sequences.
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 REFERENCE Hartley,J.L., Brasch,M.A., Temple,G.F. and Chao,D.
 AUTHORS Compositions and methods for use in recombinational cloning of nucleic acids
 TITLE Patent: JP 2002537790-A 159 12-NOV-2002;
 JOURNAL INVITROGEN CORP
 COMMENT OS Artificial Sequence
 PN JP 2002537790-A/159
 PD 12-NOV-2002
 PF 02-MAR-2000 JP 2000602252
 PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
 28-MAY-1999 US 60/136744
 PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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ORIGIN

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 Best Local Similarity 99.9%; Pred. No. 8.8e-167;
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RESULT 4
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JP 2002537790-A/180.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
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Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
AUTHORS
TITLE
Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL
Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
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Artificial Sequence
PN JP 2002537790-A/180
PD 12-NOV-2002
PR 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
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Best Local Similarity 99.9%; Pred. No. 8.7e-167;
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VERSION	BD263379.1		
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SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 4208)		
AUTHORS	Hartley, J.L., Brasch, M.A., Temple, G.F. and Chao, D.		
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids		
JOURNAL	Patent: JP 2002537790-A 157 12-NOV-2002;		
COMMENT	INVITROGEN CORP		
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DB	16784	TTAGTAA	GTATAGAGGCTGAAAATCCAGATGAGCCGACGACTTGTAAAGAGAAAGTAT	16725
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LOCUS				
DEFINITION BD263378 4204 bp DNA linear PAT 17-JUL-2003				
Compositions and methods for use in recombinational cloning of nucleic acids.				
ACCESSION BD263378				
VERSION BD263378.1 GI:33073146				
KEYWORDS JP 2002537790-A/156.				
SOURCE synthetic construct				
ORGANISM artificial sequences.				
REFERENCE 1 (bases 1 to 4204)				
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.				
TITLE Compositions and methods for use in recombinational cloning of nucleic acids				
JOURNAL Patent: JP 2002537790-A 156 12-NOV-2002;				
COMMENT INVITROGEN CORP				
OS Artificial Sequence				
PN JP 2002537790-A/156				
PD 12-NOV-2002				
PF 02-MAR-2000 JP 2000602252				
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR				
28-MAY-1999 US 60/136744				
PI JAMES L HARTLEY MICHAEL A BRASCH GARY F TEMPLE DAVID CHEO PC				
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Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JOURNAL Plant J. 27 (6), 581-590 (2001)
MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 5824)
AUTHORS Waterhouse, P.M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

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which was a derivative of pGEM-9zf(-)"
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Db 4173 TCTATATAAGGAAGTTCATTTCATTGGAGAGACACGCTCGAGGAATTCGGTACCCCA 4231
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Db 4232 ATTGGTAAGGAATAATATTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 4291

RESULT 9
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LOCUS Cloning vector PHANNIBAL.
DEFINITION Cloning vector PHANNIBAL.
ACCESSION AJ311872
VERSION AJ311872.1 GI:15982214
KEYWORDS AMP gene; ampicillin resistance protein; pdk gene; promoter.
SOURCE Cloning vector PHANNIBAL
ORGANISM Cloning vector PHANNIBAL
artificial sequences; vectors.
REFERENCE
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,
Gleave, A.P., Green, A.G., and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants

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Db 4651 AAGATAAAGTTCGAGAGTAAAGTATATATTTTAAATGAATTTGATCGAATCATGAAGATG 4710
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RESULT 11
BD263382/c
LOCUS
DEFINITION BD263382 5156 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263382
VERSION BD263382.1 GI:33073150
KEYWORDS JP 2002537790-A/160.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 5156)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 160 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/160
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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Query Match 16.9%; Score 823.8; DB 6; Length 5156;
Best Local Similarity 99.8%; Pred. No. 8.2e-111;
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RESULT 15
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LOCUS
DEFINITION      Activation-tagging vector pSKI015, complete sequence.
ACCESSION      AF187951
VERSION        AF187951.1 GI:6537289
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS      Weigel, D., Ahn, J.H., Blazquez, M.A., Borevitz, J.O.,
Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuk, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chory, J.
TITLE      Activation tagging in Arabidopsis
JOURNAL      Plant Physiol. 122 (4), 1003-1013 (2000)
MEDLINE      20223715
PUBMED      10759496
REFERENCE      2 (bases 1 to 10138)
AUTHORS      Kardailsky, I. and Weigel, D.
DIRECT SUBMISSION
SUBMITTED (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
source
1. .10138
location/qualifiers
1. .10138
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36. .2204
note="derived from pUC19"
2205. .2662
note="derived from phage f1"
2663. .2829
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2830. .2849
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2894. .4178
note="cauliflower mosaic virus 35S gene promoter enhancer
sequences (tetramer)"
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7690. .7713
note="T-DNA left border"
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note="3' end"
complement(<8785..>9420)
complement(8791..9342)
note="promotes resistance to glutamine synthetase
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complement(9421..10119)
product="mannopine synthase"
note="5' end and promoter"

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ORIGIN
Query Match      15.1%; Score 735; DB 12; Length 10138;
Best Local Similarity 100.0%; Pred. No. 6.7e-98;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4086 CTAGAGTCTGCTTTAATGAGATATGCGAGAGCGCCTATGATCGCATGATATTGCTTTCA 4145
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QY      4146 ATTCTGTTGTGACAGCTTGTAATAAACCTTGAGCATGTGTAGCTCAGATCTTACCGCCGGT 4205
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Db      8712 ATTCTGTTGTGACAGCTTGTAATAAACCTTGAGCATGTGTAGCTCAGATCTTACCGCCGGT 8653
QY      4206 TTCGGTTCAATCTTAATGAATATATCACCGTTTACTATCGTATTTTATGAATAATTTCT 4265
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QY      4386 TCGGTTTATATTACAAATCCAAATTTTAAAAAGCGCAGAACCGGTCAAACTTAAA 4445
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Db      8412 GACTGATTACATAAATCTTTATTCAAATTTCAAAGGCCCGGCTAGTATCTACGACA 8353
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QY      4806 GCAGGCATGCAAGCT 4820
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Job time : 12136.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1120.23 Seconds
(without alignments)
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Title: US-10-055-001B-23_COPY_13000_17862

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4077.2	83.8	17681	6	ABQ82143 Acceptor
3	4042	83.1	17458	6	ABQ82142 Acceptor
4	3985.4	82.0	18691	6	ABQ82130 Acceptor
5	1207.4	24.8	4470	3	AAC55521 Donor pla
6	1207.4	24.8	4470	7	ABZ58767 Destinati
7	1207.4	24.8	4892	8	ADA50329 Plasmid v
8	1207.4	24.8	4939	3	AAC55525 Donor pla
9	1207.4	24.8	5584	3	AAC55632 Donor pla
10	1207.4	24.8	5584	7	ABZ58766 Donor pla
11	1201	24.7	4428	7	ABZ58768 Destinati
12	1194.6	24.6	4627	7	ABZ58769 Destinati
13	1194.6	24.6	4627	7	ABZ58770 Destinati
14	1174.2	24.1	17681	6	ABQ82143 Acceptor
15	1089.4	22.4	17476	6	ABQ82142 Acceptor
16	1079.4	22.2	17458	6	ABQ82142 Acceptor
17	1068.2	22.0	4165	3	AAC55524 Donor pla
18	1046.2	21.5	4208	3	AAC55523 Donor pla
19	842	17.3	18691	6	ABQ82130 Acceptor
20	827	17.0	4204	3	AAC55522 Donor pla
21	823.8	16.9	5156	3	AAC55526 Donor pla
22	780	16.0	786	3	AAZ38603 Flaveria
23	780	16.0	786	9	ADD44386 Flaveria

24	738.6	15.2	7050	2	AAQ40419 Sequence
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27	713	14.7	4947	3	AAZ60627 Nucleotid
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31	709.8	14.6	6555	2	AAQ53874 Plasmid p
32	709.8	14.6	14194	4	AAQ66932 Plant sig
33	707	14.5	24596	1	AAAN50182 Complete
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41	597	12.3	6264	3	AAC55507 Destinati
42	597	12.3	6354	3	AAC55491 Destinati
43	597	12.3	6422	3	AAC55483 Destinati
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ALIGNMENTS

RESULT 1
ABQ82141
ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELISGATE 8 nucleotide sequence SEQ ID NO:24.
DE
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PR Wesley S, Waterhouse P, Helliwell C;
XX
PR WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
XX
PS Claim 15; Page 74-83; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded DNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.

XX Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 84.6%; Score 4112.4; DB 6; Length 17476;

Best Local Similarity 93.8%; Pred. No. 0;

Matches 4446; Conservative 0; Mismatches 6; Indels 290; Gaps 4;

QY	122	GCCAACTTGTACAAAAAGCTGAACGAGAAACGTAATGATATTAATCAATATATT	181
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DB	13085	AAATTAGATTTTCATAAAAAACAGACTACATATATCTGTAAACACACATATCCAGTC	13144
QY	242	ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	301
DB	13145	ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	13204
QY	302	TGTTCTTCGGGTGATCTGTCGCAACTTAGTCGACCGACAGCCCTCCAAAATGTTCTCTCAA	361
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QY	842	GAGACTTTATCTGACACGACAGCTGCACTGGCCAGGGGGATCACCACTCCGCTCGCCCGGGC	901
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QY	1082	ACGAGACGACGGGCTTCATTTCTGATGTTGTTGTTTACCAAGACCGGAGATTTGACATC	1141
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DB	14105	ATAGCACACCTCTTTTGTGACATACCTTCCGGTATCAACAGGACACAGGATTTTATTTCTCGAAG	14164
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DB	14285	GTGCACTACAGCTCACTAATACCATCTAAGTATGTTGATTCATAGTACCTGGATATGTTGT	14344
QY	1442	GTTTTACAGTATATGTTAGTCTGTTTTTATGCAAAAATCTAATTTAATATATATGATATTT	1501
DB	14345	GTTTTACAGTATATGTTAGTCTGTTTTTATGCAAAAATCTAATTTAATATATGATATTT	14404
QY	1502	ATATCATTTTACGTTTCTGTTTCAGCTTTCTTGTGACAAAAGTTGGCAATTATAGAAGCAT	1561
DB	14405	ATATCATTTTACGTTTCTGTTTCAGCTTTCTTGTGACAAAAGTTGGCAATTATAGAAGCAT	14447
QY	1562	TGCTTATCAATTTGTTGCAACGAAACAGTCACTATCAGTCAAAAATAAATCATTTATTTGC	1621
DB	14448	-----	14447
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DB	14448	-----TCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATTAATATTT	14492
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DB	14733	TTTAAATCAATAATAGTAAATTTAGCTGGTTGATGATGATGATGATGATGATGATGATGAT	14792
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DB 13505 CTAAACGTGATAAAGTCTTCTGTAATTTCTACTGTATCGACCTGCGACTGGCTGTGATA 13564
QY 662 AGGAGCCTGACATTTATATCCCGCAGAACATCAGGTTAATGGCGTTTGTGATGCAATTT 721
DB 13565 AGGAGCCTGACATTTATATCCCGCAGAACATCAGGTTAATGGCGTTTGTGATGCAATTT 13624
QY 722 TCGCGGTGCTGAGATCAGCCATCTTCTCCCGATAAACGGAGACCGGCACACTGGCCATA 781
DB 13625 TCGCGGTGCTGAGATCAGCCATCTTCTCCCGATAAACGGAGACCGGCACACTGGCCATA 13684
QY 782 TCGGTGCTCATATCGCCAGCTTTCATCCCGATATGCACACCGGGTAAAGTTCAAGG 841
DB 13685 TCGGTGCTCATATCGCCAGCTTTCATCCCGATATGCACACCGGGTAAAGTTCAAGG 13744
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DB 13745 GAGACTTTATCTGACAGCAGCGTGCACCTGGCCAGGGGATCACCATCCGTCGCCCGGCG 13804
QY 902 GTGTCAATTAATACATCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTATAG 961
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DB 13925 TTCAATAAACCGGCGACCTCAGCCATCCCTCTCGATTTCCGTTTCCAGCGTTCGCG 13984
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DB 13985 AGCAGACGACGGCTTCACTCTGCAATGTTGCTTACAGACCGGAGATATTGACATC 14044
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DB 14448 ----- 14447
QY 1622 CATCCAGCTGCAGCTCTCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATATTATTT 1681
DB 14448 -----TCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATATTATTT 14492

QY 1682 TCTTTTTCCTTTTAGTATATAAATAGTATAGTGATGTTAATTTAGTATGATATATAATA 1741
DB 14493 TCTTTTTCCTTTTAGTATATAAATAGTATAGTGATGTTAATTTAGTATGATATATAATA 14552
QY 1742 TAGTTGTTTATTAATTTGTGAAAAAATAAATTTATAAATATATCTGTTTACATAAACAACATAGT 1801
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QY 1802 AATGTAAAAAATATGACAACTGATGCTGTAAGCGAAGATATAAAGTTGAGGTAAGT 1861
DB 14613 AATGTAAAAAATATGACAACTGATGCTGTAAGCGAAGATATAAAGTTGAGGTAAGT 14672
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DB 14673 ATATTATTTTAAAGAAATTTGATCGAACATGTAAGATGATATACAGCAATTAATATTGTT 14732
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DB 14793 TAGTAAAAAATAGATAAATAAATTAATAATATATTTTATGATTAATATTGTTAT 14852
QY 2042 ATATTAATAATCTATACCATTTACTAAATATTTTAGTTTAAAAAGTTAATAATATTTTGT 2101
DB 14853 ATATTAATAATCTATACCATTTACTAAATATTTTAGTTTAAAAAGTTAATAATATTTTGT 14912
QY 2102 TAGAAATTTCCAAATCTGCTTGTAAATTTCAATAAACAATAATTAATAAACAAGCTAAG 2161
DB 14913 TAGAAATTTCCAAATCTGCTTGTAAATTTCAATAAACAATAATTAATAAACAAGCTAAG 14972
QY 2162 TAAACAAATAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATATCTAATG 2221
DB 14973 TAAACAAATAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATATCTAATG 15032
QY 2222 CTAAATATAACAAAGCGCAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCT 2281
DB 15033 CTAAATATAACAAAGCGCAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCT 15092
QY 2282 TATTAAATTTCTAAATAAATCTTGTAGTTTATTAATCTTAAATGGAATGACTATTAAT 2341
DB 15093 TATTAAATTTCTAAATAAATCTTGTAGTTTATTAATCTTAAATGGAATGACTATTAAT 15152
QY 2342 AAATGAAATTTAGTCGAACATGAATAAACAAGTAAACATGATAGATCATGTCTGTTAT 2401
DB 15153 AAATGAAATTTAGTCGAACATGAATAAACAAGTAAACATGATAGATCATGTCTGTTAT 15212
QY 2402 CAATGATCTTACATTTGGAATGATTAACAGTTGGGAAGCTGGGTTCGAAATCGATAGCTT 2461
DB 15213 CAATGATCTTACATTTGGAATGATTAACAGTTGGGAAGCTGGGTTCGAAATCGATAGCTT 15272
QY 2462 G-----GATCCTCTAGAGAGCTGCAGCTGGATGCAATAATATGATTTTATTTTCACTGA 2515
DB 15273 GCGCTGAGTTATCATCATCATAGACACACGAAATAAAGTAATCAGATTTATCAGTTA 15332
QY 2516 TAGTGACCTGTTTCGTTGCAACAAA----- 2539
DB 15333 AAGCTATGTAATATTTTGGCCATACCAATCAATTAABAAAATAGATCAGTTTAAAGAAAG 15392
QY 2540 ----- 2539
DB 15393 ATCAAAAGCTCAAAAAATAAAAAAGAAAAGGCTCTTAACCAAGAAAATGAAGAGAAA 15452
QY 2540 -----TTGATAAGCAATGCTTCTTATAATGCCAACTTTGTACAGAAAGAGCTGAA 2589
DB 15453 ACTAGAAAATTTACCTGCGCAAGCTTGGATCTCTAGACCCTTTGTACAGAAAGAGCTGAA 15512
QY 2590 CGAGAAACGTAATAAATATCAATATTAATTAATTTAGATTTTGCATATAAACAAG 2649
DB 15513 CGAGAAACGTAATAAATATCAATATTAATTAATTTAGATTTTGCATATAAACAAG 15572
QY 2650 ACTACATAATATCTGTAACAAACAAACATATCCAGTCACTATGAATCAACTATTAGTGT 2709

15573 ACTACATAAATCTGTAACAAACACATATCCAGTCACTATGAATCAACTACTTAGATGGT 15632
2710 ATTAGTGACCTGAGTCGAGTAAGTTGGCAGCATCACCGAGCGCACTTTGGCCGAATAA 2769
15633 ATTAGTGACCTGAGTCGAGTAAGTTGGCAGCATCACCGAGCGCACTTTGGCCGAATAA 15692
2770 ATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCCCTGGTGCCTCTTGATACC 2829
15693 ATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCCCTGGTGCCTCTTGATACC 15752
2830 GGAAGCCCTGGGCCAATTTTGGGGAATAAGAGAGTTGATCGGACATACCCATTTGCAC 2889
15753 GGAAGCCCTGGGCCAATTTTGGGGAATAAGAGAGTTGATCGG-----ATTTCAC 15804
2890 AACTCTTATACCTTTCTCTTACAGTCGTTCCGGCTTCATCTGGATTTTCAGGCTCTATAC 2949
15805 AACTCTTATACCTTTCTCTTACAGTCGTTCCGGCTTCATCTGGATTTTCAGGCTCTATAC 15864
2950 TTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTGGCTGTGT 3009
15865 TTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTGGCTGTGT 15924
3010 ATAAGGGAGCCCTGACATTTATATCCCGAAGATCAGGTTAATGGCTTTTGTATGTC 3069
15925 ATAAGGGAGCCCTGACATTTATATCCCGAAGATCAGGTTAATGGCTTTTGTATGTC 15984
3070 TTTTCCGGCTGGCTGAGATCAGCCACTCTTCCCGATACCGAGACCGGACACTGGCC 3129
15985 TTTTCCGGCTGGCTGAGATCAGCCACTCTTCCCGATACCGAGACCGGACACTGGCC 16044
3130 ATATCGGTGGCTCATATGCGCAGCTTCATCCCGATATGACCAACCGCGGTAAAGTTCA 3189
16045 ATATCGGTGGCTCATATGCGCAGCTTCATCCCGATATGACCAACCGCGGTAAAGTTCA 16104
3190 CGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGCGGATCACCATCGTCGCCG 3249
16105 CGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGCGGATCACCATCGTCGCCG 16164
3250 GCGGTGTCAATAATATCACTCTGTACATCCAAACAGACGATAGCGGCTCTCTCTTTA 3309
16165 GCGGTGTCAATAATATCACTCTGTACATCCAAACAGACGATAGCGGCTCTCTCTTTA 16224
3310 TAGGTGTAAACCTTAAAGTCACTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTT 3369
16225 TAGGTGTAAACCTTAAAGTCACTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTT 16284
3370 CATTTCAATAAACCAGGCGACCTCAGCCATCCCTGCTGATTTTCCGCTTTCCAGCGTTC 3429
16285 CATTTCAATAAACCAGGCGACCTCAGCCATCCCTGCTGATTTTCCGCTTTCCAGCGTTC 16344
3430 GGCACGACGACGCGGCTTCATCTGCAATGTTGCTGTACAGACCGGAGATATGAC 3489
16345 GGCACGACGACGCGGCTTCATCTGCAATGTTGCTGTACAGACCGGAGATATGAC 16404
3490 ATCATATGCTTTGAGCACTGATAGTGTGCTGCTCAACTGCTCACTGCTAATACGCTGC 3549
16405 ATCATATGCTTTGAGCACTGATAGTGTGCTGCTCAACTGCTCACTGCTAATACGCTGC 16464
3550 TTCTATGACACACCTCTTTTGAATATCTCTGTTCTTGTATGACAGATGATTTTCAGGACTA 3609
16465 TTCTATGACACACCTCTTTTGAATATCTCTGTTCTTGTATGACAGATGATTTTCAGGACTA 16524
3610 TGACATGAGGATATGAATAGGTAGATGTTTTTATTTGTGTACAAAAAGAGGCTCG 3669
16525 TGACATGAGGATATGAATAGGTAGATGTTTTTATTTTGTGTACAAAAAGAGGCTCG 16584
3670 CACCTCTTTTCTATTTCTTTTATTTATGATTTATAGGCAATTCAGCAATAGCGAGTAG 3729
16585 CACCTCTTTTCTATTTCTTTTATTTATGATTTATAGGCAATTCAGCAATAGCGAGTAG 16644
3730 GCTGGATACGACGATTCGGTTTGGAGAGAAATTTGGAGGCTGTGGTGCATAAGTTG 3789

16645 GCTGGATACGACGATTCGGTTTGGAGAGAAATTTGGAGGCTGTGGTGCAGTAAGTTG 16704
3790 GCAGCATCACCGGAAGAACATTTTGGAGGCTGTGGTGCAGTACAGGTCACATAATACCAT 3849
16705 GCAGCATCACCGGAAGAACATTTTGGAGGCTGTGGTGCAGTACAGGTCACATAATACCAT 16764
3850 CTAAGTAGTTGATTCATGACCTGAGTATGTTGTTTACAGTATATGATGCTGTT 3909
16765 CTAAGTAGTTGATTCATGACCTGAGTATGTTGTTTACAGTATATGATGCTGTT 16824
3910 TTTTATGCAAAATCTAAATTAATATATGATTTATATATATGTTTACGTTCTGTTTCAG 3969
16825 TTTTATGCAAAATCTAAATTAATATATGATTTATATATATGTTTACGTTCTGTTTCAG 16884
3970 CTTTATGTTACAAAATTTGGCAATTTAAAAAAGCATTTGCTCATCAATTTGTTGCAACGAC 4029
16885 CTTTATGTTACAAAATTTG----- 16902
4030 AGGTCATATCAGTCAAAATTAATAATCATATTGTTGGGCCCCAGATCCATGCTAGCTCAG 4089
16903 -----TCTAG 16907
4090 AGTCTGCTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATATTTGCTTTCAATTC 4149
16908 AGTCTGCTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATATTTGCTTTCAATTC 16967
4150 TGTGTTGACCGTTGTAAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGTTTCG 4209
16968 TGTGTTGACCGTTGTAAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGTTTCG 17027
4210 GTTCATTTCAATGATATATACCCGTTACTATCGTATTTTATGATTAATATTTCTCGGT 4269
17028 GTTCATTTCAATGATATATACCCGTTACTATCGTATTTTATGATTAATATTTCTCGGT 17087
4270 TCAATTTACTGATTTGATCCCTACTATATATGATCAATATATAAATGAAAAAATATAT 4329
17088 TCAATTTACTGATTTGATCCCTACTATATATGATCAATATATAAATGAAAAAATATAT 17147
4330 TGTGCTGAATAGTTTATGAGCATCTATGATGAGCGCCACCAATAACAAACAAATTCGG 4389
17148 TGTGCTGAATAGTTTATGAGCATCTATGATGAGCGCCACCAATAACAAACAAATTCGG 17207
4390 TTTTATTTATTAACAATCCAAATTTTAAABAAAGCGGAGAACCGGTCACCACTTAAAGACT 4449
17208 TTTTATTTATTAACAATCCAAATTTTAAABAAAGCGGAGAACCGGTCACCACTTAAAGACT 17267
4450 GATTACATAAATCTTTATTTCAAAATTTCAAAAGCCCCCAGGGCTAGTATCTACGACACAC 4509
17268 GATTACATAAATCTTTATTTCAAAATTTCAAAAGCCCCCAGGGCTAGTATCTACGACACAC 17327
4510 GAGCGCGAATTAATTAAGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCATGGG 4569
17328 GAGCGCGAATTAATTAAGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCATGGG 17387
4570 TGAGATTTCTTGAAGTTTCAAGTATTTGGCGCTCTACCGAAAGTTTACGGGCACTTC 4629
17388 TGAGATTTCTTGAAGTTTCAAGTATTTGGCGCTCTACCGAAAGTTTACGGGCACTTC 17447
4630 AACCCGGTCCAGCACCGCGCGGGGTAAACCGACTTTGCTGCCCCGAGAAATTAAGCAGCAAT 4689
17448 AACCCGGTCCAGCACCGCGCGGGTAAACCGACTTTGCTGCCCCGAGAAATTAAGCAGCAAT 17507
4690 TTTTATGTTATGTTGGGCCCCAAATTAAGTCAAGTCAAACTGACAGTACGACCAAT 4749
17508 TTTTATGTTATGTTGGGCCCCAAATTAAGTCAAGTCAAACTGACAGTACGACCAAT 17567
4750 CGTTGGCGGGTCCAGGCGGAATTTTGGCAAAATGTCGAGGCTCAGCAGACCTCGAG 4809
17568 CGTTGGCGGGTCCAGGCGGAATTTTGGCAAAATGTCGAGGCTCAGCAGACCTCGAG 17627
4810 GCATCAAGCTAGCTTACTAGTATGATGATTTCTTATAGTGTCACTAAATCTGC 4863
17628 GCATCAAGCTAGCTTACTAGTATGATGATTTCTTATAGTGTCACTAAATCTGC 17681

RESULT 3
ABQ82142
ID ABQ82142 standard; DNA; 17458 BP.
XX
XX ABQ82142;
AC
XX
XX
DT 11-DEC-2002 (first entry)
XX
XX
DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
XX Synthetic.
XX
XX WO200259294-A1.
XX
XX PD 01-AUG-2002.
XX
XX PF 24-JAN-2002; 2002WO-AU0000073.
XX
XX PR 26-JAN-2001; 2001US-0264067P.
XX
XX PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
PA
PI Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
XX Claim 16; Page 83-93; 104pp; English.
PS
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
XX sequence from the present invention
SQ
Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 83.1%; Score 4042; DB 6; Length 17458;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 4419; Conservative 0; Mismatches 15; Indels 308; Gaps 6;
QY 122 GCCAATCTTGTACAAAAGCTCAACGCGAAGCTAAATGATATATAATCAATATATT 181
DB 13025 GACAGTTTGTACAAAAGCTCAACGCGAAGCTAAATGATATATAATCAATATATT 13084
QY 182 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACAAACATATCCAGTC 241

Db 13085 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACAAACATATCCAGTC 13144
QY 242 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 301
Db 13145 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 13204
QY 302 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 361
Db 13205 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 13264
QY 362 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 421
Db 13265 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 13324
QY 422 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 481
Db 13325 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 13384
QY 482 ATTCATATACGCTAGTGTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTTCAACAC 541
Db 13385 ATTCATATACGCTAGTGTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTTCAACAC 13444
QY 542 TCTTATATCTTTTCTCTTACAAAGTCGTTGGCTTCTATCTGGATTTTTCAGCCTCTTACTT 601
Db 13445 TCTTATATCTTTTCTCTTACAAAGTCGTTGGCTTCTATCTGGATTTTTCAGCCTCTTACTT 13504
QY 602 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGAGACTGGCTGTGTATA 661
Db 13505 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGAGACTGGCTGTGTATA 13564
QY 662 AGGAGAGCCTGACATTTATATCCAGAAACATCAGGTTTAAATGGGCTTTTTCATGTCATTT 721
Db 13565 AGGAGAGCCTGACATTTATATCCAGAAACATCAGGTTTAAATGGGCTTTTTCATGTCATTT 13624
QY 722 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGGAGACCGGCACATCGGCCATA 781
Db 13625 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGGAGACCGGCACATCGGCCATA 13684
QY 782 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTTCAAGG 841
Db 13685 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTTCAAGG 13744
QY 842 GAGACTTTTATCTGACAGCAGACGTGCTGCTGCGAGGGGATCACCATCGCTCGCCGGGC 901
Db 13745 GAGACTTTTATCTGACAGCAGACGTGCTGCTGCGAGGGGATCACCATCGCTCGCCGGGC 13804
QY 902 GTGTCAATAATATCACTCTGTACATCCAAACAGACAGATAAACGGCTCTCTCTTTTATAG 961
Db 13805 GTGTCAATAATATCACTCTGTACATCCAAACAGACAGATAAACGGCTCTCTCTTTTATAG 13864
QY 962 GTGTAAACCTTAACTGCAATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAAT 1021
Db 13865 GTGTAAACCTTAACTGCAATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAAT 13924
QY 1022 TTCAATAAACCGGGCGAGCTCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTCCGC 1081
Db 13925 TTCAATAAACCGGGCGAGCTCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTCCGC 13984
QY 1082 ACGCAGACGACGGGCTTCATTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1141
Db 13985 ACGCAGACGACGGGCTTCATTTCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 14044
QY 1142 ATATATGCTTTCAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATAGCGTGTTC 1201
Db 14045 ATATATGCTTTCAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATAGCGTGTTC 14104
QY 1202 ATAGCACACCTCTTTTTCACATACCTTCGGGTAGTCCCGATCAACGCTCTCATTTTCGCCAA 1261
Db 14105 ATAGCACACCTCTTTTTCACATACCTTCGGGTAGTCCCGATCAACGCTCTCATTTTCGCCAA 14164
QY 1262 AAGTTGGCCCGGGCTTCCCGGTATCAACAGGACACCCAGGATTTATTTATTTCTCGGAG 1321

Db 14165 AAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACCGAGGATTTATTTATTTCTCGAAG 14224
Qy 1322 TGATCTTCCGTACACAGGTATTTATTCGGCGCAAGTGCGTCCGGTGATGCTGCCAACTTA 1381
Db 14225 TGATCTTCCGTACACAGGTATTTATTCGGCGCAAGTGCGTCCGGTGATGCTGCCAACTTA 14284
Qy 1382 GTCGACTCAGGTCTACTAATACATCTAAGTAGTGTGATTCATAGTACGTGGATATGTTGT 1441
Db 14285 GTCGACTCAGGTCTACTAATACATCTAAGTAGTGTGATTCATAGTACGTGGATATGTTGT 14344
Qy 1442 GTTTTACAGTATATGTAGTCTGTTTTTATCGAAAATCTAATTTAAATATATTTGATATTT 1501
Db 14345 GTTTTACAGTATATGTAGTCTGTTTTTATCGAAAATCTAATTTAAATATATTTGATATTT 14404
Qy 1502 ATATCAATTTTACGTTTCTCGTTTTCAGCTTTCTTTGTACAAAAGTTGGCAATTAAGAAGCAT 1561
Db 14405 ATATCAATTTTACGTTTCTCGTTTTCAGCTTTCTTTGTACAAAAGTTGGT----- 14448
Qy 1562 TGCCTATCAATTTGTTGCAACGACAGTCACTATCAGTCAAAATAAATCAATTTATTTGC 1621
Db 14449 ----- 14448
Qy 1622 CATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTATTT 1681
Db 14449 -----CTCGAGGAATTCGGTACC-----NACTGTAAGGAAATAATTTATTT 14488
Qy 1682 TCTTTTTTCTTTTAGTATAAAATAGTTAAGTAGTGTAAATAGTAGTATGATTAATAATA 1741
Db 14489 TCTTTTTTCTTTTAGTATAAAATAGTTAAGTAGTGTAAATAGTAGTATGATTAATAATA 14548
Qy 1742 TAGTTCGTTAATGTGAAATAATAATTTATATAATATTTTATATAATTTTATATAAACAATAGT 1801
Db 14549 TAGTTCGTTAATGTGAAATAATAATTTATATAATATTTTATATAATTTTATATAAACAATAGT 14608
Qy 1802 AATGTAAAAAATATACAAAGTAGTGTGAAGACGAAGAAGATAAAGTTGAGAGTAAGT 1861
Db 14609 AATGTAAAAAATATACAAAGTAGTGTGAAGACGAAGAAGATAAAGTTGAGAGTAAGT 14668
Qy 1862 ATATTAATTTTATGAATTTGATGCAACATGTGAAGATGATATCTAGCATTAATAATTTGT 1921
Db 14669 ATATTAATTTTATGAATTTGATGCAACATGTGAAGATGATATCTAGCATTAATAATTTGT 14728
Qy 1922 TTTAATCAATAAGTAAATCTAGCTAGCTGTTTGAATTAATAATCAATCAATTAATAACTA 1981
Db 14729 TTTAATCAATAAGTAAATCTAGCTAGCTGTTTGAATTAATAATCAATCAATTAATAACTA 14788
Qy 1982 TAGTAAAAATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2041
Db 14789 TAGTAAAAATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 14848
Qy 2042 ATAAATTAATAATCTATACCAATTAATAATTTTATAGTTTAAAGTTTAAATTAATAATTTGT 2101
Db 14849 ATAAATTAATAATCTATACCAATTAATAATTTTATAGTTTAAAGTTTAAATTAATAATTTGT 14908
Qy 2102 TAGAAATTTCAATCTGCTGTAAATTTATCAATAAACAATAAATAAATAAATAAATAAATAA 2161
Db 14909 TAGAAATTTCAATCTGCTGTAAATTTATCAATAAACAATAAATAAATAAATAAATAAATAA 14968
Qy 2162 TAAACAATAATCAAACTAATAAGAAACAGTAATCTAATGTAAACAAAAATATCTAATG 2221
Db 14969 TAAACAATAATCAAACTAATAAGAAACAGTAATCTAATGTAAACAAAAATATCTAATG 15028
Qy 2222 CTAAATAACAAAGCGCAAGATCTATCAATTTTATATAGTATTTTATTTTCAATCAACATCT 2281
Db 15029 CTAAATAACAAAGCGCAAGATCTATCAATTTTATATAGTATTTTATTTTCAATCAACATCT 15088
Qy 2282 TATTAATTTCTAAATAATACTTGTAGTTTATTAATCTTCAATGGAATGACTATTAATTT 2341
Db 15089 TATTAATTTCTAAATAATACTTGTAGTTTATTAATCTTCAATGGAATGACTATTAATTT 15148
Qy 2342 AATAGTAATAGTCAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTTAT 2401
Db 15149 AATAGTAATAGTCAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTTAT 15208

Qy 2402 CATTTGATCTTACATTTGGATTGATTACAGTTTGGGAAGCTGGTTTCGAAATCGATAAGCTT 2461
Db 15209 CATTTGATCTTACATTTGGATTGATTACAGTTTGGGAAGCTGGTTTCGAAATCGATAAGCTT 15254
Qy 2462 GGATCTCTAGAGAGCTGCAGCTGGATGGCAAAATAAGATTTTATTTTGACTGATAGTA 2521
Db 15255 GGATCTCTAG----- 15266
Qy 2522 CTTGTTCTGTTCAACAAATTTGATAGCAATCTTCTTTATTAATGCCAACTTTGTACAGA 2581
Db 15267 -----CCACTTTGTACAAGA 15281
Qy 2582 AAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATTAATTTAGATTTTGCATA 2641
Db 15282 AAGCTGAACGAGAAACGTAATAATGATATAATAATCAATATTAATTTAGATTTTGCATA 15341
Qy 2642 AAAACAGACTACATATACCTGTAAACACAAACATATCCAGTCACTATGAATCAACTACT 2701
Db 15342 AAAACAGACTACATATACCTGTGTAAACACAAACATATCCAGTCACTATGAATCAACTACT 15401
Qy 2702 TAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGACCTTTGCG 2761
Db 15402 TAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGACCTTTGCG 15461
Qy 2762 CCGAATAAATACCTGTGACGGAAGATCACTTCGCGAAGATAAATAAATCCTGGTGTCCCTG 2821
Db 15462 CCGAATAAATACCTGTGACGGAAGATCACTTCGCGAAGATAAATAAATCCTGGTGTCCCTG 15521
Qy 2822 TTGATACCGGAAGCCCTGGGCCCACTTTTCGCGAAGATGAGCTTGCATCGGCATACC 2881
Db 15522 TTGATACCGGAAGCCCTGGGCCCACTTTTCGCGAAGATGAGCTTGCATCGGCATACC 15574
Qy 2882 CATTTTCAAACTCTTTATATCTTTCTTTCAAGTGGTTTCGGCTTCATCTGGATTTTCAGC 2941
Db 15575 -ATTTTCAAACTCTTTATATCTTTCTTTCAAGTGGTTTCGGCTTCATCTGGATTTTCAGC 15633
Qy 2942 CTCCTATCTTACTAAACGCTGATTAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACT 3001
Db 15634 CTCCTATCTTACTAAACGCTGATTAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACT 15693
Qy 3002 GGCTGTGTATAGGAGGCTGCACATTTATTTCCCGAAGATCAAGTTTAAATGGGTTT 3061
Db 15694 GGCTGTGTATAGGAGGCTGCACATTTATTTCCCGAAGATCAAGTTTAAATGGGTTT 15753
Qy 3062 TGATGTCTATTTTCGGGTGGGTGAGATCAGGCATCTTCTTCCCGAATAACGAGACCGGCA 3121
Db 15754 TGATGTCTATTTTCGGGTGGGTGAGATCAGGCATCTTCTTCCCGAATAACGAGACCGGCA 15813
Qy 3122 CACTGGCCATATCGGTGGTGCATCATCGCGCAGCTTTCATCCCGATATGCACCCGGGT 3181
Db 15814 CACTGGCCATATCGGTGGTGCATCATCGCGCAGCTTTCATCCCGATATGCACCCGGGT 15873
Qy 3182 AAAAGTTCCGGGAGACTTTTATCTGACAGCAGACGCTGCACTGGCCAGGGGGATCAACATCC 3241
Db 15874 AAAAGTTCCGGGAGACTTTTATCTGACAGCAGACGCTGCACTGGCCAGGGGGATCAACATCC 15933
Qy 3242 GTCGCCGGGGGTGTCATTAATATCACTGTGATCATCCACAAAACAGACGATAACGGCTCT 3301
Db 15934 GTCGCCGGGGGTGTCATTAATATCACTGTGATCATCCACAAAACAGACGATAACGGCTCT 15993
Qy 3302 CTCCTTTTATAGGTGTAACCTTTAAACTGCTTTAACTGCTTCCCTGTCTCGTCAAGAAA 3361
Db 15994 CTCCTTTTATAGGTGTAACCTTTAAACTGCTTTAACTGCTTCCCTGTCTCGTCAAGAAA 16053
Qy 3362 GAGCGCTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGTATTTTCGGCTTTC 3421
Db 16054 GAGCGCTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGTATTTTCGGCTTTC 16113
Qy 3422 GAGCGCTTCAGGACGACGAGCGGCTTCATCTGCTGCTGCTTGTGCTTACAGACCGGAG 3481
Db 16114 GAGCGCTTCAGGACGACGAGCGGCTTCATCTGCTGCTTGTGCTTACAGACCGGAG 16173

CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
XX sequence from the present invention

SQ Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

Query Match 82.0%; Score 3985.4; DB 6; Length 18691;
Best Local Similarity 85.1%; Pred.No. 0;
Matches 4846; Conservative 0; Mismatches 16; Indels 831; Gaps 2;

QY 1 TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATGATCTCGGGCCCAATAATGATTT 60
DB 13000 TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATGATCTCGGGCCCAATAATGATTT 13059
QY 61 TATTTTGATGATGACCTGTTGTTGCAACAAATGATGAGCAATGCTTTTTTATAA 120
DB 13060 TATTTTGATGATGACCTGTTGTTGCAACAAATGATGAGCAATGCTTTTTTATAA 13119
QY 121 TGCCCAACTTGTACAAAAGCTGAACGAGAAACGTAAATGATATAATCAATATAT 180
DB 13120 TGCCCAACTTGTACAAAAGCTGAACGAGAAACGTAAATGATATAATCAATATAT 13179
QY 181 TAAATTAGATTTTGATATAAAACAGACTACATAACTGTAAACACAAATATCCAGT 240
DB 13180 TAAATTAGATTTTGATATAAAACAGACTACATAACTGTAAACACAAATATCCAGT 13239
QY 241 CACTATGAATCAACTTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 13240 CACTATGAATCAACTTAGATGATGATGATGATGATGATGATGATGATGATGAT 13299
QY 301 ATGTTCTTCGGGTGATGCTGCCAATAGTACGACGACGCTTCCAAATGTTCTTCA 360
DB 13300 ATGTTCTTCGGGTGATGCTGCCAATAGTACGACGACGCTTCCAAATGTTCTTCA 13359
QY 361 AACGGAATCGTGTATCAGACGCTACTCGCTATTTGCTCAATGCGGTATTAATCAATA 420
DB 13360 AACGGAATCGTGTATCAGACGCTACTCGCTATTTGCTCAATGCGGTATTAATCAATA 13419
QY 421 AAGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGACAAAATAAACAATCACTACC 480
DB 13420 AAGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGACAAAATAAACAATCACTACC 13479
QY 481 TATTCATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGAACATTTTCAAA 540
DB 13480 TATTCATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGAACATTTTCAAA 13539
QY 541 CTCCTATATCTTTCTTCAAGTGTGTTGCGCTTCACTGGAATTTTCAGCCTCTATAC 600
DB 13540 CTCCTATATCTTTCTTCAAGTGTGTTGCGCTTCACTGGAATTTTCAGCCTCTATAC 13599
QY 601 ACTAAGCGTGAATAAGTTTCTGTAATTTCTACTGTATGACCTGCGAGCTGGCTGTAT 660
DB 13600 ACTAAGCGTGAATAAGTTTCTGTAATTTCTACTGTATGACCTGCGAGCTGGCTGTAT 13659
QY 661 AAGGGAGCCTGACATTTATATTTCCCGAACAATCAGGTTAATGGGCTTTTGTATGTCAT 720
DB 13660 AAGGGAGCCTGACATTTATATTTCCCGAACAATCAGGTTAATGGGCTTTTGTATGTCAT 13719
QY 721 TTCCGGGTGGCTGAGATCAGCCTCTCTTCCCGAATAACGAGACCGGCACACTGGCCAT 780
DB 13720 TTCCGGGTGGCTGAGATCAGCCTCTCTTCCCGAATAACGAGACCGGCACACTGGCCAT 13779
QY 781 ATCGGTGGTATCATCGCCAGCTTTTCATCCCGATATGACCAACCGGTAAAGTTTCAG 840
DB 13780 ATCGGTGGTATCATCGCCAGCTTTTCATCCCGATATGACCAACCGGTAAAGTTTCAG 13839

QY 841 GGAGACTTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCGG 900
DB 13840 GGAGACTTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCGG 13899
QY 901 CGTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAACGGCTCTCTTTTATA 960
DB 13900 CGTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAACGGCTCTCTTTTATA 13959
QY 961 GGTGTAAACCTTAAACGTGATTTTACAGTCCCTGTTCTGTCAGAAAAGACCGTTCA 1020
DB 13960 GGTGTAAACCTTAAACGTGATTTTACAGTCCCTGTTCTGTCAGAAAAGACCGTTCA 14019
QY 1021 TTTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTCCAGGTCCG 1080
DB 14020 TTTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTCCAGGTCCG 14079
QY 1081 CAGCAGACACCGGGCTTCATTTGCGATGTTGTCCTTACAGACCGGAGATTTGACAT 1140
DB 14080 CAGCAGACACCGGGCTTCATTTGCGATGTTGTCCTTACAGACCGGAGATTTGACAT 14139
QY 1141 CATATATGCTTGGACAACTGATAGCTGCTGCACTGCACTGCTGATATACGTCGCT 1200
DB 14140 CATATATGCTTGGACAACTGATAGCTGCTGCACTGCACTGCTGATATACGTCGCT 14199
QY 1201 CATAGCACACCTCTTTTGGATACATCTTTCGGGTAGTCCGATCAACGCTCTCATTTCCGCA 1260
DB 14200 CATAGCACACCTCTTTTGGATACATCTTTCGGGTAGTCCGATCAACGCTCTCATTTCCGCA 14259
QY 1261 AAAGTTGGCCAGGGCTTCCGGTATCAACAGGACACCGAGATTTTATTTCTGCGAA 1320
DB 14260 AAAGTTGGCCAGGGCTTCCGGTATCAACAGGACACCGAGATTTTATTTCTGCGAA 14319
QY 1321 GTGATCTTCGGTCAACAGTATTTTATTCGGCGCAAGTCCGCTGCGTCACTGCACT 1380
DB 14320 GTGATCTTCGGTCAACAGTATTTTATTCGGCGCAAGTCCGCTGCGTCACTGCACT 14379
QY 1381 AGTCGACTACAGGTCACATAACCATCTAAGTGTGATTCATAGTCACTGGAATGTTG 1440
DB 14380 AGTCGACTACAGGTCACATAACCATCTAAGTGTGATTCATAGTCACTGGAATGTTG 14439
QY 1441 TGTTTTACAGTATTTATGATGCTGTTTATGCAAAATCTAATTTTATATATGATAT 1500
DB 14440 TGTTTTACAGTATTTATGATGCTGTTTATGCAAAATCTAATTTTATATATGATAT 14499
QY 1501 TATATCAATTTTACGTTTCTGCTCAGCTTTCTGTCACAAAGTTCGCTATTAAGAAAGCA 1560
DB 14500 TATATCAATTTTACGTTTCTGCTCAGCTTTCTGTCACAAAGTTCGCTATTAAGAAAGCA 14559
QY 1561 TTGCTTATCAATTTTGTGCAACGAGTCATCATGCTCAAAATATAAATCATTTATTG 1620
DB 14560 TTGCTTATCAATTTTGTGCAACGAGTCATCATGCTCAAAATATAAATCATTTATTG 14619
QY 1621 CCATCCAGCTGAGCTCCGAGGAATTCGCTACCCAGCTTCGTAAAGGAATTAATTAAT 1680
DB 14620 CCATCCAGCTGAGCTCCGAGGAATTCGCTACCCCA - ATTGTAAGGAATTAATTAAT 14678
QY 1681 TTTCTTTTCTTTTGTATATAAATAGTAAAGTGTAAATAGTATGATTAATTAATTAAT 1740
DB 14679 TTTCTTTTCTTTTGTATATAAATAGTAAAGTGTAAATAGTATGATTAATTAATTAAT 14738
QY 1741 ATAGTGTATTAATTTGTGAAAAAATAATTAATAATATATTTTACATAAACAACATAG 1800
DB 14739 ATAGTGTATTAATTTGTGAAAAAATAATTAATAATATATTTTACATAAACAACATAG 14798
QY 1801 TAACTAAAAAATATGACAAAGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAG 1860
DB 14799 TAACTAAAAAATATGACAAAGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAG 14858
QY 1861 TATATTTATTTTAAATGAAATTTGATCGAATGTAAGATGATATATAGCATTTAA 1914
DB 14859 TATATTTATTTTAAATGAAATTTGATCGAATGTAAGATGATATACGGCGGTAAAGGTT 14918
QY 1915 ----- 1914

Db	14919	CCACCTTTCACCATATGAATAGATCACTACCGGCGGTATTTTGGTGTATCGAGAT	14978
QY	1915	-----	1914
Db	14979	TTTCAGAGCTAAGGAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATA	15038
QY	1915	-----	1914
Db	15039	TATCCCAATGGCATCGTAAAGAACATTTTGGAGCATTTTCAGTCACTGCTCAATGATCCT	15098
QY	1915	-----	1914
Db	15099	ATAACAGACCGTTTCAGCTGGATATTACGGCCTTTTAAAGACCGCTAAGAAAAATAAGC	15158
QY	1915	-----	1914
Db	15159	ACAAGCTTTTATCCGGCCTTTATTTCACATTTCTGCCGCTGATGAATGCTCATCCGGAAT	15218
QY	1915	-----	1914
Db	15219	TCCGTATGGCAATGAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCGTTGTATACA	15278
QY	1915	-----	1914
Db	15279	CGGTTCATGAGCAAACTGAACGTTTTCATCGCTCTGGAGTGAAATACCACGACGATT	15338
QY	1915	-----	1914
Db	15339	TCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGGTGTTACGGTGAACACCTGGCCT	15398
QY	1915	-----	1914
Db	15399	ATTTCCCTAAGGGTTTATTGAGATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTT	15458
QY	1915	-----	1914
Db	15459	TCACAGTTTGTATTTAAACGTTGGCCAATATGGACAACTTCTTCGCCCCGTTTTTCACCA	15518
QY	1915	-----	1914
Db	15519	TGGGCAAAATATTAACGCAAGCGCAAGGTGCTGATCCCGCTGGCGATTCAAGTTTCATC	15578
QY	1915	-----	1914
Db	15579	ATGCGTCTGTGATGGCTTCCATGTCCGCAGATGCTTAAATGAATTAACAACAGTACTCGG	15638
QY	1915	-----	1914
Db	15639	ATGAGTGGCAGGGGGGGGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGT	15698
QY	1915	-----TATTTGTTTTTAATCAT	15758
Db	15699	ATGCGTATTTGGCGCTGATTTTGGCGTATAAGAAATATATCTGATATGTCGGGCCCAT	15758
QY	1931	AATAGTAATCTAGCTGGTTTGTAGAAATTAATATCAATGATATAAATACTAGTAAAAA	1990
Db	15759	AATAGTAATCTAGCTGGTTTGTAGAAATTAATATCAATGATATAAATACTAGTAAAAA	15818
QY	1991	TAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2050
Db	15819	TAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	15878
QY	2051	TATCTATACCACTTACTAAATATTTTGTAGTTTAAAGTTTAAATAATTTTGTAGAAATTC	2110
Db	15879	TATCTATACCACTTACTAAATATTTTGTAGTTTAAAGTTTAAATAATTTTGTAGAAATTC	15938
QY	2111	CAATCTGCTTGTAAATTTATCAATAAACAATAATTTAAATAAACAAGCTAAAGTAAACAATA	2170
Db	15939	CAATCTGCTTGTAAATTTATCAATAAACAATAATTTAAATAAACAAGCTAAAGTAAACAATA	15998
QY	2171	ATATCAAACTAATAGAAACAGTAACTAATGTAAACAAACAACTAATCTAATCTAATATAA	2230

Db	15999	ATATCAAACTAATAGAAACAGTAACTAATGTAAACAAACAACTAATCTAATCTAATATAA	16058
QY	2231	CAAAAGCCAGAGCATCTATCAATTTTATATAGTATATTTTCAATCAACATTTCTTATTAATTT	2290
Db	16059	CAAAAGCCAGAGCATCTATCAATTTTATATAGTATATTTTCAATCAACATTTCTTATTAATTT	16118
QY	2291	CTAAATATATCTGTAGCTTTTATTAACCTTCTAAATGATTTGACTATTAATTAATGAATTT	2350
Db	16119	CTAAATATATCTGTAGCTTTTATTAACCTTCTAAATGATTTGACTATTAATTAATGAATTT	16178
QY	2351	AGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTGTATCATTTGATCT	2410
Db	16179	AGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTGTATCATTTGATCT	16238
QY	2411	TACATTTGGATGTATTCAGTTGGGAAGCTGGGTTGGAATCGAATAAGCTTTGGATTCCTCT	2470
Db	16239	TACATTTGGATGTATTCAGTTGGGAAGCTGGGTTGGAATCGAATAAGCTTTGGATTCCTCT	16298
QY	2471	AGAGAGCTGACAGCTGGATGGCAATAATGATTTTATTTGACTGATAGTGAACCTGTTGCT	2530
Db	16299	AGAGAGCTGACAGCTGGATGGCAATAATGATTTTATTTGACTGATAGTGAACCTGTTGCT	16358
QY	2531	TGCAACAAATTTGATAAGCAATGCTTTCTTATAATGCAAACTTTTGTACAAGAAAGCTGAAC	2590
Db	16359	TGCAACAAATTTGATAAGCAATGCTTTCTTATAATGCAAACTTTTGTACAAGAAAGCTGAAC	16418
QY	2591	GAGAAACGTAATAATGATATAAATAATCAATATTAATAATTAAGATTTTGGATTAATAAACA	2650
Db	16419	GAGAAACGTAATAATGATATAAATAATCAATATTAATAATTAAGATTTTGGATTAATAAACA	16478
QY	2651	CTACATAATCTGTAAACAAACAACATATCCAGTCACTATGAATCAACTACTTACATGGTA	2710
Db	16479	CTACATAATCTGTAAACAAACAACATATCCAGTCACTATGAATCAACTACTTACATGGTA	16538
QY	2711	TTAGTACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCCGAATAAAA	2770
Db	16539	TTAGTACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCCGAATAAAA	16598
QY	2771	TACCTGTGACGGAAGATCACTTTCGAGAAATAAATAAATCTGCTGCTGCTGCTGCTGCTGCT	2830
Db	16599	TACCTGTGACGGAAGATCACTTTCGAGAAATAAATAAATCTGCTGCTGCTGCTGCTGCTGCT	16658
QY	2831	GGAAAGCCTTGGCCCAACTTTTGGGAAAATGAGACGTTTGTATCGGCATCTACCAATTTTACA	2890
Db	16659	GGAAAGCCTTGGCCCAACTTTTGGGAAAATGAGACGTTTGTATCGGCATCTACCAATTTTACA	16718
QY	2891	ACTCTTATATTTTCTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2950
Db	16719	ACTCTTATATTTTCTCTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16778
QY	2951	TACTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTA	3010
Db	16779	TACTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTA	16838
QY	3011	TAAGGAGCCTTGACATTTATTTCCCGAGAACATCAGGTTAAATGGCGCTTTTGTATGTCAT	3070
Db	16839	TAAGGAGCCTTGACATTTATTTCCCGAGAACATCAGGTTAAATGGCGCTTTTGTATGTCAT	16898
QY	3071	TTTCGCGGTGGCTGAGATCAAGCACTTCTTCCCGATTAACGAGACCCGACACTGGCCA	3130
Db	16899	TTTCGCGGTGGCTGAGATCAAGCACTTCTTCCCGATTAACGAGACCCGACACTGGCCA	16958
QY	3131	TATCGGTGGTCATATGCGCCAGCTTTTCAATCCCGATATACCAACCGGTTAAGTTCAC	3190
Db	16959	TATCGGTGGTCATATGCGCCAGCTTTTCAATCCCGATATACCAACCGGTTAAGTTCAC	17018
QY	3191	GGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGG	3250
Db	17019	GGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGG	17078
QY	3251	CGGTGTCAATAATATCTCTGTATATCCAAACAGACGATTAACGGCTCTCTCTTTTAT	3310
Db	17079	CGGTGTCAATAATATCTCTGTATATCCAAACAGACGATTAACGGCTCTCTCTTTTAT	17138

Qy	3311	AGTGTAACCTTTAAACTCGATTTTCAACAAGTCCCTGTGTTCTCTGTAAGCAAAAAGAGCGCGTTC	3370
Db	17139	AGGTGTAACCTTTAAACTCGATTTTCAACAAGTCCCTGTGTTCTCTGTAAGCAAAAAGAGCGCGTTC	17198
Qy	3371	ATTTCATAAACCAGGCGACCTCAGCCATCCCTTCTCGATTTTCCGCTTTTCCAGCGTTCG	3430
Db	17199	ATTTCATAAACCAGGCGACCTCAGCCATCCCTTCTCGATTTTCCGCTTTTCCAGCGTTCG	17258
Qy	3431	GCACGACAGACGCGGGTCTCAATTCGCATGGTGTGCTTTACACAGACCGAGAGATATPAGACA	3490
Db	17259	GCACGACAGACGCGGGTCTCAATTCGCATGGTGTGCTTTACACAGACCGAGAGATATPAGACA	17318
Qy	3491	TCATATAGCCTTGAGCAACTGATAGCTGTCGCTGCAACTGCTACTGTAAATACGCTGCT	3550
Db	17319	TCATATAGCCTTGAGCAACTGATAGCTGTCGCTGCAACTGCTACTGTAAATACGCTGCT	17378
Qy	3551	TCATAGCACACCTCTTTTGGACATCTCTCTGTTCTTGATGACAGATGATTTTCAGGACTAT	3610
Db	17379	TCATAGCACACCTCTTTTGGACATCTCTCTGTTCTTGATGACAGATGATTTTCAGGACTAT	17438
Qy	3611	GACACTAGCGTATGAATAGGTAGATGTTTTTATTTTGTACACAAAAAGAGGCTCGC	3670
Db	17439	GACACTAGCGTATGAATAGGTAGATGTTTTTATTTTGTACACAAAAAGAGGCTCGC	17498
Qy	3671	ACCTCTTTTTCTTATTTCTTTTTATCATTAATACGGCAATTGAGGACCAATAGCGAGTAGG	3730
Db	17499	ACCTCTTTTTCTTATTTCTTTTTATCATTAATACGGCAATTGAGGACCAATAGCGAGTAGG	17558
Qy	3731	CTGGATACGACGATTCGGTTTGAGAAGACATTTGGAAGGCTGTGCGTGCAGCTAAGTTGG	3790
Db	17559	CTGGATACGACGATTCGGTTTGAGAAGACATTTGGAAGGCTGTGCGTGCAGCTAAGTTGG	17618
Qy	3791	CAGCATCACCCGAAGAACATTTGGAAGGCTGTGCGTGCAGCTACAGTCACATTAATACCATC	3850
Db	17619	CAGCATCACCCGAAGAACATTTGGAAGGCTGTGCGTGCAGCTACAGTCACATTAATACCATC	17678
Qy	3851	TAAGTAGTGATTCATAGTGACGTGATGTTGTGTGTTTACAGTATTAATGTAGTCTGTGTT	3910
Db	17679	TAAGTAGTGATTCATAGTGACGTGATGTTGTGTGTTTACAGTATTAATGTAGTCTGTGTT	17738
Qy	3911	TTTATGCAAAATCTAATTTAAATATTTGATATTTATCATTTTACGTTTCTGCTGCTCAGC	3970
Db	17739	TTTATGCAAAATCTAATTTAAATATTTGATATTTATCATTTTACGTTTCTGCTGCTCAGC	17798
Qy	3971	TTTTTTGTACAAAGTTGGCATTAATAAAAGCATTTGCTCATCAATTTGTTGCAACGAACA	4030
Db	17799	TTTTTTGTACAAAGTTGGCATTAATAAAAGCATTTGCTCATCAATTTGTTGCAACGAACA	17858
Qy	4031	GGTCATCTACGTCAAATAAATACATTAATTTGGGGCCCGAGATCCATGCTAGCTCTAGA	4090
Db	17859	GGTCATCTACGTCAAATAAATACATTAATTTGGGGCCCGAGATCCATGCTAGCTCTAGA	17918
Qy	4091	GTCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCT	4150
Db	17919	GTCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCT	17978
Qy	4151	GTTGTGCACTGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTCTTACGCGGTTTCGG	4210
Db	17979	GTTGTGCACTGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTCTTACGCGGTTTCGG	18038
Qy	4211	TTCAATTCATAGTATATCACCCGTTTACTGTCGTTATTTTATGATGAATATATTTCTCCGTT	4270
Db	18039	TTCAATTCATAGTATATCACCCGTTTACTGTCGTTATTTTATGATGAATATATTTCTCCGTT	18098
Qy	4271	CAATTTACTGANTGTACCCCTACTTATATGTFACAAATATTAATGAAAAAATATATTT	4330
Db	18099	CAATTTACTGANTGTACCCCTACTTATATGTFACAAATATTAATGAAAAAATATATTT	18158
Qy	4331	GTGCTGAAATAGGTTTATAGCGCATCTATGATAGCGGCCACAATAACAAATTTGGGT	4390
Db	18159	GTGCTGAAATAGGTTTATAGCGCATCTATGATAGCGGCCACAATAACAAATTTGGGT	18218

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RESULTS

AAC55521
ID AAC55521 standard: DNA: 4470 BP.

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AAC55521;

DT 11-JAN-2001 (first entry)

Donor plasmid pDONR201 nucleotide sequence.

[illegible]

KW Bacteriophage lambda; att; recombination site; attB; attP; attL;
KW mutant; recombinational cloning; restriction endonuclease

mutant; recombinational cloning; entry vector; destination vector;
KW
VW
zone product targeting; fusion tag cloning; 3c

OS Bacteriop

OS Synthetic.

PN WO200052027-

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PD 08-SEP-2000.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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PF 02-MAR-2000; 2000WO-US0005432.

PR 02-MAR-1999; 99US-0122389P.

PR 23-MAR-1999; 99US-0126049P.

PR 28-MAY-1999; 99US-

PA (LIFE-) LIFE TECHNOLOGIES INC.

FA (LIFE-) LIFE TECHNOLOGIES INC.
XX

PT	Hartley, JI.	Brasch MA	Temple CE	Chao D.
XX				

1000

DR WPI; 2000-543948/49.

XX

encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is used
in the exemplification of the present invention

Query Match 24.8%; Score 1207.4; DB 3; Length 4470;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGGCTAGCATGATCTCGGGCCCCAAATAAGATTTTATTGCTGATGATGACCTGTT 84
DB 5 AGGCTAGCATGATCTCGGGCCCCAAATAAGATTTTATTGCTGATGATGACCTGTT 64
QY 85 CTTTCAACAAATTGATGAGCAATCGTTTATATGCAATTTGACAAAAGCTG 144
DB 65 CTTTCAACAAATTGATGAGCAATCGTTTATATGCAATTTGACAAAAGCTG 124
QY 145 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATAAAAAC 204
DB 125 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATAAAAAC 184
QY 205 AGACTACATATCTGTAACACACACATATCCAGTCACTATGATCACTACTTAGATG 264
DB 185 AGACTACATATCTGTAACACACACATATCCAGTCACTATGATCACTACTTAGATG 244
QY 265 GTATTAGTACCTGTAGTCGACCGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAA 324
DB 245 GTATTAGTACCTGTAGTCGACCGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAA 304
QY 325 CTTAGTCGACGACGCTTCCAAATGTTCTTCCTCAAAACGGAATCGTGTATCCAGCCTA 384
DB 305 CTTAGTCGACGACGCTTCCAAATGTTCTTCCTCAAAACGGAATCGTGTATCCAGCCTA 364
QY 385 CTCGCTATTGCTCAATGCGGTATTAATATCAATAAAGAAATAGAAAGAGGTGGCA 444
DB 365 CTCGCTATTGCTCAATGCGGTATTAATATCAATAAAGAAATAGAAAGAGGTGGCA 424
QY 445 GCCTCTTTTGTGACAAAATAAAACATCTACTATTCATATACGCTAGTGTCTAG 504
DB 425 GCCTCTTTTGTGACAAAATAAAACATCTACTATTCATATACGCTAGTGTCTAG 484
QY 505 TCGTGAATATCATCTGCATCAAGACAAATTCACAACTCTTATACCTTTCTTTCAAGT 564
DB 485 TCGTGAATATCATCTGCATCAAGACAAATTCACAACTCTTATACCTTTCTTTCAAGT 544
QY 565 CGTTGGCTTCTATCGGATTTTCAGCTCTATCTACTTAAACGTCGATTAAGTTTCTGA 624
DB 545 CGTTGGCTTCTATCGGATTTTCAGCTCTATCTACTTAAACGTCGATTAAGTTTCTGA 604
QY 625 ATTCTACTGTATCGACCTGCAGCTGGCTGTATAGGGAGCTTGACATTTATATTC 684
DB 605 ATTCTACTGTATCGACCTGCAGCTGGCTGTATAGGGAGCTTGACATTTATATTC 664
QY 685 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCGCCAC 744

DB 665 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCGCCAC 724
QY 745 TTCTTCCCGATAAACGAGACCGGCACACTGGGCCATATCGGTGTCTATCATGCGCCAGCT 804
DB 725 TTCTTCCCGATAAACGAGACCGGCACACTGGGCCATATCGGTGTCTATCATGCGCCAGCT 784
QY 805 TTCTTCCCGATAAACGAGACCGGCCTAAAGTTTACGGGAGACTTTATCTGACAGACG 864
DB 785 TTCTTCCCGATAAACGAGACCGGCCTAAAGTTTACGGGAGACTTTATCTGACAGACG 844
QY 865 TGCACTGGCCAGGGGGATCAACATCCGTTCGCGCGGGGTGTCAATAATATCACTCTGTAC 924
DB 845 TGCACTGGCCAGGGGGATCAACATCCGTTCGCGCGGGGTGTCAATAATATCACTCTGTAC 904
QY 925 ATCCACAAAACAGACGATAAAGGCTCTCTCTTTTAGTGTAAACCTTAACTGCATTTTC 984
DB 905 ATCCACAAAACAGACGATAAAGGCTCTCTCTTTTAGTGTGTAAACCTTAACTGCATTTTC 964
QY 985 ACCAGTCCCTGTTCTCGTCAAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGACCTCAG 1044
DB 965 ACCAGTCCCTGTTCTCGTCAAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGACCTCAG 1024
QY 1045 CCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGCAACGACGACGCGGCTTCATTTCT 1104
DB 1025 CCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGCAACGACGACGCGGCTTCATTTCT 1084
QY 1105 GCATGGTGTGCTTACCAGACCGGAGATATGACATCATATATGCTTGAGCAACTGATA 1164
DB 1085 GCATGGTGTGCTTACCAGACCGGAGATATGACATCATATATGCTTGAGCAACTGATA 1144
QY 1165 GCTGTGCTGTCAACTGTCACTGTAAATACGCTGTTCATAGCACACCTCTTTTGGACATA 1224
DB 1145 GCTGTGCTGTCAACTGTCACTGTAAATACGCTGTTCATAGCACACCTCTTTTGGACATA 1204
QY 1225 CTTCCGGTA 1233
DB 1205 CTTCCGGTA 1213

RESULT 6
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR201 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
FN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX

BS Disclosure; Fig 26B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
XX represents the destination plasmid pDONR201 nucleotide sequence
XX

SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 7; Length 4470;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	25	AGCTAGCATGATCTCGGCGCCCAAAATGATTTTATTTGACATGATGACCTGTT	84
DB	5	ACGCTAGCATGATCTCGGCGCCCAAAATGATTTTATTTGACATGATGACCTGTT	64
QY	85	CGTTGCAACAAATGATGAGCAATGCTTTTATATGACCACTTTGTACAAAAGCTG	144
DB	65	CGTTGCAACAAATGATGAGCAATGCTTTTATATGACCACTTTGTACAAAAGCTG	124
QY	145	AACGAGAAACGTAATGATATATAATATCAATATATAATTTAGATTTTGCATAAAAAC	204
DB	125	AACGAGAAACGTAATGATATATAATATCAATATATAATTTAGATTTTGCATAAAAAC	184
QY	205	AGACTACATAACTGTAAACACACACATATCCAGTCACTATGAATCACTACTTAGATG	264
DB	185	AGACTACATAACTGTAAACACACACATATCCAGTCACTATGAATCACTACTTAGATG	244
QY	265	GTATTAGTGACCTGTAGTCGCGCAGAGCTTCCAAATGTTCTCGGGTGATGCTGCCAA	324
DB	245	GTATTAGTGACCTGTAGTCGCGCAGAGCTTCCAAATGTTCTCGGGTGATGCTGCCAA	304
QY	325	CTTAGTCGACGACGCTTCCAAATGTTCTCTCAACGGAATCGTGTATCCAGCCTTA	384
DB	305	CTTAGTCGACGACGCTTCCAAATGTTCTCTCAACGGAATCGTGTATCCAGCCTTA	364
QY	385	CTCGCTATTGCTCAATCGCTATTATATATCAATATCAATATCAATATCAATATCA	444
DB	365	CTCGCTATTGCTCAATCGCTATTATATATCAATATCAATATCAATATCAATATCA	424
QY	445	GCCTCTTTTGTGTGACAAAATAAAACATCTACCTATTATATACGCTAGTGTATAG	504
DB	425	GCCTCTTTTGTGTGACAAAATAAAACATCTACCTATTATATACGCTAGTGTATAG	484
QY	505	TGCTGAAATCATCTGCATCAAGACAAATTCACAACTCTTATACCTTTCTCTTCAAGT	564
DB	485	TCCTGAAATCATCTGCATCAAGACAAATTCACAACTCTTATACCTTTCTCTTCAAGT	544
QY	565	CGTTGGCTTCACTGGATTTTTCAGCTCTATCTACTATACGCTGATAGATTTCTGTA	624
DB	545	CGTTGGCTTCACTGGATTTTTCAGCTCTATCTACTATACGCTGATAGATTTCTGTA	604
QY	625	ATTCTACTGTATCGACCTCGAGCTGGCTGTGTATAGGGAGCTTGACATTTATATCC	684
DB	605	ATTCTACTGTATCGACCTCGAGCTGGCTGTGTATAGGGAGCTTGACATTTATATCC	664
QY	685	CCAGAACATCAGGTTAATCGGCTTTTGTATGATCAATTTCCGGGTGGCTGAGATCAGCAC	744
DB	665	CCAGAACATCAGGTTAATCGGCTTTTGTATGATCAATTTCCGGGTGGCTGAGATCAGCAC	724
QY	745	TTCTTCCCGATAACGAGACCGGACACTGGCCATATCGTGGTTCATCATCGGCCAGCT	804
DB	725	TTCTTCCCGATAACGAGACCGGACACTGGCCATATCGTGGTTCATCATCGGCCAGCT	784

QY	805	TTATCCCGGATATGCACCAACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGC	864
DB	785	TTATCCCGGATATGCACCAACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGC	844
QY	865	TGCACTGGCCAGGGGATCACCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTAC	924
DB	845	TGCACTGGCCAGGGGATCACCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTAC	904
QY	925	ATCCACAAACAGACATAAACCGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTC	984
DB	905	ATCCACAAACAGACATAAACCGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTC	964
QY	985	ACGAGTCCCTGCTTCGCTCAGCAAAAAGCGTTTCATTTCAATAAACCGGCGGACCTCAG	1044
DB	965	ACGAGTCCCTGCTTCGCTCAGCAAAAAGCGTTTCATTTCAATAAACCGGCGGACCTCAG	1024
QY	1045	CCATCCCTTCTCTGATTTTCCGCTTTCCGACCGCTTCGGCAGCAGCAGCGGCTTCATCT	1104
DB	1025	CCATCCCTTCTCTGATTTTCCGCTTTCCGACCGCTTCGGCAGCAGCAGCGGCTTCATCT	1084
QY	1105	GCATGGTTGCTTACCAAGCCGGAGATATTTGACATATATATGCTTTGAGCAACTGATA	1164
DB	1085	GCATGGTTGCTTACCAAGCCGGAGATATTTGACATATATATGCTTTGAGCAACTGATA	1144
QY	1165	GCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGGACATA	1224
DB	1145	GCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGGACATA	1204
QY	1225	CTTCGGGTA 1233	
DB	1205	CTTCGGGTA 1213	

RESULT 7
ADA50329
ID ADA50329 standard; DNA; 4892 BP.
XX
AC ADA50329;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid vector pMK2010 DNA sequence.
XX
KW site-specific recombination; array construction; reporter gene fusion;
KW mutagenesis; protein production; protein characterisation;
KW plasmid pMK2010; ds.
XX
OS Synthetic.
XX
PN WO2003064623-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003176.
XX
PR 31-JAN-2002; 2002US-0354063P.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Kahn ML, House BL, Mortimer MW;
XX
DR WPI; 2003-679497/64.
XX
PT Moving an insert nucleic acid between vectors using site-specific
PT recombination in vivo, useful for studying the biology of the organism,
PT including array construction, reporter gene fusions, mutagenesis and
PT protein production.
XX
PS Claim 41; Page 47-51; 52pp; English.
XX
CC The invention comprises a method for moving an insert nucleic acid
CC molecule between vectors, the method involves moving an insert nucleic
CC acid from one vector to another using site-specific recombination. The

CC method of the invention is useful for studying the biology of an
CC organism, including array construction, reporter gene fusions,
CC mutagenesis, protein production and characterisation. The present DNA
CC sequence represents the plasmid vector pMK2010 of the invention.
XX
SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
Query Match 24.8%; Score 1207.4; DB 8; Length 4892;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACGTAGTAGTGAACCTGTT 84
DB |||||
5 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACGTAGTAGTGAACCTGTT 64
QY 85 CGTTGCAACAATTTGATGAGCAATGCTTTTATATGCAATGCTTGTACAAAAAGCTG 144
DB |||||
65 CGTTGCAACAATTTGATGAGCAATGCTTTTATATGCAATGCTTGTACAAAAAGCTG 124
QY 145 AACGAGAAACGTAATAATGATATATAATATCAATATATTAATTTAGATTTTGCATAAAAAC 204
DB |||||
125 AACGAGAAACGTAATAATGATATATAATATCAATATATTAATTTAGATTTTGCATAAAAAC 184
QY 205 AGACTACATAATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 264
DB |||||
185 AGACTACATAATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 244
QY 265 GTATTAGTGAACCTGTAGTGCAGCGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB |||||
245 GTATTAGTGAACCTGTAGTGCAGCGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 304
QY 325 CTTAGTCGACGAGCGCTTCCAAATGTTCTTCAACCGGAATCGTGATCCAGCCTTA 384
DB |||||
305 CTTAGTCGACGAGCGCTTCCAAATGTTCTTCAACCGGAATCGTGATCCAGCCTTA 364
QY 385 CTCGCTATTGCTCAATGCGCTTAAATCATATAAAGCAATATAGAAAAAGAGTGGGA 444
DB |||||
365 CTCGCTATTGCTCAATGCGCTTAAATCATATAAAGCAATATAGAAAAAGAGTGGGA 424
QY 445 GCCTCTTTTGTGTGACAAAATAAACAATCTACTATTATATACGTAGTGTCAATAG 504
DB |||||
425 GCCTCTTTTGTGTGACAAAATAAACAATCTACTATTATATACGTAGTGTCAATAG 484
QY 505 TCCTGAAATCATCTGCATCAAGACAATTCACAACTCTTATCTTTCTTTTCTTCAAGT 564
DB |||||
485 TCCTGAAATCATCTGCATCAAGACAATTCACAACTCTTATCTTTCTTTTCTTCAAGT 544
QY 565 CGTTCGGCTTCACTCTGGATTTTTCAGCTCTACTTACTTACAGTGTATAGTCTTCTGTA 624
DB |||||
545 CGTTCGGCTTCACTCTGGATTTTTCAGCTCTACTTACTTACAGTGTATAGTCTTCTGTA 604
QY 625 ATTCTACTGTATCGACCTGACACTGGCTGTGTATAGGGAGCGCTGACATTTATTTCC 684
DB |||||
605 ATTCTACTGTATCGACCTGACACTGGCTGTGTATAGGGAGCGCTGACATTTATTTCC 664
QY 685 CCAGACATCATGTTTAAAGCGCTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCAC 744
DB |||||
665 CCAGACATCATGTTTAAAGCGCTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCAC 724
QY 745 TTCTTCCCGGATAACGGAGACCGGACACTGCGCCATATCGGTGGTCAATCGCGCCAGCT 804
DB |||||
725 TTCTTCCCGGATAACGGAGACCGGACACTGCGCCATATCGGTGGTCAATCGCGCCAGCT 784
QY 805 TTCATCCCGGATATGACACACCGGTTAAAGTTTCAACGGGAGCTTTTATCTGACAGACAG 864
DB |||||
785 TTCATCCCGGATATGACACACCGGTTAAAGTTTCAACGGGAGCTTTTATCTGACAGACAG 844
QY 865 TGCATGCGCGGAGGATCAACATCGTTCGCGCGGCGGTGCAATAATATCACTCTGTAC 924
DB |||||
845 TGCATGCGCGGAGGATCAACATCGTTCGCGCGGCGGTGCAATAATATCACTCTGTAC 904
QY 925 ATCCCAAAACAGACATACGGCTCTCTCTTTATAGGTGTAACCTTAAACCTGATTTTC 984
DB |||||

DB 905 ATCCAAAAACAGACGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTTAAACCTGCATTTC 964
QY 985 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGAGCTCAG 1044
DB |||||
965 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGAGCTCAG 1024
QY 1045 CCATCCCTTCCCTGATTTTCCGCTTCCAGCGTTCCGACGACGACGAGCGGCTTCATTCT 1104
DB |||||
1025 CCATCCCTTCCCTGATTTTCCGCTTCCAGCGTTCCGACGACGACGAGCGGCTTCATTCT 1084
QY 1105 GCATGTTGCTGTACACAGACCGGAGATATTGACATATATATGCTTTGAGCAACTGATA 1164
DB |||||
1085 GCATGTTGCTGTACACAGACCGGAGATATTGACATATATGCTTTGAGCAACTGATA 1144
QY 1165 GCTGTCGCTGTCAACTGTCACTGTAAATACGCTTTCATAGCACACCTCTTTTGGACATA 1224
DB |||||
1145 GCTGTCGCTGTCAACTGTCACTGTAAATACGCTTTCATAGCACACCTCTTTTGGACATA 1204
QY 1225 CTTCCGGTA 1233
DB |||||
1205 CTTCCGGTA 1213
RESULT 8
AAC55525
ID AAC55525 standard; DNA; 4939 BP.
XX AAC55525;
XX
XX 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR205 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
XX WO2000052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX
XX Example 10; Fig 53; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule

CC	comprising a second recombination site that interacts with the mutated
CC	act recombination site. (I), (II), (III), primers, vectors and methods
CC	from the present invention are used for the recombinational cloning of
CC	nucleic acid molecules. They can be used for changing vectors, targeting
CC	gene products to intracellular locations, cleaving fusion tags from
CC	desired proteins, operably linking nucleic acid molecules of interest to
CC	regulatory genetic sequences, constructing genes for fusion proteins,
CC	changing copy number, changing replicons, cloning into phages and
CC	cloning. (I), (II), (III), host cells and vectors can be used in the
CC	production of polypeptides and antibodies. The present sequence is used
CC	in the exemplification of the present invention
XX	
SQ	Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;
	Query Match 24.8%; Score 1207.4; DB 3; Length 4939;
	Best Local Similarity 99.9%; Pred. No. 1.6e-164;
	Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	25 AGGCTAGCATGGATCTCGGGCCCCAAATAATGATTTTATTTGACTGATAGTGACCTGTT 84
Db	3539 ACGCTAGCATGGATCTCGGGCCCCAAATAATGATTTTATTTGACTGATAGTGACCTGTT 3598
QY	85 CGTTGCACAAATGTAGAGAAATGCTTTTATATATGCCAACTTTGTGACAAAAGCTG 144
Db	3599 CGTTGCACAAATGTAGAGCAATGCTTTTATATATGCCAACTTTGTACAAAAGCTG 3658
QY	145 AACGAGAAACGTAAATGATATAAATCAATATATTAATTAATTTAGATTTTCGATAAAAC 204
Db	3659 AACGAGAAACGTAAATGATATAATATCAATATATTAATTTAGATTTTGCATAAAAC 3718
QY	205 AGACTACATAATACTGTAAAAACAACATATCCAGTCACCTATGAATCAACTACTTAGATG 264
Db	3719 AGACTACATAATACTGTAAAAACAACATATCCAGTCACCTATGAATCAACTACTTAGATG 3778
QY	265 GTATTAGTAGACCTGTAGTCGACGACAGCCTCCAAATGTTCTTCGGTGATGCTGCCAA 324
Db	3779 GTATTAGTAGACCTGTAGTCGACGACAGCCTTCCAAATGTTCTTCGGTGATGCTGCCAA 3838
QY	325 CTTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTA 384
Db	3839 CTTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTA 3898
QY	385 CTGCTATTGTCTCAATGCGGTATTAATATCATAAAAAGAAAATGAAGAAAGAGGTGCGA 444
Db	3899 CTGCTATTGTCTCAATGCGGTATTAATATCATAAAAAGAAAATGAAGAAAGAGGTGCGA 3958
QY	445 GCCTCTTTTGTGTGACAAAATAAAAAACATCTACCTATTCAATACGCTAGTGTCTATAG 504
Db	3959 GCCTCTTTTGTGTGACAAAATAAACATCTACCTATTCAATACGCTAGTGTCTATAG 4018
QY	505 TCTGAAAAATCATCTGCATCAAGAACAAATTTACAACTCTTTATCTTTTCTCTTACAAGT 564
Db	4019 TCTGAAAAATCATCTGCATCAAGAACAAATTTCAAACTCTTTATCTTTTCTCTTACAAGT 4078
QY	565 CGTTCGGCTTTCATCTGGATTTTCAGCCTCTATCTTACTAAACGTGATAAAGTTTCTGTGA 624
Db	4079 CGTTCGGCTTTCATCTGGATTTTCAGCCTCTATCTTACTAAACGTGATAAAGTTTCTGTGA 4138
QY	625 ATTTCTACTGTATCGACCTCGACACTGGCTGTGTATAGGGAGGCTTGACATTTTATATTC 684
Db	4139 ATTTCTACTGTATCGACCTCGACACTGGCTGTGTATAGGGAGGCTTGACATTTTATATTC 4198
QY	685 CCAGAACATCAGGTTAATGGGTTTTTGATGTCATTTTTCGGGTGGCTGAGATCAGCCAC 744
Db	4199 CCAGAACATCAGGTTAATGGGTTTTTGATGTCATTTTTCGGGTGGCTGAGATCAGCCAC 4258
QY	745 TTCTTCCCGGATACGGAGACCGGCACATCGGCCATATCGGTGGTGCATCATGCGCCAGCT 804
Db	4259 TTCTTCCCGGATACGGAGACCGGCACATCGGCCATATCGGTGGTGCATCATGCGCCAGCT 4318
QY	805 TTCTTCCCGGATACGCCACCGGGTAAAGTTACGGGAGACTTTATCTGAACAGCAGACG 864
Db	4319 TTCTTCCCGGATACGCCACCGGGTAAAGTTACGGGAGACTTTATCTGAACAGCAGACG 4378

at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

XX
SQ

Query Match 24.8%; Score 1207.4; DB 3; Length 5584;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGCTAGCATGGATCTCGGGCCCAAAATGAATTTATTTGACTGATGAGCTGTT 84
DB 5580 AGCTAGCATGGATCTCGGGCCCAAAATGAATTTATTTGACTGATGAGCTGTT 5521

QY 85 CGTTGCAACAATGATGAGCAATGCTTTTATATGCGCAACTTTGTAACAAAAAGCTG 144
DB 5520 CGTTGCAACAATGATGAGCAATGCTTTTATATGCGCAACTTTGTAACAAAAAGCTG 5461

QY 145 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATAAAAAC 204
DB 5460 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATAAAAAC 5401

QY 205 AGACTACATATATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 264
DB 5400 AGACTACATATATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 5341

QY 265 GTATTAGTACCTTAGTGCAGCGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB 5340 GTATTAGTACCTTAGTGCAGCGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 5281

QY 325 CTTAGTCGACGACAGCGCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTA 384
DB 5280 CTTAGTCGACGACAGCGCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTA 5221

QY 385 CTCGCTATTGCTCTCAATCGCTATTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 444
DB 5220 CTCGCTATTGCTCTCAATCGCTATTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 5161

QY 445 GCCTCTTTTGTGTGACCAATTAACACATCTACTATTATATACGCTAGTGTATAG 504
DB 5160 GCCTCTTTTGTGTGACCAATTAACACATCTACTATTATATACGCTAGTGTATAG 5101

QY 505 TCCTGAAATCATCTGCATCAAGAACAAATTCACAACTCTTATACCTTTTCTTCAAGT 564
DB 5100 TCCTGAAATCATCTGCATCAAGAACAAATTCACAACTCTTATATCTTTCTTCAAGT 5041

QY 565 CGTTGGCTTCACTGGATTTTACGCTCTATCTACTTACTTAAACGTTAAGTTCTGTGA 624
DB 5040 CGTTGGCTTCACTGGATTTTACGCTCTATCTACTTACTTAAACGTTAAGTTCTGTGA 4981

QY 625 ATTTCTACTGTATCGACCTGCGAGCTGCTGTGTATAGGGAGCTGACATTTATTTCC 684
DB 4980 ATTTCTACTGTATCGACCTGCGAGCTGCTGTGTATAGGGAGCTGACATTTATTTCC 4921

QY 685 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGCGTGGCTGAGATCAGCCAC 744
DB 4920 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGCGTGGCTGAGATCAGCCAC 4861

QY 745 TTCTTCCCGATACGAGACGCGCACACTCGGCATATCGGTGTCATCATCGGCAGCT 804
DB 4860 TTCTTCCCGATACGAGACGCGCACACTCGGCATATCGGTGTCATCATCGGCAGCT 4801

QY 805 TTCACTCCCGATATACACACCGGTAAGTTTACGGGAGACTTTTATCTGACAGCAGG 864
DB 4800 TTCACTCCCGATATACACACCGGTAAGTTTACGGGAGACTTTTATCTGACAGCAGG 4741

QY 865 TGCATCGCGCAGGGGATACCATCCGTCGCCCGGCGGTGTCATAATACTCTGTAC 924
DB 4740 TGCATCGCGCAGGGGATACCATCCGTCGCCCGGCGGTGTCATAATACTCTGTAC 4681

QY 925 ATCCAAACAGACATTAACGCTCTCTCTTTTATAGTGTAAACCTTAACTGCACTTC 984
DB 4680 ATCCAAACAGACATTAACGCTCTCTCTTTTATAGTGTAAACCTTAACTGCACTTC 4621

QY 985 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGCTTCATTTCAATAACCGGGCGACTCAG 1044
DB 4620 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGCTTCATTTCAATAACCGGGCGACTCAG 4561

QY 1045 CCATCCCTTCTGATTTTCCGCTTTCAGCGTTCCGACGAGCAGCAGCGGCTTCATTTCT 1104
DB 4560 CCATCCCTTCTGATTTTCCGCTTTCAGCGTTCCGACGAGCAGCAGCGGCTTCATTTCT 4501

QY 1105 GCATGGTTGTGCTTACACAGACCGGAGATATTGACATCATATATGCTTGAGCACTGATA 1164
DB 4500 GCATGGTTGTGCTTACACAGACCGGAGATATTGACATCATATATGCTTGAGCACTGATA 4441

QY 1165 GCTGTCGCTGCAACTGCTGCACTGTAATAGCTGCTTCTATAGCACACACCTCTTTTGGACATA 1224
DB 4440 GCTGTCGCTGCAACTGCTGCACTGTAATAGCTGCTTCTATAGCACACACCTCTTTTGGACATA 4381

QY 1225 CTTGCGGTA 1233
DB 4380 CTTGCGGTA 4372

RESULT 10
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
DT
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX
OS Nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 18B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a

CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 7; Length 5584;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGGCCCAATAATGATTTTATTTGACGTAGTGACCTGTT 84
DB |||||
QY 5580 ACCTAGCATGATCTCGGGCCCAATAATGATTTTATTTGACGTAGTGACCTGTT 5521
DB |||||
QY 85 CGTTGCAACAAATGATGACGAATGCTTTTATAATGCAACTTTTGTACAAAAAGCTG 144
DB |||||
QY 5520 CGTTGCAACAAATGATGACGAATGCTTTTATAATGCAACTTTTGTACAAAAAGCTG 5461
DB |||||
QY 145 AACGGAACGTAATGATATATAATATCAATATATTAATAGATTTTGCATAAACAC 204
DB |||||
QY 5460 AACGGAACGTAATGATATATAATATCAATATATTAATAGATTTTGCATAAACAC 5401
DB |||||
QY 205 AGACTACATAATCTGTAAACACACATATCCAGTCACATGAATCAACTACTTAGATG 264
DB |||||
QY 5400 AGACTACATAATCTGTAAACACACATATCCAGTCACATGAATCAACTACTTAGATG 5341
DB |||||
QY 265 GTATTAGTACCTGTAGTCAGCGACAGCGCTCCAAATGTTCTCGGGTGTAGTCCCAA 324
DB |||||
QY 5340 GTATTAGTACCTGTAGTCAGCGACAGCGCTCCAAATGTTCTCGGGTGTAGTCCCAA 5281
DB |||||
QY 325 CTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAACCGAATCGTGTATCCAGCCTA 384
DB |||||
QY 5280 CTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAACCGAATCGTGTATCCAGCCTA 5221
DB |||||
QY 385 CTGCTATTGTTCTCTAATCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCA 444
DB |||||
QY 5220 CTGCTATTGTTCTCTAATCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCA 5161
DB |||||
QY 445 GCCTCTTTTGTGTGACAAATATAAACAATCTACCTATTATATACGTAGTGATAG 504
DB |||||
QY 5160 GCCTCTTTTGTGTGACAAATATAAACAATCTACCTATTATATACGTAGTGATAG 5101
DB |||||
QY 505 TCTGAAAAATCATCTGCATCAAGAACAAATTTCAAACTCTTATACCTTTTCTCTTACAAGT 564
DB |||||
QY 5100 TCTGAAAAATCATCTGCATCAAGAACAAATTTCAAACTCTTATACCTTTTCTCTTACAAGT 5041
DB |||||
QY 565 CGTTCCGCTTCATCTGGATTTTCAGCTCTATCTTACTAAAGTGAATAAGTTCTCTGTA 624
DB |||||
QY 5040 CGTTCCGCTTCATCTGGATTTTCAGCTCTATCTTACTAAAGTGAATAAGTTCTCTGTA 4981
DB |||||
QY 625 ATTCTTACTGTATCGACCTGACAGCTGGCTGTGTATAGGGAGCTTGACATTTATATCC 684
DB |||||
QY 4980 ATTCTTACTGTATCGACCTGACAGCTGGCTGTGTATAGGGAGCTTGACATTTATATCC 4921
DB |||||
QY 685 CCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCAC 744
DB |||||
QY 4920 CCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCAC 4861
DB |||||
QY 745 TTCTTCCCGATTAACGAGACCGGACACGTGGCCATATCGTGGTCAATCATATGCGCCAGT 804
DB |||||
QY 4860 TTCTTCCCGATTAACGAGACCGGACACGTGGCCATATCGTGGTCAATCATATGCGCCAGT 4801
DB |||||
QY 805 TTCTTCCCGATTAACGAGACCGGATTAAGTTTACCGGGAGACTTTTATCTGACAGACAG 864
DB |||||
QY 4800 TTCTTCCCGATTAACGAGACCGGATTAAGTTTACCGGGAGACTTTTATCTGACAGACAG 4741
DB |||||

QY 865 TGCATCTGCGCAGGGGGATCAACATCCGTCGCCCGCGGCGTGTCAATAATATCACTCTGTAC 924
DB |||||
QY 4740 TGCATCTGCGCAGGGGGATCAACATCCGTCGCCCGCGGCGTGTCAATAATATCACTCTGTAC 4681
DB |||||
QY 925 ATCCCAAAACAGACAGATTAACGGCTCTCTCTTTATAGTGTAAACCTTAAACTGCATTTTC 984
DB |||||
QY 4680 ATCCCAAAACAGACAGATTAACGGCTCTCTCTTTATAGG-GTAAACCTTAAACTGCATTTTC 4621
DB |||||
QY 985 ACCAGTCCCTGTCTGTCGTACGAAAGACGGCTTCATTTCAATTAACCGGCGACCTCAG 1044
DB |||||
QY 4620 ACCAGTCCCTGTCTGTCGTACGAAAGACGGCTTCATTTCAATTAACCGGCGACCTCAG 4561
DB |||||
QY 1045 CCATCCCTCTCTGATTTTCCGCTTTCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCT 1104
DB |||||
QY 4560 CCATCCCTCTCTGATTTTCCGCTTTCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCT 4501
DB |||||
QY 1105 GCATGTTGTGCTTACACAGACGGAGATTTGACATCATATATATGCTTTGAGCACTGATA 1164
DB |||||
QY 4500 GCATGTTGTGCTTACACAGACGGAGATTTGACATCATATATGCTTTGAGCACTGATA 4441
DB |||||
QY 1165 GCTGTCGTGTCAACTGTCACGTGTAATACGCTGCTTCAATAGCACACCTCTTTTGGACATA 1224
DB |||||
QY 4440 GCTGTCGTGTCAACTGTCACGTGTAATACGCTGCTTCAATAGCACACCTCTTTTGGACATA 4381
DB |||||
QY 1225 CTTCCGGGTA 1233
DB |||||
QY 4380 CTTCCGGGTA 4372
DB |||||

RESULT 11
ABZ58768
ID ABZ58768 standard; DNA; 4428 BP.
XX
AC ABZ58768;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 27B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to

CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence
XX
SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 24.7%; Score 1201; DB 7; Length 4428;
Best Local Similarity 99.6%; Pred. No. 1.3e-163;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACTGATGAGCCTGTT 84
DB 842 ACCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACTGATGAGCCTGTT 901
QY 85 CGTTGCAACAATGATGAGCAATGCTTTTATATGCAACTTTGTTACAAAAAGCTG 144
DB 902 CGTTGCAACAATGATGAGCAATGCTTTTATATGCAACTTTGTTACAAAAAGCTG 961
QY 145 AAGGAGAAACGTAAATATGATATAATATCAATATATTAATAGATTTTGCATAAAAAC 204
DB 962 ATATCGAAACGTAAATATGATATAATATCAATATATTAATAGATTTTGCATAAAAAC 1021
QY 205 AGACTACATAATCTCTAAACAACAATATCCAGTCACCTATGAAATCAACTACTTAGATG 264
DB 1022 AGACTACATAATCTCTAAACAACAATATCCAGTCACCTATGAAATCAACTACTTAGATG 1081
QY 265 GTATTAGTACCTGTAGTCAGCGACAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB 1082 GTATTAGTACCTGTAGTCAGCGACAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 1141
QY 325 CTTAGTCGACCGACAGCGCTTCCAAATGTTCTCTCAAAAGGAATCGTGTATCCAGCCTA 384
DB 1142 CTTAGTCGACCGACAGCGCTTCCAAATGTTCTCTCAAAAGGAATCGTGTATCCAGCCTA 1201
QY 385 CTGCTATTGTTCTCAATCGCGTATTAAATCATAAAAAGAAATPAGAAAAAGAGGTGCGA 444
DB 1202 CTGCTATTGTTCTCAATCGCGTATTAAATCATAAAAAGAAATPAGAAAAAGAGGTGCGA 1261
QY 445 GCTCTTTTTTGTGTCAGAAATPAAAAACATCTACCTATTTCATATAGCTGTGTCATAG 504
DB 1262 GCTCTTTTTTGTGTCAGAAATPAAAAACATCTACCTATTTCATATAGCTGTGTCATAG 1321
QY 505 TCCTGAAATCATCTGCATCAAGACAAATTTCAAACTCTTATACATTTTCTCTTACAAGT 564
DB 1322 TCCTGAAATCATCTGCATCAAGACAAATTTCAAACTCTTATACATTTTCTCTTACAAGT 1381
QY 565 CGTTGCGCTTCATCTGGATTTTTCAGCGCTCTATACCTTAAACGCTGATAAAGTTTCTGTA 624
DB 1382 CGTTGCGCTTCATCTGGATTTTTCAGCGCTCTATACCTTAAACGCTGATAAAGTTTCTGTA 1441
QY 625 ATTCTACTGTATCGACCTGCGACATGGCTGTCTATAAGGAGCGCTGACATTTATATTC 684
DB 1442 ATTCTACTGTATCGACCTGCGACATGGCTGTCTATAAGGAGCGCTGACATTTATATTC 1501
QY 685 CCAGAACATCAGGTTAATGCGGTTTTTGATGTCAATTTTCGCGGTGGCTGAGATCAGCCAC 744
DB 1502 CCAGAACATCAGGTTAATGCGGTTTTTGATGTCAATTTTCGCGGTGGCTGAGATCAGCCAC 1561
QY 745 TTCTTCCCGATTAACGAGACCGGCACTGGCGCATATCGTGGTGTATATGCGCCAGCT 804
DB 1562 TTCTTCCCGATTAACGAGACCGGCACTGGCGCATATCGTGGTGTATATGCGCCAGCT 1621
QY 805 TTCTATCCCGATATGACACACCGGTTAAAGTTTACCGGGAGCTTTATCTGACAGAGAGC 864
DB 1622 TTCTATCCCGATATGACACACCGGTTAAAGTTTACCGGGAGCTTTATCTGACAGAGAGC 1681
QY 865 TGCACTGGCCAGGGGATACCATCGTCCGCGCGGGCGTGTCAATATATCACTCTGTATC 924
DB 1682 TGCACTGGCCAGGGGATACCATCGTCCGCGCGGGCGTGTCAATATATCACTCTGTATC 1741
QY 925 ATCCACAAACAGAGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTC 984

DB 1742 ATCCACAAACAGACAGATAAAGCGCTCTCTTTTATAGGTAAACCTTAAACTGCATTTTC 1801
QY 985 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAG 1044
DB 1802 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAG 1861
QY 1045 CCATCCCTTCCGTGATTTTCCGCTTTCCAGCGTTCCGCGACGACGAGCGGGCTTCAATCT 1104
DB 1862 CCATCCCTTCCGTGATTTTCCGCTTTCCAGCGTTCCGCGACGACGAGCGGGCTTCAATCT 1921
QY 1105 GCATGTTGTGCTTACCGACCGGAGATATTGACATCATATATATGCTTTGAGCAACTGATA 1164
DB 1922 GCATGTTGTGCTTACCGACCGGAGATATTGACATCATATATATGCTTTGAGCAACTGATA 1981
QY 1165 GCTGTCGCTGTCACCTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGACATA 1224
DB 1982 GCTGTCGCTGTCACCTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGACATA 2041
QY 1225 CTTCCGGGTA 1233
DB 2042 CTTCCGGGTA 2050

RESULT 12
ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX AC ABZ58769;
XX DT 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR212(F) nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KM nucleic acid isolation; ds.
XX OS Synthetic.
XX PN WO200295055-A2.
XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US015947.
XX PR 21-MAY-2001; 2001US-0291973P.
XX PA (INVI-) INVITROGEN CORP.
XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX DR
XX PT Inserting a population of nucleic acids into a second target molecule for
XX PT selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid.
XX PS Disclosure; Fig 28B-C; 273pp; English.
XX CC The invention relates to inserting a population of nucleic acids into a
XX CC second target molecule. The method involves (a) mixing a first population
XX CC of nucleic acid comprising one or more recombination sites with a target
XX CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX CC the first population to recombine with the first target nucleic acid
XX CC molecules to form a second population; (c) mixing the second population
XX CC of nucleic acid with a second target nucleic acid; and (d) causing some
XX CC or all of the nucleic acid molecules of the second population to
XX CC recombine with some or all of the second target nucleic acid molecules to
XX CC form a third population of nucleic acid. The method is useful for
XX CC selecting and isolating nucleic acid molecules. The present sequence
XX CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.6%; Score 1194.6; DB 7; Length 4627;
Best Local Similarity 99.7%; Pred. No. 1.1e-162;
Matches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 ATGGATCTCGGCGCCCAATAATGATTTTATTTGACTGATAGTACCTGTTGCTTGCAA 92
DB 1 AUGGATCTCGGCGCCCAATAATGATTTTATTTGACTGATAGTACCTGTTGCTTGCAA 60

QY 93 CAAATGATGAGCAATGCTTTTATAATGCGCAACTTTGTACAAAAAAGCTGACAGAA 152
DB 61 CAAATGATGAGCAATGCTTTTATAATGCGCAACTTTGTACAAAAAAGCTGATATCGAA 120

QY 153 ACCTAAATGATATTAATATCAATATATTAATATGATTTTGCATAAAAAAGCTATCA 212
DB 121 ACCTAAATGATATTAATATCAATATATTAATATGATTTTGCATAAAAAAGCTATCA 180

QY 213 TAATCTGTAAAAACACAAATATCCAGTCACTATGAATCAATCACTTATGATGGTATAGT 272
DB 181 TAATCTGTAAAAACACAAATATCCAGTCACTATGAATCACTTATGATGGTATAGT 240

QY 273 GACCTGTAGTCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTCG 332
DB 241 GACCTGTAGTCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTCG 300

QY 333 ACCGACAGCTTCCAAATGTTCTTCACACGGAATCGTCTGATCCAGCTACTCGCTAT 392
DB 301 ACCGACAGCTTCCAAATGTTCTTCACACGGAATCGTCTGATCCAGCTACTCGCTAT 360

QY 393 TGFCTCAATGCCGTATTAATATCAATAAAAAGAAATAGAAAAAGAGGTGCGAGCTCTTT 452
DB 361 TGFCTCAATGCCGTATTAATATCAATAAAAAGAAATAGAAAAAGAGGTGCGAGCTCTTT 420

QY 453 TTTGTGTGACAAATAAAAACATCTACCTATTCATATAGCTAGTGTATAGTCCTGAAA 512
DB 421 TTTGTGTGACAAATAAAAACATCTACCTATTCATATAGCTAGTGTATAGTCCTGAAA 480

QY 513 ATCATCTGCATCAAGAACAAATTTCAACATCTTTATATCTTTCTTACAAAGTCTCGGC 572
DB 481 ATCATCTGCATCAAGAACAAATTTCAACATCTTTATATCTTTCTTACAAAGTCTCGGC 540

QY 573 TTCACTCGAATTTTCAGCTCTATATCTTACTAAACGTGATAAAGTTTCTGTATTTCTAC 632
DB 541 TTCACTCGAATTTTCAGCTCTATATCTTACTAAACGTGATAAAGTTTCTGTATTTCTAC 600

QY 633 TGTATCGACTCGACAGCTGCTGTATATAGGAGCTGACATTTATATCCCAAGCA 692
DB 601 TGTATCGACTCGACAGCTGCTGTATATAGGAGCTGACATTTATATCCCAAGCA 660

QY 693 TCAGGTTAATGGCGTTTTCATGCTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTCC 752
DB 661 TCAGGTTAATGGCGTTTTCATGCTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTCC 720

QY 753 CGATACGAGACCGGACACTGGCCATATCGTGTGTCATATGCGCCAGCTTTTATCC 812
DB 721 CGATACGAGACCGGACACTGGCCATATCGTGTGTCATATGCGCCAGCTTTTATCC 780

QY 813 CGATATGACACCGGTTAAGTTTCAGGAGACTTTATCTGACAGACAGCTGCTGG 872
DB 781 CGATATGACACCGGTTAAGTTTCAGGAGACTTTATCTGACAGACAGCTGCTGG 840

QY 873 CCAGGGGATCACCATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCAAA 932
DB 841 CCAGGGGATCACCATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCAAA 900

QY 933 ACAGACGATAACGGCTCTCTTTTATAGTGTAACCTTAACTGATTTTACAGTCC 992
DB 901 ACAGACGATAACGGCTCTCTTTTATAGTGTAACCTTAACTGATTTTACAGTCC 960

QY 993 CTGTTCTGTCAGCAAAAGCGCTTCATTTCAATAAAGCGGACCTCAGGCATCCCT 1052
DB 961 CTGTTCTGTCAGCAAAAGCGCTTCATTTCAATAAAGCGGACCTCAGGCATCCCT 1020

QY 1053 TCCTGATTTTTCGCTTTTCCAGCGTTTCGGCAGCAGACGCGGCTTTCATTTGCTGATGGTT 1112

DB 1021 TCCTGATTTTCCGCTTTCCAGCGTTCCGACGACGACGCGGCTTCATTTCTGCTGGTT 1080

QY 1113 GTGCTTACAGACCGGAGATATTGACATATATATGCTTGGAGCACTGATAGCTGTGC 1172

DB 1081 GTGCTTACAGACCGGAGATATTGACATATATATGCTTGGAGCACTGATAGCTGTGC 1140

QY 1173 TGTCAACTGTCTCTCTAATAGCTCTTCATAGCAACCTCTTTTGTACATATCTTCGGGT 1232

DB 1141 TGTCAACTGTCTCTCTAATAGCTCTTCATAGCAACCTCTTTTGTACATATCTTCGGGT 1200

QY 1233 A 1233

DB 1201 A 1201

RESULT 13
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX
AC ABZ58770;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212(R) nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
XX
DR
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 29B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(R) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.6%; Score 1194.6; DB 7; Length 4627;
Best Local Similarity 99.7%; Pred. No. 1.1e-162;
Matches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 ATGGATCTCGGCGCCCAATAATGATTTTATTTGACTGATAGTACCTGTTGCTTGCAA 92
DB 1 ATGGATCTCGGCGCCCAATAATGATTTTATTTGACTGATAGTACCTGTTGCTTGCAA 60

QY 93 CAAATTGATGAGCAATGCTTTTATTAATGSCCAACTTTGTACAAAAGAGCTGAACGAGAA 152
Db |||||
QY 61 CAAATTGATGAGCAATGCTTTTATTAATGSCCAACTTTGTACAAAAGAGCTGAATATCGAA 120
Db |||||
QY 153 ACCTAAATGATATAATATCAATATATTAATATAGATTGATATAAAAACAGACTACA 212
Db |||||
QY 121 ACCTAAATGATATAATATCAATATATTAATATAGATTGATATAAAAACAGACTACA 180
QY 213 TAATAGCTGTAACACACACATATCCAGTCACTATGATCACTACTATAGTATAGTATAGT 272
Db |||||
QY 181 TAATAGCTGTAACACACACATATCCAGTCACTATGATCACTACTATAGTATAGTATAGT 240
Db |||||
QY 273 GACCTGTAGTGCAGCCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTGC 332
Db |||||
QY 241 GACCTGTAGTGCAGCCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTGC 300
QY 333 ACCGACAGCCTTCCAAATGTTCTTCCTCAACCGAAATCGTGTATCCAGCCTACTCGCTAT 392
Db |||||
QY 301 ACCGACAGCCTTCCAAATGTTCTTCCTCAACCGAAATCGTGTATCCAGCCTACTCGCTAT 360
QY 393 TGTCTCAATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTT 452
Db |||||
QY 361 TGTCTCAATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTT 420
QY 453 TTTGTGTGACAAATATAAATCTACTTATCATATAGCTAGTGTCTATAGTCTCTGAAA 512
Db |||||
QY 421 TTTGTGTGACAAATATAAATCTACTTATCATATAGCTAGTGTCTATAGTCTCTGAAA 480
QY 513 ATCATCTGATCAAGAACAAATTTCAACCTTTATATCTTTCTTTCAAGTGTCTTCGCG 572
Db |||||
QY 481 ATCATCTGATCAAGAACAAATTTCAACCTTTATATCTTTCTTTCAAGTGTCTTCGCG 540
QY 573 TTCATCTGATTTTCAAGCTCTATATCTTACTTAAACGTGATTAAGTCTTCTGTAATTTCTAC 632
Db |||||
QY 541 TTCATCTGATTTTCAAGCTCTATATCTTACTTAAACGTGATTAAGTCTTCTGTAATTTCTAC 600
QY 633 TGTATCGACCTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTTCCCGAGAA 692
Db |||||
QY 601 TGTATCGACCTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTTCCCGAGAA 660
QY 693 TCAGTTAATGGGTTTGTATGTCATTTTTCGGGTGGCTGAGATCAGGACATTTCTTCC 752
Db |||||
QY 661 TCAGTTAATGGGTTTGTATGTCATTTTTCGGGTGGCTGAGATCAGGACATTTCTTCC 720
QY 753 CGATAACGAGACCGGCACACTGGCCATATCGTGTGTCATATGSCCAGCTTTCTATCC 812
Db |||||
QY 721 CGATAACGAGACCGGCACACTGGCCATATCGTGTGTCATATGSCCAGCTTTCTATCC 780
QY 813 CGATATGCAACCGGTTAAAGTTCACGGAGACTTTTATCTGACAGCAGACGTGCACTGG 872
Db |||||
QY 781 CGATATGCAACCGGTTAAAGTTCACGGAGACTTTTATCTGACAGCAGACGTGCACTGG 840
QY 873 CCAGGGGGATCACCTCCGTCGCGGGGTGTCAATATATCACTCTGTATATCCACAA 932
Db |||||
QY 841 CCAGGGGGATCACCTCCGTCGCGGGGTGTCAATATATCACTCTGTATATCCACAA 900
QY 933 ACAGAGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCACTTCCACAGTCC 992
Db |||||
QY 901 ACAGAGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCACTTCCACAGTCC 960
QY 993 CTGTTCTCTGACAAAAGAGCGGTTCAATTAATAAACCGGCGACCTCAGCCATCCCT 1052
Db |||||
QY 961 CTGTTCTCTGACAAAAGAGCGGTTCAATTAATAAACCGGCGACCTCAGCCATCCCT 1020
QY 1053 TCTGATTTTCCGCTTCCAGCTTCCGACCGCAGAGCGGCTTCACTTCTGATGTT 1112
Db |||||
QY 1021 TCTGATTTTCCGCTTCCAGCTTCCGACCGCAGAGCGGCTTCACTTCTGATGTT 1080
QY 1113 GTGCTTACAGACCGGAGATATTGACATCATATATGCTTGTAGCACTGATAGTGTGCG 1172
Db |||||
QY 1081 GTGCTTACAGACCGGAGATATTGACATCATATATGCTTGTAGCACTGATAGTGTGCG 1140

QY 1173 TGTCAACTGTCACTGTATATACGCTCTTCATAGCACACCTCTTTTGACATACTTCGGGT 1232
Db |||||
QY 1141 TGTCAACTGTCACTGTATATACGCTCTTCATAGCACACCTCTTTTGACATACTTCGGGT 1200
Db |||||
QY 1233 A 1233
Db 1201 A 1201
RESULT 14
ABQ82143/c
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
XX
PR 29-NOV-2001; 2001US-0333743P.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Wesley S, Waterhouse P, Helliwell C;
XX
DR WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 17; Page 93-102; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;
Query Match 24.1%; Score 1174.2; DB 6; Length 17681;
Best Local Similarity 59.5%; Pred. No. 8.5e-160;

Matches 2327; Conservative 0; Mismatches 1508; Indels 78; Gaps 17;

QY	122	GCACCTTTGTACAAAAGCTGAAACGAGAAACGTAAATGATATATAATATCAATATAT	181	QY	1193	CCCTGCTTCATAGACACCTCTTTTGTGACATACCTTCGGGTAGTG-----CCGATCAACGTC	1248
Db	16904	GACAAAGTTTGACAAAAGAGCTGAAACGAGAAACGTAAATGATATATAATATCAATATAT	16845	Db	15845	AGATGAAGCCGCAACGACTTGTGAAGAGAAAGATATAAGAGTTGTGAAATCCCGATCAACGTC	15786
QY	182	AAATTTAGATTTTGCATAAAAACAGACTACATATCTGTAAACACAAATATCCAGTC	241	QY	1249	TCATTTTTCGCAAAAGTTGGCCACGGCTTCCTCGGTATCAACAGGACACACAGGATTTAT	1308
Db	16844	AAATTTAGATTTTGCATAAAAACAGACTACATATCTGTAAACACAAATATCCAGTC	16785	Db	15785	TCATTTTTCGCAAAAGTTGGCCACGGCTTCCTCGGTATCAACAGGACACACAGGATTTAT	15726
QY	242	ACTATGAATCAACTACTTAGATGGTATTTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	301	QY	1309	TTATTTCTCGAAGTGATCTTCCGTACAGGTATTTATTTGGCGCAAGTGCGTCCGGTGA	1368
Db	16784	ACTATGAATCAACTACTTAGATGGTATTTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	16725	Db	15725	TTATTTCTCGAAGTGATCTTCCGTACAGGTATTTATTTGGCGCAAGTGCGTCCGGTGA	15666
QY	302	TGTTCTTCGGGTGATGCTGCAACTTAGTGACCGACAGCTTCGAAATGTTCTCTCAA	361	QY	1369	TGCTGCCAACTTAGTGACCTACAGGTCACTAATCACTAAGTAGTAGTTGATTCATAGTGA	1428
Db	16724	TGTTCTTCGGGTGATGCTGCAACTTAGTGACCGACAGCTTCGAAATGTTCTCTCAA	16665	Db	15665	TGCTGCCAACTTAGTGACCTACAGGTCACTAATCACTAAGTAGTAGTTGATTCATAGTGA	15606
QY	362	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCGGTATTAATCATAAAA	421	QY	1429	CTGGATATGTTGTTTACAGTATTTAGTAGTCTGTGTTTTTTTATGCAAAATCTAATTTAA	1488
Db	16664	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCGGTATTAATCATAAAA	16605	Db	15605	CTGGATATGTTGTTTACAGTATTTAGTAGTCTGTGTTTTTATGCAAAATCTAATTTAA	15546
QY	422	AGAAATPAAGAAAAGGTCGAGCCTCTTTTGTGTGACAAATAAATAACATCTACCT	481	QY	1489	TATATGTATTTATATATATTTTACAGTTCTCGTTTCTCGTTTCTGTTGACAAAGTTGGCAT	1548
Db	16604	AGAAATPAAGAAAAGGTCGAGCCTCTTTTGTGTGACAAATAAATAACATCTACCT	16545	Db	15545	TATATGTATTTATATATTTTACAGTTCTCGTTTCTCGTTTCTGTTGACAAAGTTGGCAT	15486
QY	482	ATTATATAGCTAGTGTATGCTAGTCTGCTGAAATCATCTGATCAAGACAAATTTCAAC	541	QY	1549	TATAAGAAAGCATTCGTTATCAATTTGTGTGCAACGACAGGTCACTATCAGTCAAAATAA	1608
Db	16544	ATTATATAGCTAGTGTATGCTAGTCTGCTGAAATCATCTGATCAAGACAAATTTCAAC	16485	Db	15485	GAGGATCCAGCTGTGACAGGTAAATTTCTAGTTTTTCTCTTCAATTTCTTCTGTTGAGGA	15426
QY	542	TCTTATATCTTTCTTTACAAAGTCGTTCCGCTTCATCTGATTTTTCAGCCTCTATACCTA	601	QY	1609	AATCATTTATTTCCCATCCAGCTGCAGCT-----CCTCGAGGAATTCGGTACCCAGCTTGG	1664
Db	16484	AAAAAGAGGTGCTGATGAA--GCAGCGTATTACAGTGACAGTTGACAGCGACAGCTAT	16428	Db	15425	CCCTTTCTCTTTTATTTTGTAGCTTTGATCTTTCTTTAACTGATCTATTTTTTAA	15366
QY	602	CTAAACGTGATAAAGTTCTCTGTAATTTCTACTGATTCGACCTCGACAGCTGGTGTGATA	661	QY	1665	TAAGGAATAATATTTTCTTTTCTTTTGTAGTATAAATAAGTTAAAGTAGTTAAATTA	1724
Db	16427	CAGTTGCTCAAGGCATATATATGATGTCATATCTCCGCTCTGTAAGCAACCAACATCGA	16368	Db	15365	TTGATTTGTTTATGCGGCAAAATATACATAGCTTTTAACTGATATCTGATTTACTTTTTC	15306
QY	662	AGGAGCCTCACATTTATATTTCCCGACACATCAGGTTAATGCGTTTGTGATCATTT	721	QY	1725	GTATGATTAATAATAATATAGTTTGTATTAATCTGTAAGAAAAATAATTTATAATATATTT	1784
Db	16367	ATGAAGCCCTGCTCTGCGTGCC---GAACGCTGGAAGCGGAAATTCAGGAAGGATGG	16311	Db	15305	GTGTTCTATGATGATGATGATGATACTGCGCGCAAGCTTATCGATTCGAAACCCAGCTTC	15246
QY	722	TCGCGGTGGTGTAGATCAGCACCTTCTTCCCGATACAGGAGACCGGCACACTGGCCATA	781	QY	1785	TACATAAAACACATAGTAAATGTAAGAAAAATATGCAAGTAGTGTGTAAGACGAAGAAT	1844
Db	16310	CTGAGGTCCGCGGTTTATTTGAAATGAACGGCTCTTTTGTGACGAGAACAGGG-----	16257	Db	15245	CCAACTGTAATCAATCCAAATGTAAGATCAATGATAACACAAATGACATGATCTATCATGT	15186
QY	782	TGCGGTGTCATCATGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG	841	QY	1845	AAAAGTTGAGAGTAAGTATATTTTAAAGAAATTTGATCGAATGTAAGATGATATA	1904
Db	16256	ACTGGTGAATGCAATTTAAGGTTTACACCTATAAAGAGAGAGCGGTATATCGTCTGTTT	16197	Db	15185	TACCTTGTGTTTTCATGTTTCGACTAATTCATTTAATTAATAGTCAATCCATTTAGAAATT	15126
QY	842	GAGACTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGATCACCATCCGTCGCGCCGGGC	901	QY	1905	CTAGCATTAATATTTGTTTAAATCATATAGTAAATTTCTAGCTGGTTTGTATGAATTAATA	1964
Db	16196	GTGATGTACAGAGTGATATTTATGACACCGCCGGCGACGGATGGTATCCCTCTGGCC	16137	Db	15125	AATAAACTACAAGTATTTATTTAGAAATTTAATAAGATGTTGATTGAAATAATACTATA	15066
QY	902	GTGCAATAATATCATCTCTGTACATCCAAACAGAGGATAACGGCTCTCTCTTTTATAG	961	QY	1965	TCATGATGATAAA-----TACTATAGTAAATAAAGATAAATAAATAAATAAATAAT	2014
Db	16136	AGTGACAGTCTGTGTGATATAAGTCTCCCGTGAACTTTACCCGGTGGTGATATCGGG	16077	Db	15065	TAAAATGATAGATCTTCGCGCTTGTATATATTAGCATTTAGATTATGTTTTTTTACATTAGA	15006
QY	962	GTGTAACCTTAACTGATTTTCACG-----AGTCCCTGTTCTCGTCAGCAAAAGAGCC	1015	QY	2015	ATTTTTTTTATGATTAATAGTCTTTTATTAATAATATCTATACCATTTACTTAAATATTT	2074
Db	16076	GATGAAGCTGGCGATGATGACACCGATATGCGCCAGTGTGCGGTCCTCGGTATCGGG	16017	Db	15005	TTACTGTTTCTATAGTTTGATTTATTTTGTACTTTTGTAGCTTTGTTTATTTATTTTGT	14946
QY	1016	GTTTCAATTAATAACCGGGGACCTCAGCCATCCCTTCTGATTTTTCGCTTTTCCAGCG	1075	QY	2075	TAGTTTAAAGTTAAATAATTTTGTGAGAAATTTCCAATCTGCTTGTAAATTTATCAATA	2134
Db	16016	GAAGAAGTGCTGATCTCAGCCACCGGAAATGACATCAAAACGCCATTTACCTGATG	15957	Db	14945	TATTGATTAATTAACAGCAGATTGGAAATTTCTTAACAAAAATTTTATTAACTTTTAACTA	14886
QY	1076	TTC---GGCAGCAGACGAGCGGCTTCATTTCTGATGTTGTGCTTACCGAGACCGAGAT	1132	QY	2135	AACAAAAATTAATAAACAAGCTAAAGTAAACAAATAA-----TATCAAACTAATTAAGAAC	2189
Db	15956	TTCTGGGGAATATAAATGTGAGGCTCCCTTTATACACAG-----CCAGTCTGCAGGT	15906	Db	14885	AAATATTTAGTAATGGTATAGATATTTAATTAATAAATACTATTAATCAATAAAAAAAT	14826
QY	1133	ATTGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATAA	1192	QY	2190	AGTATCTAATCTAACAACACATATCTAACTAATAATAAAGCGCAAGATCTATCA	2249
Db	15905	CGATACAGTAGAAATACAGAACTTTTATCACGCTTTAGTAGTATTTTATCATTTGATTAATTC	15846	Db	14825	ATTATTTTAATTTATTTTCTTTATTTTCTATAGTATTTTATCATTTGATTAATTAATTC	14766

QY 2250 TTTTATATAGTATTTTTCATCAACATCTCTTATTAAT-TTCTAAATATATCTTGTAGT 2308
Db 14765 ATCAAAACGAGCTAGAAATCTATTAATGATTAATAAACAATAATTAATGCTAGTATATCATCT 14706
QY 2309 TTTTATTAATCTCTAAATGGATGAGTATTAATTAATGAATTAAGTCAAGATGAATAAAC 2368
Db 14705 TACATGTCGATCAATTCATTAATAAATAATATATCTTACTCTCAACTTTTATCTTCTTCG 14646
QY 2369 AAGGTAAATGATAGATCAATGTCATGTTGTATCAATGATCTTACATTTGGATGATTAAC 2428
Db 14645 TCTTACACATCACTGTGCATATTTTTCATATTAATAAATAATATTAATTAATTAATTAACAT 14586
QY 2429 AGTTGGGAAGCTGGTTCGAATCGATAGCTTGGATCCTCTAGAGAGCTGACCTGGAT 2488
Db 14585 TTATTAATATTTTTCACAATTAATAACAATATATTAATTAATTAATTAATTAATTAACAT 14526
QY 2489 GGCATAATATGATTTATTTTGAAGTGAAGTGAAGCTGCTGCTGCAACAAATTTGATAAGC 2548
Db 14525 CACTTAACATATTTTATCTAAAGGAAAGAAAGAAATAATTTTCTTACCAAGCTGGG 14466
QY 2549 AATGCTTTCTTATTAATGCAACTTTGTACAAGAGCTGAACGAGAAACGTAATAATGATA 2608
Db 14465 GTACCGAAATCTCTGAGACCACTTTGTACAAGAAAGCTGAACGAGAAACGTAATAATGATA 14406
QY 2609 TAAATATCAATATATTAATTAATGATTTTGTCAATAAAGACAGACTACATAATCTGTAAAC 2668
Db 14405 TAAATATCAATATATTAATTAATGATTTTGTCAATAAAGACAGACTACATAATCTGTAAAC 14346
QY 2669 CACAACATATCAAGTCACTATGAATCAACTACTTAGATGGTATTAAGTCACTGTAGTCGA 2728
Db 14345 CACAACATATCAAGTCACTATGAATCAACTACTTAGATGGTATTAAGTCACTGTAGTCGA 14286
QY 2729 CTAAGTTGGAGCATCAACGAGAGCACTTTGGCCGAATAAATACCTGTGACGAGATC 2788
Db 14285 CTAAGTTGGAGCATCAACGAGAGCACTTTGGCCGAATAAATACCTGTGACGAGATC 14226
QY 2789 ACTTCGAGAAATAAATAATCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2848
Db 14225 ACTTCGAGAAATAAATAATCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14166
QY 2849 TTTGGCGAAATGAGACGCTGTGATGCGCACTACCCATTTTCACAACCTCTTATCTTCTCT 2908
Db 14165 TTTGGCGAAATGAGACGCTGTGATGCGCACTACCCGAAAGTATGTCAAAAAGAGGTGTGCTA 14106
QY 2909 TACAAGTCTGTTGGCTTCACTGCTGCTTTCAGCTCTTATCTTATCAACGCTGAATAAGT 2968
Db 14105 TGAA--GCAGCGTATACAGTGACAGTGTGACGAGCAGCTATCAGTTGTCTCAAGGCAT 14049
QY 2969 TTCTGTAAATTTCTACTGTATCGACCTGACAGCTGCTGTGATTAAGGGAGCCTGACATTT 3028
Db 14048 ATATGATGTCATATCTCCGGTCTGCTGATGACACACCATGAGATGAAGCCGCTGCTCT 13989
QY 3029 ATATTTCCCGAAGCATCAGTTTAATGGCGTTTTCATGTCATTTTCGGGTGGCTGAGAT 3088
Db 13988 GCGTGC--GAACGCTGGAAGCGGAAATCAGGAAGGATGGCTGAGGTGCGCCGGTT 13932
QY 3089 CAGCACTCTTCTCCCGATAACGAGACCGGACACTGCGCATATCGGTGTCATCATGTC 3148
Db 13931 TATTGAATGAACGCTCTTTTCTGCTGAGAGACAGG-----ACTGGTGAATGCTAGT 13878
QY 3149 GCCAGCTTTTCACTCCCGATGATGACACCGGGTAAAGTTTCAAGGAGACTTTATCTGACA 3208
Db 13877 TTAAGTTTACACCTATAAAGAGAGAGCGGTTATCTGCTGTTTGGATGTACAGAGTG 13818
QY 3209 GCAGAGTGTGATGGCCAGGGGATCACCATCGCTGCGCCGGCGGTGTCAATAATATCATC 3268
Db 13817 ATATTTATGACAGCGCCGGGCGACGATGGTGTATCCCTTGGCCAGTGCACGCTGCTGT 13758
QY 3269 TCTGTACATCCCAACACAGAGATACGCTCTCTCTTTTATAGGTAAACCTTAAACT 3328
Db 13757 CAGATAAAGTCTCCCGTGAACCTTTACCCCGTGTGATATCGGGGATGAAGAGCTGGCGCA 13698
QY 3329 GCATTTTCAAC-----AGTCCCTGTTCTGCTCAGCAAAAGAGCGGTTTCATTTCAATAAAC 3382

Db 13697 TGAAGACCGATATGCGCAGTGTCCGGTCTCCGTTATCGGGAGAGTGGCTGATC 13638
QY 3383 CGGGCAGCTCAGCCATCCCTTCTGATTTTCGCTTTCCAGGTTT---GGCAGCGAGA 3439
Db 13637 TCAGCCACCGGAAATGACATCAAAACGCCATTAACCTGATGTTCTGGGGAATATAAA 13578
QY 3440 CGAGGGCTTCATCTGCTG---TTGTGCTTACAGACCGGAGATATTGACATCATAT 3496
Db 13577 TGTGAGCTCCCTTATACACAGCAGTCTCGAGTGTGATACAGTAGAAAATTACAGAACT 13518
QY 3497 ATGCTTTGACCACTGATAGCTGCTGCTGCTCAACTGTCACTGTAATACGCTGCTCATAG 3556
Db 13517 TTATCAGTTTAGTATAGAGCTGAAATCCAGATGAAGCCGAAACGACTTGTGAAGA 13458
QY 3557 CACACCTCTTTTGAACATCTTCTGTTCTTGTAGTGCAGATGATTTTCAAGTATGACACT 3616
Db 13457 GAAAGTATTAAGAGTTTGTGAATTTGTTCTTGTGATGACAGATGATTTTTCAGGACTATGACACT 13398
QY 3617 AGCGTATCAATAGTAGATGTTTATTTTGTACACAAAAGAGGCTCGCACCTCT 3676
Db 13397 AGCGTATCAATAGTAGATGTTTATTTTGTACACAAAAGAGGCTCGCACCTCT 13338
QY 3677 TTTTCTTATTTCTTTTATGATTAATACGGCATTTAGGCAATAGCGAGTAGCTGGAT 3736
Db 13337 TTTTCTTATTTCTTTTATGATTAATACGGCATTTAGGCAATAGCGAGTAGCTGGAT 13278
QY 3737 ACAGAGTTCGTTTGAAGAAACATTTGGAAGCTGTCGGTGCAGTAAGTTGGCAGCAT 3796
Db 13277 ACAGAGTTCGTTTGAAGAAACATTTGGAAGCTGTCGGTGCAGTAAGTTGGCAGCAT 13218
QY 3797 CACCCGAGAAACATTTTGAAGGCTGTCGGTGCAGTACAGGTCACTAATACCATCTAAGTA 3856
Db 13217 CACCCGAGAAACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACTAATACCATCTAAGTA 13158
QY 3857 GTTGATTCATAGTCACTGGATATGTTGTTTACAGTATTATGATGCTGTTTTTTATG 3916
Db 13157 GTTGATTCATAGTCACTGGATATGTTGTTTACAGTATTATGATGCTGTTTTTTATG 13098
QY 3917 CAAATCTAATTTAATATATGATTTATATCAATTTTACGTTTCTCGTTACGCTTTTTT 3976
Db 13097 CAAATCTAATTTAATATATGATTTATATCAATTTTACGTTTCTCGTTACGCTTTTTT 13038
QY 3977 GTACAAAGTTGGC 3989
Db 13037 GTACAACTTGTCT 13025

RESULT 15

ABQ82141/c

ID ABQ82141 standard; DNA; 17476 BP.

XX ABQ82141;

AC ABQ82141;

DT 11-DEC-2002 (first entry)

XX

DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX

KW Chimeric nucleic acid construct; recombinational cloning; silencing;

KW recombination site; double stranded RNA; plant; ds.

XX

OS Synthetic.

XX

PN WO200259294-A1.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-AU0000073.

XX

PR 26-JAN-2001; 2001US-0264067P.

XX

PR 29-NOV-2001; 2001US-0333743P.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.


```
XX PI Wesley S, Waterhouse P, Helliwell C;
XX DR WPI; 2002-682669/73.
XX PT New vectors comprising operably linked DNA fragments having an origin of
XX PT replication, a selectable marker and a chimeric DNA construct, useful for
XX PT silencing target nucleic acids and for producing large amounts of double-
XX PT stranded RNA.
XX PS Claim 15; Page 74-83; 104pp; English.
XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
XX CC selectable marker region capable of being expressed in the recipient cell
XX CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
XX CC region capable of being recognized by RNA polymerases of a eukaryotic
XX CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
XX CC fourth recombination sites; (iii) 3' transcription terminating and
XX CC polyadenylation region functional in the eukaryotic cell. The first and
XX CC fourth recombination sites, or the second and third recombination sites
XX CC are capable of reacting with a same recombination site, and preferably
XX CC are identical. The first and second recombination sites, or the third and
XX CC fourth recombination sites, do not recombine with each other or with a
XX CC same recombination site. The vector is useful for producing large amounts
XX CC of double-stranded RNA which can be used for silencing target nucleic
XX CC acid sequences. The vectors can also be used to convert a DNA fragment
XX CC into an inverted repeat structure. Plants transformed with a vector from
XX CC the present invention can be used in a conventional breeding scheme to
XX CC produce more plants with the same characteristics or to introduce a
XX CC chimeric gene for reduction of the phenotypic expression of nucleic
XX CC acids. The present sequence represents an acceptor vector nucleotide
XX CC sequence from the present invention
XX SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 22.4%; Score 1089.4; DB 6; Length 17476;
Best Local Similarity 59.4%; Pred. No. 1.2e-147;
Matches 2314; Conservative 0; Mismatches 1336; Indels 243; Gaps 18;

QY 122 GCCAACTTTGTACAAAAGAGCTGAACGAGAAACGCTAAATATGATATAAATATCAATATATT 181
DB 16699 GACAAAGTTTGTACAAAAGAGCTGAACGAGAAACGCTAAATATGATATAAATATCAATATATT 16640

QY 182 AAATTAGATTTTGCATATAAAGAGCTGACATACATTAATCTGTAACACACATATCCAGTC 241
DB 16639 AAATTAGATTTTGCATATAAAGAGCTGACATACATTAATCTGTAACACACATATCCAGTC 16580

QY 242 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAGAGCTTCCAAA 301
DB 16579 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAGAGCTTCCAAA 16520

QY 302 TGTTCCTGGGTGATGCTGCCAACTTAGTCGACGAGAGCTTCCAAATGTTCTCTCAA 361
DB 16519 TGTTCCTGGGTGATGCTGCCAACTTAGTCGACGAGAGCTTCCAAATGTTCTCTCAA 16460

QY 362 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATCGCTATTAAATCATATAAA 421
DB 16459 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATCGCTATTAAATCATATAAA 16400

QY 422 AGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAATAAATAAATCATCTACCT 481
DB 16399 AGAAATAGAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAATAAATAAATCATCTACCT 16340

QY 482 ATTATATAGCTAGTGTGATAGTCTGAAATCATCTGATCAAGAAACAATTTCAACAC 541
DB 16339 ATTATATAGCTAGTGTGATAGTCTGAAATCATCTGATCAAGAAACAATTTCAACAC 16280

QY 542 TCTTATACTTTTCTCTTACAGTCGTTTCGCTTTCATCTGATTTTCAGCTCTTATCTTA 601
DB 16279 AAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGAGCTAT 16223

QY 602 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCGAGACTGGCTGTGTATA 661
DB 16222 CAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAAGCACAAACCATGAGA 16163

QY 662 AGGAGAGCTGACATTTATATTTCCCGCAACATCAGGTTAATGGCGTTTTTGTATGTCTATT 721
DB 16162 ATGAAGCCCGTCTGCTCGTGC---GAAAGCTGGAAGCGGAAATCAGNAGGATGG 16106

QY 722 TCGCGGTGGTGTAGATCAGGCACCTTTCTTCCCGATAAACGAGAGCCGACACATGGCCATA 781
DB 16105 CTGAGGTGCGCCCGTTTTATTGAATGAACGCTCTTTTGTGTGACGAGAACAGGG----- 16052

QY 782 TCGGTGTGTCATCATCGCCAGCTTTTCATCCCGATATGACCCCGGTAAAGTTACGG 841
DB 16051 ACTGGTGAATGCAAGTTTAAGTTTACACCTATATAAAGAGAGAGCCGTTATCGTCTGTTT 15992

QY 842 GAGACTTTTATCTGACAGCAGACGCTGCACTGGCCAGGCGGATCACCCTCGCCCGGGC 901
DB 15991 GTGGATGTACAGAGTGATATTATTGACAGCCCGGCGAGCGATGGTGATCCCCCTGGCC 15932

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DB 15931 AGTCACGCTCTGCTGTGATGATAAAGTCTCCCGTGAACCTTTACCCGGTGGTGACATACGG 15872

QY 962 GTGTAAACCTTAAACTGCTATTTCAAC-----AGTCCCTGTCTCTCGTCAGCAAAAGAGCC 1015
DB 15871 GATGAAGCTGGCGCATGATGACACACCGATATGCGCAGTGTGCGGTCTCGTTATCGGG 15812

QY 1016 GTTCATTTCAATAAACCGGCGAGCCTCAGCCATCCCTTCCTGATTTTCCGCTTTTCAGAG 1075
DB 15811 GAAGAAGTGGTGATCTCAGCCACCGGAAATGACATCAAAAACGCAATTAACCTGATG 15752

QY 1076 TTC---GGCAGCAGACGAGCGGCTTCTATCTGATGTTGTGCTTACCAGACCGGAGAT 1132
DB 15751 TTCTGGGGAATATAAATGTGAGGCTCCCTTATACACAG-----CCAGTCTGCGAGT 15701

QY 1133 ATTGACATCATATATGCTTGCAGCAACTGATAGCTGCTCGCTGCTCAACTGTCACTGTATA 1192
DB 15700 CGATACAGTAGAATTAACAGAACTTTTACAGTTTAGTAGATATAGAGGCTGAAATCC 15641

QY 1193 CGCTGCTTATAGCAGACCTCTTTTTCATATCTTGGGTTAGTG-----CCGATCAAGTCT 1248
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DB 15580 TCATTTTGGCCAAAGTTGGCCAGGCTTCCCGATCAACAGGACACACAGGATTTAT 15521

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DB 15520 TTATTTGCGAAGTATCTCCGTCACAGTATTATTTCGCGCAAAAGTGGTGGGTGA 15461

QY 1369 TGCTGCCAACTTAGTCGATACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGA 1428
DB 15460 TGCTGCCAACTTAGTCGATACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGA 15401

QY 1429 CTGGATATGTTGTGTTTACAGTATTATGATAGTCTGTTTATGCAAAATCTAATTTAA 1488
DB 15400 CTGGATATGTTGTGTTTACAGTATTATGATAGTCTGTTTATGCAAAATCTAATTTAA 15341

QY 1489 TATATGATATTTATATCATTTTACGTTTCTCGTTACGTTCTTGTGACAAAGTTGGCAT 1548
DB 15340 TATATGATATTTATATCATTTTACGTTTCTCGTTACGTTCTTGTGACAAAGTTGGCT-- 15283

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DB 15282 --TAGAGGATCAAGCTTATCGATTT----- 15259

QY 1609 AATCATTTTGGCATCCAGCTCGAGGATCTCGGAGAAATTCGGTACCCCGCTGGTAAG 1668
DB 15258 -----CGAACCCAGCTTCCCAA- 15242

QY 1669 GAAATATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1728
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15241 -CTGTAATCAATCCAAATGTAAGATCAATGATACACAAATGACATGATCTATCAATGTTAC 15183
1729 GATTATAATAATAGTGTGTTATTAATGTTGAAAAAATAATTTATAAATATATGTTTACA 1788
15182 CTGTGTTATTCATGTTGACATAATTCATTTAATTAATAGTCAATCCATTTAGAAGTTAAT 15123
1789 TAAACAACATAGTAATGTAAGAAAAATATGACAAGTGATGCTGTAAGACGAAGAATAAAA 1848
15122 AAACTACAGATATTTTAGAATTTAATAGAAATGTTGATGGAATTAATTAATTAATATAA 15063
1849 GTTGAGAGTAAGTATATTTTAAATGAATTTGATCGAACAATGTAAGATGATATACATAG 1908
15062 AATGATAGATCTTGGCTTTTGTTATATTTAGCATTTAGATTTAGTTTGTGTACATTAGATTA 15003
1909 CATTAATATTTGTTTAAATCATATAGTAATCTAGCTGGTTTGATGAAATTAATAATACAA 1968
15002 CTGTTTCTTATTTAGTTTGATATATTTTGTGTACTTTAGCTTGTATTTAATAATTTTGTAT 14943
1969 TGATAAAATACATATAGTAAAAAATAAGATAAATAAATTAATAATATTTTATATGATT 2028
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2029 AATAGTTTATTAATAATTAATAATCTATATACCATTTACTAATAATTTTATGTTTAAAGTTA 2088
14882 TATTTAGTAATGGTATAGATATTTAATTTATATATAATAAATCTATTAATCATAAAAAATAT 14823
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14642 TACATCATCTTGTATATTTTATCATTTTATCATTTACTATGTTGTTTATGTAACAATATATTA 14583
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14522 TTAACATATTTTATACATAA----- 14504
2449 AATCGATAAGCTTGGATCTCTAGAGAGCTGCAGCTGGATGGCAAAATATGATTTTATTT 2508
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2509 TGACTGATAGTGAGCTGTTGCTGTGCAAAATGATAGCAATGCTTTCTTATAATGCCA 2568
14475 CCAAGCTGGGTACCGAAT-----TCCTCGAGACC 14446
2569 ACTTGTACAGAAAGCTGACGAGAAACGTAAATGATATAAATATCAATATATTAAT 2628
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2749 GACGCACCTTTGGCGGAATAAATACCTGTGACGGAAGATCACTTCGCGAAGATAAATAAT 2808

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2809 CTGTGTTCTCCTGTTGATATACGGGAAGCCCTTGGGCCAACTTTTGGCGAAATAATGAGAGTT 2868
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2869 GATCGGCACATACCCATTTTCAACTCTTATATCTTTCTTACAAAGTCGTTGCGCTTCAT 2928
14145 GATCGGCACATACCCGAAGTATGTCAAAAAGAGGTGCTGTATGAA---GACGCGTATTACA 14089
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13797 CGACGGATGTTGATCCCTCGCCAGTGCAGCTGCTGTGTCAGATAAGTCTCCCGTGAA 13738
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13617 ATCAAAAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTGTCAGCTCCCTTATACAC 13558
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QY 3877 TATGTTGTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATAT 3936
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Db 13137 TATGTTGTTTACAGTATTATGAGTCTGTTTTTATGCAAAATCTAATTTAATATAT 13078
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QY 3937 TGATATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTGTACAAAAGTTGTC 3989
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Db 13077 TGATATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTGTACAAAAGTTGTC 13025
|||

Search completed: May 7, 2004, 18:28:01
Job time : 1169.23 secs


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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid DNA designated as pUD884
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1869
;   OTHER INFORMATION: /note= "Coding region of a
;   OTHER INFORMATION: truncated bt2 (cryIab) gene, also designated as the bt884 ge
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1877..2110
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA gene 7."
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2480..3005
;   OTHER INFORMATION: /note= "35S promoter sequence
;   OTHER INFORMATION: derived from Cauliflower mosaic virus."
;   FEATURE:
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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;   NAME/KEY: misc_feature
;   LOCATION: 3666..4491
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA octopine synthase gene."
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 5684..6541
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;   OTHER INFORMATION: Patent No. 5952547
;   OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7155..7639
;   OTHER INFORMATION: /note= "TR1' and TR2' promoter
;   OTHER INFORMATION: derived from Agrobacterium T-DNA."
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; US-08-232-016-22
;
; Query Match 15.0%; Score 729.6; DB 2; Length 7639;
; Best Local Similarity 98.8%; Pred. No. 6e-140;
; Matches 735; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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; QY 4072 GATCATGCTAGCTAGAGTCTCTTATGAGATATGAGACGCGCTATGATCGCAT 4131
; DB 3764 GACCCATCGCGCTAGAGTCTCTTATGAGATATGAGACGCGCTATGATCGCAT 3823
;
; QY 4132 GATATTTCTTCAATTCCTGTTGTCAGCTGTGTAATAAATCTGAGCATGTAGCTCAGA 4191
; DB 3824 GATATTTCTTCAATTCCTGTTGTCAGCTGTGTAATAAATCTGAGCATGTAGCTCAGA 3883
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; QY 4192 TCCTTACCGCGGTTTCGGTTCATTCATGATGATATATCACCCTTATCTCGTATTTT 4251
; DB 3884 TCCTTACCGCGGTTTCGGTTCATTCATGATGATATATCACCCTTATCTCGTATTTT 3943
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; QY 4252 ATGATATATATCTCGGTTCAATTTACTGATGTACCTACTTACTTATATGTACATATT 4311
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; QY 4312 AAAATGAAACAAATATATTGCTGAATAGGTTTATAGCGCATCTATCATAGAGCGCA 4371
; DB 4004 AAAATGAAACAAATATATTGCTGAATAGGTTTATAGCGCATCTATCATAGAGCGCA 4063
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; QY 4372 CAATAACAACAATTCGGTTTATTATTATTAACAATCCAAATTTAAAAAGCGGCAAGACC 4431
; DB 4064 CAATAACAACAATTCGGTTTATTATTATTAACAATCCAAATTTAAAAAGCGGCAAGACC 4123

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; QY 4492 TAGTATCTACGACACACACCGGCGGAACTAATAAGCTTCACTGAAGGAACTCCGGTTC 4551
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; QY 4552 CCGCGCGCGCGATGGGTGAGATTCCTTGAAGTTGAGTATTGGCGCTCCGCTCTACCGA 4611
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; QY 4612 AAGTTACGGGCACCATTTCAACCGCGTCCAGCAGCGCGCGGTAACCGACTTGTGCCCC 4671
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; QY 4672 CGAGAAATTATGACGCAATTTTTTGTGTATGTGGGCCCCCAAAATGAAGTGAGGTCAAACC 4731
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; DB 4424 TTGACAGTGACGCAAAATCGTTGGGCGGTCGAGCGGGAATTTTGGCACAACATGTCGAG 4483
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; QY 4792 GCTCAGCAGGACCTCGAGGCATGC 4815
; DB 4484 GCTCAGCAGGACCTCGAGGCATGC 4507
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; RESULT 3
; US-08-064-121-1
; Sequence 1. Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Peury, Sharon E
; REGISTRATION NUMBER: 35,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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Qy	4573	GAATCCTTGAAGTTGAGTATTGGCCGTCCTACCGGAAAGTTACGGGCACCAATTCAC	4633
Db	2753	GAATCCTTGAAGTTGAGTATTGGCCGTCCTACCGGAAAGTTACGGGCACCAATTCAC	2812
Qy	4633	CCGGTCAGCACGCGCGCGGTAACCGACTTGTGCCCCGAGAAATATGACGATTTTT	4692
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RESULT 4			
US-08-478-015-1			
; Sequence 1, Application US/08478015			
; Patent No. 5712135			
; GENERAL INFORMATION:			
; APPLICANT: D'HALLUIN, Kathleen			
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING			
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Burns, Doane, Swecker & Mathis			
; STREET: P.O. Box 1404			
; CITY: Alexandria			
; STATE: Virginia			
; COUNTRY: United States			
; ZIP: 22313-1404			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/478,015			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: EP 90403332.1			
; FILING DATE: 23-NOV-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: EP 91401888.2			
; FILING DATE: 08-JUL-1991			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/064,121			
; FILING DATE: 23-JUN-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: McGowan, Malcolm K.			
; REGISTRATION NUMBER: 39,300			
; REFERENCE/DOCKET NUMBER: 010830-088			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (703) 836-6620			
; TELEFAX: (703) 836-2021			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 5399 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: circular			
; MOLECULE TYPE: DNA (genomic)			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; ORIGINAL SOURCE:			
; ORGANISM: plasmid pDE108			
; FEATURE:			
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OTHER INFORMATION: /label= pUC18
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FEATURE:
NAME/KEY: -
LOCATION: 2101..3160
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OTHER INFORMATION: /label= pUC18
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US-08-478-015-1
Query Match 14.6%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 66-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 2333 TGTGACGTTGTAAATAAAGCTGAGATGTTAGCTCAGATCCTTACCGCGGTTTCGGTT 2392
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; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
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; OTHER INFORMATION: /label= pUC18
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; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
; OTHER INFORMATION: Cauliflower mosaic virus isolate CabBB-JI"
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Wed May 12 08:20:59 2004

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; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine"
; OTHER INFORMATION: phosphotransferase gene"
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; NAME/KEY: -
; LOCATION: 2101...3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; NAME/KEY: -
; LOCATION: 3161...5399
; OTHER INFORMATION: /label= pUC18
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US-08-475-975-1

Query Match 14.6%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 2273 CTTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTGCTTTCAATTCTGT 2332
QY 4153 TGTGCAAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212
DB 2333 TGTGCAAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 2392
QY 4213 CATTCATGAATATATACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCA 4272
DB 2393 CATTCATGAATATATACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCA 2452
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QY 4333 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATAAACAATTCGGTTT 4392
DB 2513 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATAAACAATTCGGTTT 2572
QY 4393 TATTATCAATCCAAATTTTAAATAAGGCGCAGAACCGGTCAACCTAAAGACTGAT 4452
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RESULT 6
US-08-084-889-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLSCULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
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; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
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; NAME/KEY: -
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; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
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; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
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US-09-084-889-1
Query Match 14.6%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 68-136; Indels 0; Gaps 0;
Matches 711; Conservative 0; Mismatches 2;

QY 4093 CCTGCTTTAATCAGATATCGAGAGCCCTATGATCGCATGATATTTGCTTTCAATTCGT 4152
DB |||||
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RESULT 7
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; Sequence 2, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
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; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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; ORGANISM: plasmid pVEL14 (replicable in E.coli)
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; OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"
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US-08-351-413-2

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Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 8
US-09-025-583-2
; Sequence 2, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
FEATURE:
NAME/KEY: -
LOCATION: 1..396
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
FEATURE:
NAME/KEY: -
LOCATION: complement (397..751)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: complement (752..1024)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -
LOCATION: 1608..2440
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-J1"

FEATURE:
NAME/KEY: 2441..3256
LOCATION: 2441..3256 /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
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NAME/KEY: 3257..4315
LOCATION: 3257..4315 /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: 4316..6555
LOCATION: 4316..6555 /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2

Query Match 14.6%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 6.4e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4093 CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT 4152
Db 3429 CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT 3488
QY 4153 TGTGCAAGTTGTAATAAAGCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212
Db 3489 TGTGCAAGTTGTAATAAAGCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3548
QY 4213 CATTCCTAATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA 4272
Db 3549 CATTCCTAATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA 3608
QY 4273 ATTTACTGATGTACCGTACTACTATATGATGAGCGCCCAATTAACAAACAAATTGGGTT 4332
Db 3609 ATTTACTGATGTACCGTACTACTATATGATGAGCGCCCAATTAACAAACAAATTGGT 3668
QY 4333 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATTAACAAACAAATTGGGTT 4392
Db 3669 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATTAACAAACAAATTGGGTT 3728
QY 4393 TATTATTACAAATCCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 4452
Db 3729 TATTATTACAAATCCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 3788
QY 4453 TACATAAATCTTATTCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 4512
Db 3789 TACATAAATCTTATTCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 3848
QY 4513 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGTTCCCGCGCGCGCATGGGTGA 4572
Db 3849 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGTTCCCGCGCGCGCATGGGTGA 3908
QY 4573 GATTCTCTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 4632
Db 3909 GATTCTCTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 3968
QY 4633 CCGGTCCAGCACGCGCGCGGTAAACCGACTTGTCTGCCGAGAAATTATGCAGCATTTT 4692
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QY 4753 TGGCGGGTCCAGGGCGGAATTTTCCGACAAACATGTGAGGCTCAGCAGGACCT 4805
Db 4089 TGGCGGGTCCAGGGCGGAATTTTCCGACAAACATGTGAGGCTCAGCAGGACCT 4141

RESULT 9

US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 14.6%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 8e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4093 CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT 4152
Db 9830 CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT 9889
QY 4153 TGTGCAAGTTGTAATAAAGCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212
Db 9890 TGTGCAAGTTGTAATAAAGCTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT 9949
QY 4213 CATTCCTAATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA 4272
Db 9950 CATTCCTAATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA 10009
QY 4273 ATTTACTGATGTACCGTACTACTATATGATGAGCGCCCAATTAACAAACAAATTGGT 4332
Db 10010 ATTTACTGATGTACCGTACTACTATATGATGAGCGCCCAATTAACAAACAAATTGGT 10069
QY 4333 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATTAACAAACAAATTGGGTT 4392
Db 10070 GCTGAATAGTTTATAGCGACATCTATGATAGCGCCCAATTAACAAACAAATTGGGTT 10129
QY 4393 TATTATTACAAATCCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 4452
Db 10130 TATTATTACAAATCCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 10189
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Db 10190 TACATAAATCTTATTCAAATTTTAAATAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 10249
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Db 10250 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGTTCCCGCGCGCGCATGGGTGA 10309
QY 4573 GATTCTCTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 4632
Db 10310 GATTCTCTGAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 10369
QY 4633 CCGGTCCAGCACGCGCGCGGTAAACCGACTTGTCTGCCGAGAAATTATGCAGCATTTT 4692
Db 10370 CCGGTCCAGCACGCGCGCGGTAAACCGACTTGTCTGCCGAGAAATTATGCAGCATTTT 10429
QY 4693 TTGTTGATGTGGGCCCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT 4752
Db 10430 TTGTTGATGTGGGCCCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT 10489
QY 4753 TGGCGGGTCCAGGGCGGAATTTTCCGACAAACATGTGAGGCTCAGCAGGACCT 4805
Db 10490 TGGCGGGTCCAGGGCGGAATTTTCCGACAAACATGTGAGGCTCAGCAGGACCT 10542

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Db 7230 CATTCATATGATATATACCGGTTACTATCGTATTTTATGAAATATATTCCTCGTTCA 7289
QY 4273 ATTACTGATGATGACCTACTACTATATGATACATATTAATGAAATGAAACATATATGT 4332
Db 7290 ATTACTGATGATGACCTACTACTATATGATACATATTAATGAAATGAAACATATATGT 7349
QY 4333 GGTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATAACAAACAATTCGGTTT 4392
Db 7350 GGTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATAACAAACAATTCGGTTT 7409
QY 4393 TATTATCAAAATCCAAATTTTAAAAAGCGGAGAACCCGGTCAAACTTAAAGACTGAT 4452
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QY 4513 CGGCGAACCTAAATGACCTTCACTGAAGGGAACCTCCGGTTCCTCCGCGCGCGCATGGTGA 4572
Db 7530 CGGCGAACCTAAATGACCTTCACTGAAGGGAACCTCCGGTTCCTCCGCGCGCGCATGGTGA 7589
QY 4573 GATTCCTGAAAGTTGAGTATGCGCTCGCTCTACCGAAAGTTACGGGCAACATTCAC 4632
Db 7590 GATTCCTGAAAGTTGAGTATGCGCTCGCTCTACCGAAAGTTACGGGCAACATTCAC 7649
QY 4633 CCGGTCACGACGCGCGCGGTAACCG 4660
Db 7650 CCGGTCACGACGCGCGCGGTAACAG 7677

RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 11.6%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.7e-106;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4093 CTTGCTTTTAAAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 4152
Db 14394 CTTGCTTTTAAAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 14335
QY 4153 TGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212
Db 14334 TGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 14275
QY 4213 CATTCATATGATATATACCGGTTACTATCGTATTTTATGAAATATATTCCTCGTTCA 4272
Db 14274 CATTCATATGATATATACCGGTTACTATCGTATTTTATGAAATATATTCCTCGTTCA 14215
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QY 4333 GGTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCCAATAACAAACAATTCGGTTT 4392
Db 14154 GGTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCCAATAACAAACAATTCGGTTT 14095
QY 4393 TATTATCAAAATCCAAATTTTAAAAAGCGGAGAACCCGGTCAAACTTAAAGACTGAT 4452
Db 14094 TATTATCAAAATCCAAATTTTAAAAAGCGGAGAACCCGGTCAAACTTAAAGACTGAT 14035
QY 4453 TACATAAATCTTATTCAAATTTTAAAAAGCGGAGAACCCGGTCAAACTTAAAGACTGAT 4512
Db 14034 TACATAAATCTTATTCAAATTTTAAAAAGCGGAGAACCCGGTCAAACTTAAAGACTGAT 13975
QY 4513 CGGCGAACCTAAATGACCTTCACTGAAGGGAACCTCCGGTTCCTCCGCGCGCGCATGGTGA 4572
Db 13974 CGGCGAACCTAAATGACCTTCACTGAAGGGAACCTCCGGTTCCTCCGCGCGCGCATGGTGA 13915
QY 4573 GATTCCTGAAAGTTGAGTATGCGCTCGCTCTACCGAAAGTTACGGGCAACATTCAC 4632
Db 13914 GATTCCTGAAAGTTGAGTATGCGCTCGCTCTACCGAAAGTTACGGGCAACATTCAC 13855
QY 4633 CCGGTCACGACGCGCGGTAACCG 4660
Db 13854 CCGGTCACGACGCGCGGTAACAG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION NUMBER: PCT/BE93/00051
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,614
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/BE93/00051
/ FILING DATE: 02-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: VANMA10.001APC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 420 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: both
/ MOLECULE TYPE: Genomic DNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
/ NAME/KEY: Coding Sequence
/ LOCATION: 1..378
/ OTHER INFORMATION:
/
/ US-08-379-614-2

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Best Local Similarity 99.7%; Pred. No. 1.1e-57;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 654 TGTGTATAAGGGAGCCTTGACATTTATATTCCTCCAGAACATCAGGTTAATGGCGTTTGA 713
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QY 714 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACAC 773
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QY 834 GTTCACGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTC 893
Db 223 GTTCACGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTC 164
QY 894 GCCCGGGCTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACCGCTCTCTC 953
Db 163 GCCCGGGCTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACCGCTCTCTC 104
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RESULT 14

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US-09-225-152A-2/c
/ Sequence 3, Application US/09225152A
/ Patent No. 6180407
/ GENERAL INFORMATION:
/ APPLICANT: Bernard, Philippe
/ APPLICANT: Gabant, Philippe
/ TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
/ FILE REFERENCE: VANMA10.001CPI
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/ CURRENT APPLICATION NUMBER: US/09/225,152A
/ CURRENT FILING DATE: 1998-01-04
/ PRIOR APPLICATION NUMBER: 08/379614
/ PRIOR FILING DATE: 1995-07-20
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 420
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(378)
/ OTHER INFORMATION: ccdB gene of pKIL 18.
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/ US-09-225-152A-2

Query Match          6.7%; Score 325.4; DB 3; Length 420;
Best Local Similarity 99.7%; Pred. No. 1.1e-57;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 654 TGTGTATAAGGGAGCCTTGACATTTATATTCCTCCAGAACATCAGGTTAATGGCGTTTGA 713
Db 403 TGTGTATAAGGGAGCCTTGACATTTATATTCCTCCAGAACATCAGGTTAATGGCGTTTGA 344
QY 714 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACAC 773
Db 343 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACAC 284
QY 774 TGGCCATATCGGTGGTCATATGCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 833
Db 283 TGGCCATATCGGTGGTCATATGCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 224
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Db 223 GTTCACGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTC 164
QY 894 GCCCGGGCTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACCGCTCTCTC 953
Db 163 GCCCGGGCTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACCGCTCTCTC 104
QY 954 TTTTATAGGTGTAACCTTAACTGCA 980
Db 103 TTTTATAGGTGTAACCTTAACTGCA 77

RESULT 15
US-08-379-614-3/c
/ Sequence 3, Application US/08379614
/ Patent No. 5910438
/ GENERAL INFORMATION:
/ APPLICANT: Bernard, Philippe
/ APPLICANT: Gabant, Philippe
/ TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/379,614
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/BE93/00051
/ FILING DATE: 02-AUG-1993
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ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKil 19
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...378
OTHER INFORMATION:
US-08-379-614-3

Query Match 6.6%; Score 323.2; DB 2; Length 416;
Best Local Similarity 99.1%; Pred. No. 3e-57; Mismatches 0; Indels 0; Gaps 0;
Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db |||||
QY 715 GTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACACT 774
Db |||||
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QY 102 TTTATAGGTGTAACCTTAAACTGCATT 75
Db |||||

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Job time : 213.004 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1296.69 Seconds

(without alignments)
16988.923 Million cell updates/sec

Title: US-10-055-001B-23_COPY_13000_17862

Perfect score: 4863

Sequence: 1 ttctattggagagacagc.....ataggtcacataatcgc 4863

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	4863	100.0	17862	15	US-10-055-001A-23	Sequence 23, Appl
2	4112.4	84.6	17476	15	US-10-055-001A-24	Sequence 24, Appl
3	4112.4	84.6	17476	15	US-10-385-546-7	Sequence 7, Appl
4	4077.2	83.8	17691	15	US-10-055-001A-26	Sequence 26, Appl
5	4042	83.1	17458	15	US-10-055-001A-25	Sequence 25, Appl
6	3985.4	82.0	18621	15	US-10-055-001A-13	Sequence 13, Appl
7	1645	33.8	17862	15	US-10-055-001A-23	Sequence 23, Appl
8	1207.4	24.8	4470	15	US-10-151-690-21	Sequence 21, Appl
9	1207.4	24.8	4892	16	US-10-357-268-1	Sequence 1, Appl
10	1207.4	24.8	5584	15	US-10-151-690-61	Sequence 61, Appl
11	1201	24.7	4428	15	US-10-151-690-62	Sequence 62, Appl
12	1194.6	24.6	4627	15	US-10-151-690-63	Sequence 63, Appl
13	1194.6	24.6	4627	15	US-10-151-690-64	Sequence 64, Appl
14	1174.2	24.1	17691	15	US-10-055-001A-26	Sequence 26, Appl

c 15	1089.4	22.4	17476	15	US-10-055-001A-24	Sequence 24, Appl
c 16	1089.4	22.4	17476	15	US-10-385-546-7	Sequence 7, Appl
c 17	1079.4	22.2	17458	15	US-10-055-001A-25	Sequence 25, Appl
c 18	842	17.3	18691	15	US-10-055-001A-13	Sequence 13, Appl
c 19	780	16.0	786	15	US-10-385-521-9	Sequence 9, Appl
c 20	737.8	15.2	2116	12	US-10-644-335-3	Sequence 3, Appl
c 21	737.8	15.2	2873	15	US-10-356-088-55	Sequence 55, Appl
c 22	737.8	15.2	2873	15	US-10-353-454-38	Sequence 38, Appl
c 23	736.2	15.1	3002	15	US-10-353-454-57	Sequence 57, Appl
c 24	735.8	15.1	3034	15	US-10-356-088-48	Sequence 48, Appl
c 25	735.8	15.1	3034	15	US-10-353-454-31	Sequence 31, Appl
c 26	713	14.7	4947	9	US-09-118-276-21	Sequence 21, Appl
c 27	710.2	14.6	7599	15	US-10-027-880-5	Sequence 5, Appl
c 28	703.4	14.5	2867	15	US-10-176-884-9	Sequence 9, Appl
c 29	703.4	14.5	2867	15	US-10-177-478-20	Sequence 20, Appl
c 30	597	12.3	1846	15	US-10-023-208-63	Sequence 63, Appl
c 31	597	12.3	5558	15	US-10-241-596-137	Sequence 137, App
c 32	597	12.3	6464	15	US-10-151-690-20	Sequence 20, Appl
c 33	597	12.3	7278	17	US-10-097-034A-37	Sequence 37, Appl
c 34	597	12.3	9249	16	US-10-389-120-2	Sequence 2, Appl
c 35	597	12.3	10463	16	US-10-389-120-1	Sequence 1, Appl
c 36	597	12.3	12789	13	US-10-686-778-9	Sequence 9, Appl
c 37	593.8	12.2	11180	9	US-09-887-576-581	Sequence 581, App
c 38	505.8	10.4	4470	15	US-10-151-690-21	Sequence 21, Appl
c 39	505.8	10.4	4892	16	US-10-357-268-1	Sequence 1, Appl
c 40	505.8	10.4	5584	15	US-10-151-690-61	Sequence 61, Appl
c 41	499.4	10.3	4428	15	US-10-151-690-62	Sequence 62, Appl
c 42	492.6	10.1	4627	15	US-10-151-690-63	Sequence 63, Appl
c 43	492.6	10.1	4627	15	US-10-151-690-64	Sequence 64, Appl
c 44	478.8	9.8	528	15	US-10-162-214-4	Sequence 4, Appl
c 45	323.4	6.7	2877	13	US-09-861-925-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match	100.0%;	Score 4863;	DB 15;	Length 17862;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4863;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATCGATCTCGGGCCCAAAATAATGATTT	60	
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Db	13060	TATTTTGACTAGTAGTACCTGTTGTTGCAACAAATGATGAGCAATGCTTTTTTATAA	13119	
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Db 17560 GCGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCCCTCCGCTCTACCGAAAGTTACGG 17619
Qy 4621 GCACATTAACCCCGTCCAGCACGCGCGCGGGTAAACGGACTTCGTCGCCCGGAGAAATTA 4680
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Qy 4681 TCAGCATTTTTCGTTGATGTGGGCCCAATGAAGTGCAGGTCAAAACCTTGACAGTG 4740
Db 17680 TCAGCATTTTTCGTTGATGTGGGCCCAATGAAGTGCAGGTCAAAACCTTGACAGTG 17739
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Qy 4801 GACCTGCGAGCATGAAGCTAGCTTACTAGTATGCATATCTATAGTGTCAACCTAAATC 4860
Db 17800 GACCTGCGAGCATGAAGCTAGCTTACTAGTATGCATATCTATAGTGTCAACCTAAATC 17859
Qy 4861 TGC 4863
Db 17860 TGC 17862

RESULT 2
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATES
US-10-055-001A-24

Query Match 84.6%; Score 4112.4; DB 15; Length 17476;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 4446; Conservative 0; Mismatches 6; Indels 290; Gaps 4;
Qy 122 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 181
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Qy 182 AAATTAGATTTTGCATAAAAAAAGAGACTACATTAATCTGTAAACACACATATCCAGTC 241
Db 13085 AAATTAGATTTTGCATAAAAAAAGAGACTACATTAATCTGTAAACACACATATCCAGTC 13144
Qy 242 ACTATGAATCAACTTACTAGTATGTTAGTACCTGTAGCTGCACGACGAGCCTCCCAA 301
Db 13145 ACTATGAATCAACTTACTAGTATGTTAGTACCTGTAGCTGCACGACGAGCCTCCCAA 13204
Qy 302 TGTTCCTCGGGTATGCTGCCAACTTAGTGCAGCAGAGCCTTCCCAATGTCTTCTCAA 361
Db 13205 TGTTCCTCGGGTATGCTGCCAACTTAGTGCAGCAGAGCCTTCCCAATGTCTTCTCAA 13264
Qy 362 ACGAAATCGTGTATCGAGCCTACTCGCTATGTTCCTCAATGCGGTATTAATCATAA 421
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Qy 482 ATTCATATACGCTAGTGTCTAGTCCCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC 541
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Db 15300 AAGCTGAACGAGAAACGTAATAATGATATAAATAATCAATATATTAATTTAGATTTTGCATA 15359
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QY 2702 TAGATGGTATTAAGTGAACCTGTGACGGAAGATCACTTCCGAGAAATAAATAAATCCCTGGTGTCCCTG 2761
Db 15420 TAGATGGTATTAAGTGAACCTGTGACGGAAGATCACTTCCGAGAAATAAATAAATCCCTGGTGTCCCTG 15479
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Db 15652 CTCCTATACTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGAGACT 15711
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QY 3542 TACGCTGCTTTCATAGCACACCTTTTGTGACATCTTCTGTTCTTGTGATGAGATGATTTT 3601
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Db 16312 CAGGACTATGACACTAGCGTATATGAATAGTGTATGTTTATTTTGTGACACAAAAA 16371
QY 3662 GAGGCTCGACCTCTTTTCTTTTATGATTTAATACGCGATTTGAGGACAATA 3721

Db 16372 GAGGCTCGACCTCTTTCTTTATTTCTTTTATGATTTAAATACGGCAATGAGGACAAATA 16431
Qy 3722 GCGAGTAGGCTGGATACGACGATTCGGTTTGGAGAGAAACATTTGGAAGGCTGTGGTTCGA 3781
Db 16432 GCGAGTAGGCTGGATACGACGATTCGGTTTGGAGAGAAACATTTGGAAGGCTGTGGTTCGA 16491
Qy 3782 CTAAGTTGGCAGCATCACCGGAAGAACATTTGGAGAGGCTGTGGTTCGACATCAGGTCACT 3841
Db 16492 CTAAGTTGGCAGCATCACCGGAAGAACATTTGGAGAGGCTGTGGTTCGACATCAGGTCACT 16551
Qy 3842 AATACATCTAAGTAGTTGATTTCAATGACGATGATGTTGTTTACATGATTAATGT 3901
Db 16552 AATACATCTAAGTAGTTGATTTCAATGACGATGATGTTGTTTACATGATTAATGT 16611
Qy 3902 AGCTGTGTTTTATGCAAAATCTAATTTAATATATTTGATATTTATATATATTTTACGTTTC 3961
Db 16612 AGCTGTGTTTTATGCAAAATCTAATTTAATATATTTGATATTTATATATATTTTACGTTTC 16671
Qy 3962 TCGTTTCAGCTTTTGTACAAAGTTGGCAATTTAAAAAGCAATGCTCATCAATTTGTTG 4021
Db 16672 TCGTTTCAGCTTTTGTACAAAGTTG----- 16697
Qy 4022 CAAGGAACAGGTCACTATCAGTCAMAAATAAAATCATTATTTGGGGCCCGAGATCCATGCT 4081
Db 16698 ----- 16697
Qy 4082 AGCTCTAGAGTCTGCTTTTAATGAGATATCGGAGAGCGCTATGATCGCATGATATTGCT 4141
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Qy 4142 TTCAATCTGTTGTCACAGCTGTGAAAAACCTGAGCATGTGTAGTTCAGATCCTTACCGC 4201
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Db 17115 GACACACGAGCGGCACTTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCCCGCGG 17174
Qy 4562 CGCATGGGTGAGATTCCTTGAAGTTGATATTTGGCCGTCGCTACCGGAAAGTTACGGG 4621
Db 17175 CGCATGGGTGAGATTCCTTGAAGTTGATATTTGGCCGTCGCTACCGGAAAGTTACGGG 17234
Qy 4622 CACCATTTCAACCGGTCGACGACGCGCGGGTTAACGGACTTGTCTGCCCGCGAGATTAT 4681
Db 17235 CACCATTTCAACCGGTCGACGACGCGCGGGTTAACGGACTTGTCTGCCCGCGAGATTAT 17294
Qy 4682 GCACATTTTTCGTTGATGTTGGGCCCCAAATGAAAGTGAGGTTCAAACTTTGACAGTGA 4741
Db 17295 GCACATTTTTCGTTGATGTTGGGCCCCAAATGAAAGTGAGGTTCAAACTTTGACAGTGA 17354
Qy 4742 CGACAAATCGTTGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGG 4801
Db 17355 CGACAAATCGTTGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGG 17414

Qy 4802 ACTGCGAGGCAATGCAAGCTAGCTTACTAGTGATGCATATTTCTATAGTGTCACTAAATCT 4861
Db 17415 ACTGCGAGGCAATGCAAGCTAGCTTACTAGTGATGCATATTTCTATAGTGTCACTAAATCT 17474
Qy 4862 GC 4863
Db 17475 GC 17476
RESULT 3
US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 84.6%; Score 4112.4; DB 15; Length 17476;

Best Local Similarity 93.8%; Pred. No. 0;

Matches 4446; Conservative 0; Mismatches 6; Indels 290; Gaps 4;

Qy 122 GCCAATTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAATAATCAATATATT 181
Db 13025 GACAAAGTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAATAATCAATATATT 13084
Qy 182 AAATTAGATTTTGGCATAAAAAACAGACTACATAATCTGTAAAAACAACTATCCAGTC 241
Db 13085 AAATTAGATTTTGGCATAAAAAACAGACTACATAATCTGTAAAAACAACTATCCAGTC 13144
Qy 242 ACTATGAATCAACTACTTAGATGTTAGTGAACCTGTAGTCGACGAGAGCCCTTCCAA 301
Db 13145 ACTATGAATCAACTACTTAGATGTTAGTGAACCTGTAGTCGACGAGAGCCCTTCCAA 13204
Qy 302 TGTTCCTGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTTCAA 361
Db 13205 TGTTCCTGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTCAA 13264
Qy 362 ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGCTCAATGCCGTATTAATCATATAA 421
Db 13265 ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGCTCAATGCCGTATTAATCATATAA 13324
Qy 422 AGAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGACAAAAATAAAAATCACTACCT 481
Db 13325 AGAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGACAAAAATAAAAATCACTACCT 13384
Qy 482 ATTTCATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCAATCAAGAAACAAATTTCAACAC 541
Db 13385 ATTTCATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCAATCAAGAAACAAATTTCAACAC 13444
Qy 542 TCTTATATCTTTCTTCTTACAGTCGTTCCGGCTTCATCTGGAATTTTCAGCCTCTATCTT 601
Db 13445 TCTTATATCTTTCTTCTTACAGTCGTTCCGGCTTCATCTGGAATTTTCAGCCTCTATCTT 13504
Qy 602 CTAAACGCTATAAAGTTTCTGTAATTTCTCTGTATCGACCTGCGACCTGGCTGTGTATA 661
Db 13505 CTAAACGCTATAAAGTTTCTGTAATTTCTCTGTATCGACCTGCGACCTGGCTGTGTATA 13564

QY	662	AGGAGCCTGACATTTATATCCCCAGAACATCAGGTTAATGCGGTTTTTGATGTCATTT	721
Db	13565	AGGAGCCTGACATTTATATCCCCAGAACATCAGGTTAATGCGGTTTTTGATGTCATTT	13624
QY	722	TCGGGTGGCTGAGATCAGCCACTTTCTCCCGATAAOCGAGACCGGCACACTGGCCATA	781
Db	13625	TCGGGTGGCTGAGATCAGCCACTTTCTCCCGATAAOCGAGACCGGCACACTGGCCATA	13684
QY	782	TCGGTGGTCATCATCGGCCAGCTTTTCATCCCGATATGCACACCGGTAAGTTCAACGG	841
Db	13685	TCGGTGGTCATCATCGGCCAGCTTTTCATCCCGATATGCACACCGGTAAGTTCAACGG	13744
QY	842	GAGACTTTATCTGACAGCAGACGTGCACATGGCCAGGGGATCACCATCCGTCGCCCGGC	901
Db	13745	GNAGCTTTATCTGACAGCAGACGTGCACATGGCCAGGGGATCACCATCCGTCGCCCGGC	13804
QY	902	GGTCAATAATATACCTCTGTGTATCCACAAACAGACGATACGGCTCTCTCTTTATAG	961
Db	13805	GGTCAATAATATACCTCTGTGTATCCACAAACAGACGATACGGCTCTCTCTTTATAG	13864
QY	962	GTGTAACCTTAAACTGTCAATTTACACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTAT	1021
Db	13865	GTGTAACCTTAAACTGTCAATTTACACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTAT	13924
QY	1022	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCGGCTTTCAGCGTTGGC	1081
Db	13925	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCGGCTTTCAGCGTTGGC	13984
QY	1082	AGCAGACAGCGGCTTCAITCTGCATGGTTGTCTTACCAGACCGGAGATATGCATC	1141
Db	13985	AGCAGACAGCGGCTTCAITCTGCATGGTTGTCTTACCAGACCGGAGATATGCATC	14044
QY	1142	ATATATGCCCTTGAGCAACTGATAGCTGTCGCTGTCACTGTCACTGTAAACGCTGCTTC	1201
Db	14045	ATATATGCCCTTGAGCAACTGATAGCTGTCGCTGTCACTGTAAACGCTGCTTC	14104
QY	1202	ATAGCACACCTCTTTTTTGACATACCTTCGGGTAGTGC CGATCAAGCTCTCATTTTCGCCAA	1261
Db	14105	ATAGCACACCTCTTTTTTGACATACCTTCGGGTAGTGC CGATCAAGCTCTCATTTTCGCCAA	14164
QY	1262	AGTTTGGCCCGAGGCTTCCCGGTATCAACAGGAGACACAGATTTATTTCTTCGCAAG	1321
Db	14165	AGTTTGGCCCGAGGCTTCCCGGTATCAACAGGAGACACAGATTTATTTCTTCGCAAG	14224
QY	1322	TGATCTTCCGTCACAGTATTTTATTCGGCCAAAGTCGCGGTGATGCTGCCAACTTA	1381
Db	14225	TGATCTTCCGTCACAGTATTTTATTCGGCCAAAGTCGCGGTGATGCTGCCAACTTA	14284
QY	1382	GTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTT	1441
Db	14285	GTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTT	14344
QY	1442	GTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTTAATAATATTGATATTT	1501
Db	14345	GTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAAATTTAATAATATTGATATTT	14404
QY	1502	ATATCATTTTACGTTTCTCGTTCAGCTTCTGTGTACAAAGTTGGCATTTAAGAAGCAT	1561
Db	14405	ATATCATTTTACGTTTCTCGTTCAGCTTCTGTGTACAAAGTTGGCATTTAAGAAGCAT	14464
QY	1562	TGCTTATCAATTTGTTTCGACGACAGGTCACTATCAGTCAAAATAAAATCATTTATGTC	1621
Db	14448	-----TCTCGAGGAATTCGGTACCCACCTTGGTAAGGAATAATATTT	14447
QY	1622	CATCCAGGTGAGCTCCTTCGAGGAATTCGGTACCCACCTTGGTAAGGAATAATATTT	1681
Db	14448	-----TCTCGAGGAATTCGGTACCCACCTTGGTAAGGAATAATATTT	14492
QY	1682	TCCTTTTCCCTTTAGTATAAAATAGTTAAAGTAGTATGTTAAATAGTATATAATAATA	1741
Db	14493	TCCTTTTCCCTTTAGTATAAAATAGTTAAAGTAGTATGTTAAATAGTATATAATAATA	14552

1742	QY	TAGTGTGTTATAATCTGFAAAAAATTAATTTATAAATATATTTGTTTACATAAAACAACATAGT	1801
14553	Db	TAGTGTGTTATAATCTGFAAAAAATTAATTTATAAATATATTTGTTTACATAAAACAACATAGT	14612
1802	QY	AATGTAAAAAANAATATGACAAGTGATGTCTGTAAGACGAAGAGATAAAAAGTCTGAGAGTAAGT	1861
14613	Db	AATGTAAAAAANAATATGACAAGTGATGTGTAAAGACGAAGAGATAAAGGTTGAGAGTAAGT	14672
1862	QY	ATATATATTTTAAATGAAATTTGATCGGAACATGTAAAGATGATATCTAGCATTAAATATTGTT	1921
14673	Db	ATATATATTTTAAATGAAATTTGATCGGAACATGTAAAGATGATATCTAGCATTAAATATTGTT	14732
1922	QY	TTTTAATCATAAATAGTAATTTCTAGCTGGTTGAGTGAATTAATAATATCAATGATAAATACTA	1981
14733	Db	TTTTAATCATAAATAGTAATTTCTAGCTGGTTGAGTGAATTAATAATATCAATGATAAATACTA	14792
1982	QY	TAGTAAAAATAAGATAAATAAATTAATAATAATATTTTTTTTATGATTAATAGTTTATTTAT	2041
14793	Db	TAGTAAAAATAAGATAAATAAATTAATAATAATATTTTTTTTATGATTAATAGTTTATTTAT	14852
2042	QY	ATAATTTAAATATCTATACCATTTACTAAATATTTTAGTTTAAAGTTAAATAATTTTGT	2101
14853	Db	ATAATTTAAATATCTATACCATTTACTAAATATTTTAGTTTAAAGTTAAATAATTTTGT	14912
2102	QY	TAGAAATTCGAATCTGCTTGTGTAATTTATCAATATAACAAATATTAATAACAGCTAAAG	2161
14913	Db	TAGAAATTCGAATCTGCTTGTGTAATTTATCAATATAACAAATATTAATAACAGCTAAAG	14972
2162	QY	TAAACAATAATATCAAACTTAATAGAACAGTAAATCTAATGTAACAAAAACATAATCTAATG	2221
14973	Db	TAAACAATAATATCAAACTTAATAGAACAGTAAATCTAATGTAACAAAAACATAATCTAATG	15032
2222	QY	CTAATATAACAAAGCGAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATTCT	2281
15033	Db	CTAATATAACAAAGCGAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATTCT	15092
2282	QY	TATTAATTTCTAAATAATATCTGTAGTGTTTATTAACCTCTAAATCGGATTGACTATTAAT	2341
15093	Db	TATTAATTTCTAAATAATATCTGTAGTGTTTATTAACCTCTAAATCGGATTGACTATTAAT	15152
2342	QY	AAATGAATTTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTTGTTAT	2401
15153	Db	AAATGAATTTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTTGTTAT	15212
2402	QY	CATTGATCTTACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTT	2461
15213	Db	CATTGATCTTACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTT	15272
2462	QY	GGATCTCTAGAGAGCTGACGTGGATGGCAATAATGATTTTATTTGACTGATAGTGA	2521
15273	Db	GGATCTCTAGAGAGCTGACGTGGATGGCAATAATGATTTTATTTGACTGATAGTGA	15284
2522	QY	CCTGTTCTGTTGCAACAAATTTGATAAGCAATGCTTTCTTATATATGCCAACCTTTGTACAAGA	2581
15285	Db	-----CCACTTTGTACNAGA15299-----	15299
2582	QY	AAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATTAATAATTAGATTTTGCAATA	2641
15300	Db	AAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATTAATAATTAGATTTTGCAATA	15359
2642	QY	AAAAACAGACTACATAATACTATGTAATAACAAACAATATCCAGTCACTATGAATCAACTACT	2701
15360	Db	AAAAACAGACTACATAATACTATGTAATAACAAACAATATCCAGTCACTATGAATCAACTACT	15419
2702	QY	TAGATGGTATTTAGTGACCTGTGTCGACTAAGTTGCGACATCAACCGACGCACTTTGGG	2761
15420	Db	TAGATGGTATTTAGTGACCTGTGTCGACTAAGTTGCGACATCAACCGACGCACTTTGGG	15479
2762	QY	CCGAATAAATACTGTGACGGAAGATCACTTTGCGAGAAATAAATAAATCTCTGGTGTCCCTG	2821
15480	Db	CCGAATAAATACTGTGACGGAAGATCACTTTGCGAGATAAATAAATAAATCTCTGGTGTCCCTG	15533
2822	QY	TTGATATACCGGAAGCCCTGGGCCAACCTTTTGGCGAAATGAGACGTTGATGGCACTATACC	2881

15540 TTGATACCGGGAAGCCCTGGGCAACTTTTGGCGAAATGAGACGCTTGATCGG----- 15592
2882 CATTTCACAACTTATCTTTCTCTTACAGTCGTTCCGGCTTCATCTGGATTTTCAGC 2941
15593 -ATTTTCACAACTTATCTTTCTCTTACAGTCGTTCCGGCTTCATCTGGATTTTCAGC 15651
2942 CTTCTATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTGAGACT 3001
15652 CTCCTATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTGAGACT 15711
3002 GCGTGTGTATAAGGAGCCCTGACATTTATTTATTTCCCGAGAACATCATGTTTAAATGGCGTTT 3061
15712 GCGTGTGTATAAGGAGCCCTGACATTTATTTATTTCCCGAGAACATCATGTTTAAATGGCGTTT 15771
3062 TGAATGTCATTTTCCGGGTGGCTGAGATCAGGCACCTTCTTCCCGAGAACATCATGTTTAAATGGCGTTT 3121
15772 TGAATGTCATTTTCCGGGTGGCTGAGATCAGGCACCTTCTTCCCGAGAACATCATGTTTAAATGGCGTTT 15831
3122 CACTGGCCATATCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGTT 3181
15832 CACTGGCCATATCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGTT 15891
3182 AAGTTTCACGGGAGCTTTATCTGACAGCAGCTGCTGCGCCAGGCGGATCACCATCC 3241
15892 AAGTTTCACGGGAGCTTTATCTGACAGCAGCTGCTGCGCCAGGCGGATCACCATCC 15951
3242 GTCCGCGGCGGTGCAATAATATCACTCTGTACATCCCAACACAGCAGATACCGCTCT 3301
15952 GTCCGCGGCGGTGCAATAATATCACTCTGTACATCCCAACACAGCAGATACCGCTCT 16011
3302 CTCCTTTATAGGTGTAACCTTAAACCTGATTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 3361
16012 CTCCTTTATAGGTGTAACCTTAAACCTGATTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 16071
3362 GAGCGCTTCATTTCAATAACCGGCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3421
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3422 CAGCGTTCCGACGACGACGAGCGGCTTCAATCTGATGTTTGTCTTACAGACCGGAG 3481
16132 CAGCGTTCCGACGACGACGAGCGGCTTCAATCTGATGTTTGTCTTACAGACCGGAG 16191
3482 ATATTGACATCATATGCTTGGAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3541
16192 ATATTGACATCATATGCTTGGAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16251
3542 TACGCTGCTTATAGCACACCTCTTTTGTGACATCTTCTGTTCTTGTATGACATGATTTT 3601
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16312 CAGGACTATGACATAGGATATGAAATAGGATAGTGTATTTTGTGACACAAATA 16371
3662 GAGGCTGACCTCTTTTCTTATTTCTTTTATGATTTTATGATTTTATGATTTTATGATTTT 3721
16372 GAGGCTGACCTCTTTTCTTATTTCTTTTATGATTTTATGATTTTATGATTTTATGATTTT 16431
3722 GCGAGTAGGCTGGATACGACGATTCGCTTTGAGAGAACATTTGGAAGGCTGTCGGT CGA 3781
16432 GCGAGTAGGCTGGATACGACGATTCGCTTTGAGAGAACATTTGGAAGGCTGTCGGT CGA 16491
3782 CTAAGTTGGGAGCATCACCGAGAACATTTGGAAGGCTGTCGGTTCGACTACAGTCACT 3841
16492 CTAAGTTGGGAGCATCACCGAGAACATTTGGAAGGCTGTCGGTTCGACTACAGTCACT 16551
3842 AATACCTCTAGTAGTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 3901
16552 AATACCTCTAGTAGTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 16611
3902 AGTCGTGTTTTTATGCAAAATCTAATTTAATAATTTATGATTTTATGATTTTATGATTTTATG 3961

16612 AGTCGTGTTTTTATGCAAAATCTAATTAATATATGATTTTATGATTTTATGATTTTATGATTTT 16671
3962 TCGTTACGCTTTTGTGACAAAGTTGGCATATATAAAAGCATTTGCTCACTAATTTGTTG 4021
16672 TCGTTACGCTTTTGTGACAAAGTTG----- 16697
4022 CAACGACAGGTCACTATCAGTCAAAATAAAATCAATTAATTTGGGGCCGAGATCCATGCT 4081
16698 ----- 16697
4082 AGCTCTAGAGTCCCTGCTTTAATGAGATATGCGAGACGCTTATGATGCGATGATTTGCT 4141
16698 ---TCTAGAGTCCCTGCTTTAATGAGATATGCGAGACGCTTATGATGCGATGATTTGCT 16754
4142 TTAATTTCTGTTGTGACAGTTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 4201
16755 TTAATTTCTGTTGTGACAGTTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 16814
4202 CGGTTTCGGTTTCATTTAATGAATATATACCCGTTACTATCGTATTTTATGAATAATA 4261
16815 CGGTTTCGGTTTCATTTAATGAATATATACCCGTTACTATCGTATTTTATGAATAATA 16874
4262 TTCTCCGTTCAATTTACTGATTTGTAACCTACTACTATGATGTAATAATTAATAATA 4321
16875 TTCTCCGTTCAATTTACTGATTTGTAACCTACTACTATGATGTAATAATTAATAATA 16934
4322 CAATATATGCTGTAATAGGTTTATAGGACATCTATGATAGAGCGCACATAAACA 4381
16935 CAATATATGCTGTAATAGGTTTATAGGACATCTATGATAGAGCGCACATAAACA 16994
4382 CAATTTCCGTTTATTTATTTACAAATCCAAATTTTAAATAAGGCGGACAAACCGTCAAACT 4441
16995 CAATTTCCGTTTATTTATTTACAAATCCAAATTTTAAATAAGGCGGACAAACCGTCAAACT 17054
4442 AAAAGACTGATTAATAAATCTTATTAATTTTAAATAAGGCGGCTAGTATCTAC 4501
17055 AAAAGACTGATTAATAAATCTTATTAATTTTAAATAAGGCGGCTAGTATCTAC 17114
4502 GACACACGAGCGGCGAACTAATAAGTTTCACTGAAAGGAACTCCGGTTTCCCGCGCGG 4561
17115 GACACACGAGCGGCGAACTAATAAGTTTCACTGAAAGGAACTCCGGTTTCCCGCGCGG 17174
4562 CGCATGGGTGAGATCTCTTTGAAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGG 4621
17175 CGCATGGGTGAGATCTCTTTGAAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGG 17234
4622 CACCATTAACCGGTCCAGCAGCGCGCGGCTAACCGACTTGTCTGCCCGCGAGATTTAT 4681
17235 CACCATTAACCGGTCCAGCAGCGCGCGGCTAACCGACTTGTCTGCCCGCGAGATTTAT 17294
4682 GCAGCATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4741
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4742 CGCAAAATCGTTGGCGGTTCCAGGCGGAAATTTTGGCAACATGTCGAGGCTCAGCAG 4861
17355 CGCAAAATCGTTGGCGGTTCCAGGCGGAAATTTTGGCAACATGTCGAGGCTCAGCAG 17414
4802 ACCTGAGGCGCATCAGAGTACTTACTAGTGTGATTTTCTATAGTGTCACTTAATCT 4861
17415 ACCTGAGGCGCATCAGAGTACTTACTAGTGTGATTTTCTATAGTGTCACTTAATCT 17474
4862 GC 4863
17475 GC 17476

RESULT 4

US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.

; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 83.8%; Score 4077.2; DB 15; Length 17681;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 68; Indels 309; Gaps 5;
122 GCGAATCTTGTACAAAAAGCTGACGAGAAAGCTAAATGATATAAATATCAATATTT 181
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13385 ATTCAATAGCTAGTGTATAGTCGCAAAATCATCTGCATCAAGAACAAATTTCAAC 13444
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13445 TCTTATATCTTTCTCTTACAGTGGTTCGGCTTCATCTGGATTTTCAGCCCTCTATCTTA 13504
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13505 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGATA 13564
662 AGGAGCCCTGACATTTATATTCGCCAGAACATCAGGTTAAATGGCGTTTGTGATGTCATTT 721
13565 AGGAGCCCTGACATTTATATTCGCCAGAACATCAGGTTAAATGGCGTTTGTGATGTCATTT 13624
722 TCGGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 781
13625 TCGGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 13684
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13685 TCGGTGGTTCATCATGCGCCAGCTTTTCATCCCGGATATGACACACCGGGTAAAGTTTCAGG 13744
842 GAGACTTTATCTGACAGCAGCTGCTGCGCAGGGGATCCATCCGTCGCGCCGGC 901
13745 GAGACTTTATCTGACAGCAGCTGCTGCGCAGGGGATCCATCCGTCGCGCCGGC 13804

QY 902 GTGTCAATAATATCACTGTGTACATCCACAAACAGACGATACCGCTCTCTCTTTATAG 961
DB 13805 GTGTCAATAATATCACTGTGTACATCCACAAACAGACGATACCGCTCTCTCTTTATAG 13864
QY 962 GTGTAAACCTTAAACCTGCAATTTACAGTCCCTGTTCTGTCAGCAAAAGACCGCTTCAT 1021
DB 13865 GTGTAAACCTTAAACCTGCAATTTACAGTCCCTGTTCTGTCAGCAAAAGACCGCTTCAT 13924
QY 1022 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCGGC 1081
DB 13925 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCGGC 13984
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DB 13985 ACGCAGACGACGGGCTTCATTTCTGATGTTGTCTTACACAGACCGGAGATATTCACATC 14044
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DB 14045 ATATATGCTTGAGCAACTGATAGTGTGCTGTCACCTGTCACCTGTCATGATACGCTGCTTC 14104
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QY 1322 TGATCTTCGGTCAAGGATTTTATTTGGCGCAAGTGGCTGCGGTGATGCTGCCAACTTA 1381
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QY 1382 GTCGACTCAGGTCATTAATACCATCTAAGTAGTTGATTCATAGTACCTGATGATGTTGT 1441
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QY 1502 ATATCATTTTACGTTTCTGTTTCAGCTTCTGTCACAAAGTTGGCATTATTAAGAAAGCAT 1561
DB 14405 ATATCATTTTACGTTTCTGTTTCAGCTTCTGTCACAAAGTTGGCATTATTAAGAAAGCAT 14447
QY 1562 TGCTTATCAATTTGTTGCAACGAAAGTCATCTCAGTCAAAATCAATTTATTTTC 1621
DB 14448 ----- 14447
QY 1622 CATCCAGCTGACGCTCCTCAGGAAATTCGGTACCCAGCTTCGTAAGGAAATAATTTATTT 1681
DB 14448 -----TCGAGGAAATTCGGTACCCAGCTTCGTAAGGAAATAATTTATTT 14492
QY 1682 TCTTTTTCCTTTTGTAGTATAAATAAGTAAAGTATGATTAATAGTATGATTAATAATA 1741
DB 14493 TCTTTTTCCTTTTGTAGTATAAATAAGTAAAGTATGATTAATAGTATGATTAATAATA 14552
QY 1742 TAGTGTATTAATTTGTCAAAAATAAATTTATAAATATTTGTTTACATAAACACATAGT 1801
DB 14553 TAGTGTATTAATTTGTCAAAAATAAATTTATAAATATTTGTTTACATAAACACATAGT 14612
QY 1802 AATGTAAAAAATAATGACAAAGTATGTAAGAGAGAGAGATAAAGTTGACAGTAAGT 1861
DB 14613 AATGTAAAAAATAATGACAAAGTATGTAAGAGAGAGATAAAGTTGACAGTAAGT 14672
QY 1862 ATATTTATTTTATGATTTTGTATCGAACATGTAAGTATGATATAGTATGATTAATTTGT 1921
DB 14673 ATATTTATTTTATGATTTTGTATCGAACATGTAAGTATGATATAGTATGATTAATTTGT 14732
QY 1922 TTTAATCATTAATAGTAAATTTCTAGCTGGTTTGTGATTAATTAATATCAATGATTAATAACTA 1981
DB 14733 TTTAATCATTAATAGTAAATTTCTAGCTGGTTTGTGATTAATTAATATCAATGATTAATAACTA 14792
QY 1982 TAGTAAAAATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2041


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4090 AGTCCTGCTTTAATGAGATATGCGAGACCCCTATGATCGCATGATATTTGCTTCAATTC 4149
16908 AGTCCTGCTTTAATGAGATATGCGAGACCCCTATGATCGCATGATATTTGCTTCAATTC 16967
4150 TGTTGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCTCTTACCGCGGTTTCG 4209
16968 TGTTGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCTCTTACCGCGGTTTCG 17027
4210 GTTCATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATATCTCCGT 4269
17028 GTTCATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATATCTCCGT 17087
4270 TCAATTTACTGATGTGACCTACTATATATGTACAAATATTTAAATGAAACAATATAT 4329
17088 TCAATTTACTGATGTGACCTACTATATATGTACAAATATTTAAATGAAACAATATAT 17147
4330 TGTGCTGATAGTTTATAGGACATCTATAGAGCGCCACAATAACAAACAATTTGCG 4389
17148 TGTGCTGATAGTTTATAGGACATCTATAGAGCGCCACAATAACAAACAATTTGCG 17207
4390 TTTTATTTATCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 4449
17208 TTTTATTTATCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 17267
4450 GATTACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 4509
17268 GATTACATAAATCTTATTTCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 17327
4510 GAGCGCGCACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCATGG 4569
17328 GAGCGCGCACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCATGG 17387
4570 TGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGACCATTC 4629
17388 TGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGACCATTC 17447
4630 AACCCGCTCCAGCAGCGCGCGGTAACCGACTTGTGCTCCCGAGAAATTTATGCGCAT 4689
17448 AACCCGCTCCAGCAGCGCGCGGTAACCGACTTGTGCTCCCGAGAAATTTATGCGCAT 17507
4690 TTTTGTGTATGTGGSCCCCAATGAAGTGCAGGTCAAACTTGACAGTGACGACAAAT 4749
17508 TTTTGTGTATGTGGSCCCCAATGAAGTGCAGGTCAAACTTGACAGTGACGACAAAT 17567
4750 CGTTGGCGGGTCAGCGCGAAATTTTCGCAACATGTCGAGGCTCAGAGGACCTGCAG 4809
17568 CGTTGGCGGGTCAGCGCGAAATTTTCGCAACATGTCGAGGCTCAGAGGACCTGCAG 17627
4810 GCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTAAATCTGC 4863
17628 GCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTAAATCTGC 17681

RESULT 5
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELUGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
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; FEATURE:
; OTHER INFORMATION: acceptor vector PHELLSGATE11
US-10-055-001A-25

Query Match      83.1%; Score 4042; DB 15; Length 17458;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 4419; Conservative 0; Mismatches 15; Indels 308; Gaps 6;

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DB 13025 GACAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAATATAT 13084
QY 182 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAAATATCCAGTC 241
DB 13085 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAAATATCCAGTC 13144
QY 242 ACTATGAATCAACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 301
DB 13145 ACTATGAATCAACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 13204
QY 302 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTCTCAA 361
DB 13205 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTCTCAA 13264
QY 362 ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGTCTCAATGCCGTATTAATCATATAAA 421
DB 13265 ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGTCTCAATGCCGTATTAATCATATAAA 13324
QY 422 AGAATATAGAAAGAGGTCGAGGCTCTTTTGTGTGACAAATATAAATATCAATCTACCT 481
DB 13325 AGAATATAGAAAGAGGTCGAGGCTCTTTTGTGTGACAAATATAAATATCAATCTACCT 13384
QY 482 ATTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTCACAAC 541
DB 13385 ATTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTCACAAC 13444
QY 542 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCAATCGGATTTTTCAGCTCTTACTTATA 601
DB 13445 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCAATCGGATTTTTCAGCTCTTACTTATA 13504
QY 602 CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACACTGGCTGTGTATA 661
DB 13505 CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACACTGGCTGTGTATA 13564
QY 662 AGGAGCCCTGACATTTATATTTCCCAAGAACATCAGGTTAATGCCGTTTGTGATGTCATTT 721
DB 13565 AGGAGCCCTGACATTTATATTTCCCAAGAACATCAGGTTAATGCCGTTTGTGATGTCATTT 13624
QY 722 TCCGCGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGACACTGGGCATA 781
DB 13625 TCCGCGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGACACTGGGCATA 13684
QY 782 TCCGCGTGGCTGATCGCCAGCTTTTCTATCCCGCATATGCACCAACCGGGTAAAGTTACCGG 841
DB 13685 TCCGCGTGGCTGATCGCCAGCTTTTCTATCCCGCATATGCACCAACCGGGTAAAGTTACCGG 13744
QY 842 GAGACTTTATPCTCAGACGACAGCTGCACTGGCGCAGGGGATACCATTCCTGCCCGCGGC 901
DB 13745 GAGACTTTATPCTCAGACGACAGCTGCACTGGCGCAGGGGATACCATTCCTGCCCGCGGC 13804
QY 902 GTGTCAATATATATCTCTCTGATATCAACAAACAGACGATAACGGCTCTCTCTTTTATAG 961
DB 13805 GTGTCAATATATATCTCTCTGATATCAACAAACAGACGATAACGGCTCTCTCTTTTATAG 13864
QY 962 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTCTGTCAGCAAAAGAGCGGTTTAT 1021
DB 13865 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTCTGTCAGCAAAAGAGCGGTTTAT 13924
QY 1022 TTCAATAAACCGGCGACCTCAGCCATCTCTGATTTTTCGCTTTCCAGGTTTCGGC 1081
DB 13925 TTCAATAAACCGGCGACCTCAGCCATCTCTGATTTTTCGCTTTCCAGGTTTCGGC 13984
QY 1082 ACGCAGACGACGGGCTTCTTCTGATGTTGTGCTTTACAGACCGGAGATATTGACATC 1141
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[illegible]


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/ OTHER INFORMATION: attP1 recombination site (complement)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (17610)..(16855)
/ OTHER INFORMATION: ccdB selection marker (complement)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (16551)..(16319)
/ OTHER INFORMATION: attP2 recombination site (complement)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (14650)..(16258)
/ OTHER INFORMATION: pdk2 intron 2
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (15002)..(15661)
/ OTHER INFORMATION: chloramphenicol resistance gene
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (14387)..(14619)
/ OTHER INFORMATION: attP2 recombination site
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (13675)..(13980)
/ OTHER INFORMATION: ccdB selection marker (complement)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (13048)..(13279)
/ OTHER INFORMATION: attP1 recombination site
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (17922)..(18687)
/ OTHER INFORMATION: octopine synthase gene terminator region
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (264)..(496)
/ OTHER INFORMATION: nopaline synthase gene promoter
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (497)..(1442)
/ OTHER INFORMATION: nptII coding region
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1443)..(2148)
/ OTHER INFORMATION: nopaline synthase gene terminator
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2149)..(2706)
/ OTHER INFORMATION: a left T-DNA border region
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/ US-10-055-001A-13
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/ Query Match 82.0%; Score 3985.4; DB 15; Length 18691;
/ Best Local Similarity 85.1%; Pred. No. 0; Mismatches 16; Indels 831; Gaps 2;
/ Matches 4846; Conservative 0;
/
/ QY 1 TTTTCAATTTGGAGAGGACGCTCGAGGCTAGCATGGATCTCGGGCCCCCAATAATGATTT 60
/ DB 13000 TTTTCAATTTGGAGAGGACGCTCGAGGCTAGCATGGATCTCGGGCCCCCAATAATGATTT 13059
/
/ QY 61 TATTTTGACTGATGATGACCTGTTGTCGCAAAATTCGATGAGCAATGCTTTTATATAA 120
/ DB 13060 TATTTTGACTGATGATGACCTGTTGTCGCAAAATTCGATGAGCAATGCTTTTATATAA 13119
/
/ QY 121 TGCCAACTTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 180
/ DB 13120 TGCCAACTTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 13179
/
/ QY 181 TAAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGT 240
/ DB 13180 TAAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGT 13239
/
/ QY 241 CACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGAGCGGACGCTTCCAA 300
/ DB 13240 CACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGAGCGGACGCTTCCAA 13299
/
/ QY 301 ATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTCTTTCTCA 360
/ DB 13300 ATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTCTTTCTCA 13359
/
/ QY 361 AACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATCGGTATTAAATCATATAA 420
/ DB 13360 AACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATCGGTATTAAATCATATAA 13419
/
/ QY 421 AAGAAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACTATACC 480
/ DB 13420 AAGAAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAACTATACC 13479
/
/ QY 481 TATTCATATAGCTAGTGTCTGTAATCTCTGAAATCATCTGATCAAGAACTATTCACAA 540
/ DB 13480 TATTCATATAGCTAGTGTCTGTAATCTCTGAAATCATCTGATCAAGAACTATTCACAA 13539
/
/ QY 541 CTCCTTATACCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGGATTTTCAGCCTCTATACTT 600
/ DB 13540 CTCCTTATACCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGGATTTTCAGCCTCTATACTT 13599
/
/ QY 601 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGAGCTGGCTGTGAT 660
/ DB 13600 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGAGCTGGCTGTGAT 13659
/
/ QY 661 AAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTGTGATGTCATT 720
/ DB 13660 AAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTGTGATGTCATT 13719
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/ QY 721 TTCGGGTGGCTGAGATCAGCCACTTCTTCCCGCAATAACGAGACCCGGCACACCTGGCCAT 780
/ DB 13720 TTCGGGTGGCTGAGATCAGCCACTTCTTCCCGCAATAACGAGACCCGGCACACCTGGCCAT 13779
/
/ QY 781 ATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATGACACCCGCGTAAAGTTACAG 840
/ DB 13780 ATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATGACACCCGCGTAAAGTTACAG 13839
/
/ QY 841 GGAGACTTTTATCTGACAGCAGCTGACCTGCCAGGGGGATCACCATCCGTCGCCCGGG 900
/ DB 13840 GGAGACTTTTATCTGACAGCAGCTGACCTGCCAGGGGGATCACCATCCGTCGCCCGGG 13899
/
/ QY 901 CGTGTCAATAATATCACTCTGTATACATCCAAAACAGAGATACCGGCTCTCTCTTTTATA 960
/ DB 13900 CGTGTCAATAATATCACTCTGTATACATCCAAAACAGAGATACCGGCTCTCTCTTTTATA 13959
/
/ QY 961 GGTGTAAACCTTAACTGCATTTTCAGTCCCTGTTCTCTGTCAGCAAAAGACGGTCA 1020
/ DB 13960 GGTGTAAACCTTAACTGCATTTTCAGTCCCTGTTCTCTGTCAGCAAAAGACGGTCA 14019
/
/ QY 1021 TTTCAATAAACCGGGCGACCTCAGCATCCCTTCTGATTTTCCGCTTTCAGCGCTTCGG 1080
/ DB 14020 TTTCAATAAACCGGGCGACCTCAGCATCCCTTCTGATTTTCCGCTTTCAGCGCTTCGG 14079
/
/ QY 1081 CACGACAGACGCGGCTTCACTTGTGATGTTGTGTACAGACCGGAGATATTGACAT 1140
/ DB 14080 CACGACAGACGCGGCTTCACTTGTGATGTTGTGTACAGACCGGAGATATTGACAT 14139
/
/ QY 1141 CATATATGCTTTGACAACTGATAGCTGCTGCTCACTGTCACTGTAAATACGCTGCTT 1200
/ DB 14140 CATATATGCTTTGACAACTGATAGCTGCTGCTCACTGTCACTGTAAATACGCTGCTT 14199
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/ QY 1201 CATAGCACACCTCTTTTGTGACATCTCGGCTAGTGGCGGATCAACGCTCTCACTTTTCGCCA 1260
/ DB 14200 CATAGCACACCTCTTTTGTGACATCTCGGCTAGTGGCGGATCAACGCTCTCACTTTTCGCCA 14259
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/ QY 1261 AAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACAGATTTATTTATTTCTGCGAA 1320
/ DB 14260 AAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACAGATTTATTTATTTCTGCGAA 14319
/
/ QY 1321 GTGATCTTCGCTCAGAGTATTATTTCGGCGCAAGTCGGTGTGATGCTGCCCACTT 1380
/ DB 14320 GTGATCTTCGCTCAGAGTATTATTTCGGCGCAAGTCGGTGTGATGCTGCCCACTT 14379
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QY 1381 AGTCGACTACAGGTCACATAATACCACTAAGAGTGTGATGACTGATGATGTTG 1440
DB |||||
14380 AGTCGACTACAGGTCACATAATACCACTAAGAGTGTGATGACTGATGATGTTG 14439
QY |||||
1441 TGTTTTACAGTATATATAGTCTGTTTTTATGCAAAATCTAATTTAATATATTCATATT 1500
DB |||||
14440 TGTTTTACAGTATATATAGTCTGTTTTTATGCAAAATCTAATTTAATATATTCATATT 14499
QY |||||
1501 TATATCATTTTACGTTTCTGTTCCAGTCTTCTGTAACAAAGTGGCATTATTAAGAAAGCA 1560
DB |||||
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QY |||||
1561 TTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATCAATTTATTG 1620
DB |||||
14560 TTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATCAATTTATTG 14619
QY |||||
1621 CCATCCAGCTGAGCTCCCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATATATT 1680
DB |||||
14620 CCATCCAGCTGAGCTCCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATATATT 14678
QY |||||
1681 TTCTTTTTTCTTTTGTATATAAATAGTTPAAGTGATGTTTAATTTAGTATGATTTAATAAT 1740
DB |||||
14679 TTCTTTTTTCTTTTGTATATAAATAGTTPAAGTGATGTTTAATTTAGTATGATTTAATAAT 14738
QY |||||
1741 ATAGTTGTTTATTAATTTGTGAAAAATAATTTTATATAATATTTGTTTACATAAACAATAG 1800
DB |||||
14739 ATAGTTGTTTATTAATTTGTGAAAAATAATTTTATATAATATTTGTTTACATAAACAATAG 14798
QY |||||
1801 TAAATGTAATAAATAATGACAAGTGATGTTGAAGACGAAGATAAAGTTTCAGAGTAAAG 1860
DB |||||
14799 TAAATGTAATAAATAATGACAAGTGATGTTGAAGACGAAGATAAAGTTTCAGAGTAAAG 14858
QY |||||
1861 TATATATTTTAAATGAATTTGATTCGAACATGTAAGATGATATCTAGCAATTAA 1914
DB |||||
14859 TATATATTTTAAATGAATTTGATTCGAACATGTAAGATGATATCGGCCGTAAGAGGTT 14918
QY |||||
1915 ----- 1914
DB 14919 CCAACTTTCCACATAATGAAATAAGATCACTACCGGGCGTATTTTTTGGAGTTATCGAGAT 14978
QY |||||
1915 ----- 1914
DB 14979 TTTTCAGGACCTAAGGAAGCTAATAATGGAAGAAAATCACTGATATACCACCGTTGATA 15038
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1915 ----- 1914
DB 15039 TATCCCAATGGCATCGTAAGAACAATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACCT 15098
QY |||||
1915 ----- 1914
DB 15099 ATAAACGAGACGTTGAGCTGGATATATACGGCTTTTAAAGACCGTAAGAAAAATAAGC 15158
QY |||||
1915 ----- 1914
DB 15159 ACAAAGTTTATCCGGCTTTTATTCACATTTCTTGGCCGCTGATGATGCTCATCCGGAAT 15218
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1915 ----- 1914
DB 15219 TCCGTATGGCAATGAAGAAGCGGTGAGCTGGTGAATGGAATGTTTCACCTTTGTACA 15278
QY |||||
1915 ----- 1914
DB 15279 CCGTTTTCCATGAGCAAACTGAACCGTTTTTCATCGCTCTGGAGTGAATACCAGCAGATT 15338
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DB 15459 TCACCAGTTTTGATTTAAACGTCGCCAATATGGACAACTTCTTCGCCCCCGTTTTTCACCA 15518
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15759 AATAGTAATTTCTAGCTGGTTTGTGATGAATTAATTAATCAATGATAAATACTATAGTAAAAA 15818
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DB |||||
15819 TAAAGTAATAATAAATTAATAATAATTTTTTTTATGATTAAATAGTTTATATATAATTTAAA 15878
QY 2051 TATCTATACCATTAATAATAATTTTGTGTTAAAAAGTTTAATAAATAATTTTGTAGAAATTC 2110
DB 15879 TATCTATACCATTAATAATAATTTTGTGTTAAAAAGTTTAATAAATAATTTTGTAGAAATTC 15938
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QY 2171 ATATCAAACTAATAAGAACAGTAATCTAATGTGAACAAAACATAATCTAATGTCTAATAATA 2230
DB 15999 ATATCAAACTAATAAGAACAGTAATCTAATGTGAACAAAACATAATCTAATGTCTAATAATA 16058
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DB 16059 CAAAGCGCAAGATCTATCATTTTATATAGTATATATTTTCAATCAACATCTCTTATTTAAATTT 16118
QY 2291 CTAAATATATCTGTAGTTTTTATTAACCTTCAATAATGGAATTCACATTTAATTTAAATGAATTT 2350
DB 16119 CTAAATATATCTGTAGTTTTTATTAACCTTCAATAATGGAATTCACATTTAATTTAAATGAATTT 16178
QY 2351 AGTCGAACATGAATAAACAAGCTAACATGATAGATCATGTCTATTGTGTTATCAATGTATCT 2410
DB 16179 AGTCGAACATGAATAAACAAGCTAACATGATAGATCATGTCTATTGTGTTATCAATGTATCT 16238
QY 2411 TACATTTGGATTTGATTAAGTTGGGAAGCTGGTTTCGAAATCGATAAGCTTTGGATCTCT 2470
DB 16239 TACATTTGGATTTGATTAAGTTGGGAAGTTGGTTTCGAAATCGATAAGCTTTGGATCTCT 16298
QY 2471 AGAGAGCTGCAGCTGGATGGCAATAATAATTTTATTTTGTAGTATGATGATCTGCTGCT 2530
DB 16299 AGAGAGCTGCAGCTGGATGGCAATAATAATTTTATTTTATTTTGTAGTATGATGATCTGCT 16358
QY 2531 TGCAACAAATTTGATTAAGCAATGCTTTCTTATAATGCCAACTTTTGTACAAAGAAAGCTGAAC 16418
DB 2591 GAGAAACGTAATAATGATATAATTAATTAATTAATTAATTAATTTTGTACATAAACAAGCA 2650
DB 16419 GAGAAACGTAATAATGATATAATTAATTAATTAATTAATTTTGTACATAAACAAGCA 16478
QY 2651 CTACATAATCTGTAAAAACACAAATATCCAGTCACTATGAATCAACTTCTAGATGGTA 2710
DB 16479 CTACATAATCTGTAAAAACACAAATATCCAGTCACTATGAATCAACTTCTAGATGGTA 16538
QY 2711 TTAGTGACCTGTAGTCGATGAATTTGGCAGCATCACCCGACGCACTTTTGGCCCGCAATAA 2770

Db 16539 TTAGTGACCTGTAGTGCATAGTTGGCAGCATCACCCGAGCGACTTTGCGCGCAATAAAA 16598
QY 2771 TACCTGTGACGGAAGATCACTTGGCAGATAAATAAATCCTGGTGTCCCTGTGTATACCG 2830
Db 16599 TACCTGTGACGGAAGATCACTTGGCAGATAAATAAATCCTGGTGTCCCTGTGTATACCG 16658
QY 2831 GGAAGCCCTGGCCCAACTTTTGGCGAAATGAGCGTTGATGGCAGTACCCATTTCACA 2890
Db 16659 GGAAGCCCTGGCCCAACTTTTGGCGAAATGAGCGTTGATGGCAGTACCCATTTCACA 16718
QY 2891 ACTCTTATATCTTTCTCTTACAGTCCGTTCGCGCTTCATCTGGATTTTTCAGCCTCTATACT 2950
Db 16719 ACTCTTATATCTTTCTCTTACAGTCCGTTCGCGCTTCATCTGGATTTTTCAGCCTCTATACT 16778
QY 2951 TACTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACTGAGACTGGCTGTGTA 3010
Db 16779 TACTAAACGTGATAAAGTTCTCTGTAATTTCTACTGTATCGACTGAGACTGGCTGTGTA 16838
QY 3011 TAAGGAGCCTGACATTTATATCCCGAAGACATCAGGTTAATGGCGTTTTTGTATGTCAT 3070
Db 16839 TAAGGAGCCTGACATTTATATCCCGAAGACATCAGGTTAATGGCGTTTTTGTATGTCAT 16898
QY 3071 TTTTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGCCACACTGGCCA 3130
Db 16899 TTTTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGCCACACTGGCCA 16958
QY 3131 TATCGGTGTCATCATGCGCAGCTTTTATCCCGATATGCAACCGGGTAAAGTTTAC 3190
Db 16959 TATCGGTGTCATCATGCGCAGCTTTTATCCCGATATGCAACCGGGTAAAGTTTAC 17018
QY 3191 GGGAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCGCCCGG 3250
Db 17019 GGGAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCGCCCGG 17078
QY 3251 GGGTGTCAATAATPATCACTGTGATATCCAAACAGAGATAAAGGCTCTCTCTTTAT 3310
Db 17079 GGGTGTCAATAATPATCACTGTGATATCCAAACAGAGATAAAGGCTCTCTCTTTAT 17138
QY 3311 AGGTGTAAACCTTAACTGATTCACAGTCCCTGCTTCTGTCAGCAAAAAGCGCTTC 3370
Db 17139 AGGTGTAAACCTTAACTGATTCACAGTCCCTGCTTCTGTCAGCAAAAAGCGCTTC 17198
QY 3371 ATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCAGCGCTTCG 3430
Db 17199 ATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCAGCGCTTCG 17258
QY 3431 GCACGACGACGCGGCTTCAATTCGATGTTGTTGCTTACAGACCGGAGATATTGACA 3490
Db 17259 GCACGACGACGCGGCTTCAATTCGATGTTGTTGCTTACAGACCGGAGATATTGACA 17318
QY 3491 TCATATATGCTTGTAGCACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCT 3550
Db 17319 TCATATATGCTTGTAGCACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCT 17378
QY 3551 TCATAGCACACCTCTTTTGTACATCTCTGTTCTTGTATGATGATGATTTTTCAGGACTAT 3610
Db 17379 TCATAGCACACCTCTTTTGTACATCTCTGTTCTTGTATGATGATGATTTTTCAGGACTAT 17438
QY 3611 GACACTAGGCTATATGAATAGTGTAGTGTGCTGCTCACTGTCACTGTAAATACGCTGCT 3670
Db 17439 GACACTAGGCTATATGAATAGTGTAGTGTGCTGCTCACTGTCACTGTAAATACGCTGCT 17498
QY 3671 ACCTCTTTTCTTTTATTTTATGATTTTAAACGGCATTTAGGACAAATAGGAGTAGG 3730
Db 17499 ACCTCTTTTCTTTTATTTTATGATTTTAAACGGCATTTAGGACAAATAGGAGTAGG 17558
QY 3731 CTGGATACGACGATTCGGTTTGTAGAGAAACATTTGGAAGGCTGCTCGTCACTAAAGTTGG 3790
Db 17559 CTGGATACGACGATTCGGTTTGTAGAGAAACATTTGGAAGGCTGCTCGTCACTAAAGTTGG 17618
QY 3791 CAGCATCACCGAAGAACATTTGGAGGCTGCTCGTCACTACAGGTCACTAAATACCATC 3850

Db 17619 CAGCATCACCGAAGAACATTTGGAGGCTGCTCGTCACTACAGGTCACTAAATACCATC 17678
QY 3851 TAAGTAGTGTGATTCATAGTGACTGGAATATGTGTGTGTTTTTACAGTATTAATGATGCTGTTT 3910
Db 17679 TAAGTAGTGTGATTCATAGTGACTGGAATATGTGTGTGTTTTTACAGTATTAATGATGCTGTTT 17738
QY 3911 TTTATGCAAAATCTAAATTTAATATATATGATATTTATATCATTTTACGTTTCTCGTTTCAGC 3970
Db 17739 TTTATGCAAAATCTAAATTTAATATATATGATATTTATATCATTTTACGTTTCTCGTTTCAGC 17798
QY 3971 TTTTGTGACAAAGTTGGCATTTATAAAAGCAATTTGCTCATCAATTTGTTGCAACGAACA 4030
Db 17799 TTTTGTGACAAAGTTGGCATTTATAAAAGCAATTTGCTCATCAATTTGTTGCAACGAACA 17858
QY 4031 GGTCACTATCAGTCAAAATAAATCAATTTATTTGGGCCCCGAGATCCATGCTAGCTCTAGA 4090
Db 17859 GGTCACTATCAGTCAAAATAAATCAATTTATTTGGGCCCCGAGATCCATGCTAGCTCTAGA 17918
QY 4091 GTCCCTGCTTTAATGAGATATGCGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCT 4150
Db 17919 GTCCCTGCTTTAATGAGATATGCGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCT 17978
QY 4151 GTTGTGACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGG 4210
Db 17979 GTTGTGACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGG 18038
QY 4211 TTCAATTTCAATGAATATATCATCCGTTACTCTGTTATTTTATGAATATATTTCTCGGTT 4270
Db 18039 TTCAATTTCAATGAATATATCATCCGTTACTCTGTTATTTTATGAATATATTTCTCGGTT 18098
QY 4271 CAATTTACTGATTTGACCCCTACTACTTATATGTACAATATTTAAAAATGAAAACAATATTT 4330
Db 18099 CAATTTACTGATTTGACCCCTACTACTTATATGTACAATATTTAAAAATGAAAACAATATTT 18158
QY 4331 GTGCTGAATAGTGTATAGCGACATCTATGATAGAGCGCCAAATAAACAATTTGGT 4390
Db 18159 GTGCTGAATAGTGTATAGCGACATCTATGATAGAGCGCCAAATAAACAATTTGGT 18218
QY 4391 TTTTATTTTACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAAAGACTG 4450
Db 18219 TTTTATTTTACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAAAGACTG 18278
QY 4451 ATTTACATAAATCTTATTTCAAAATTTTCAAAAGGCCCCCAGGGGCTTAGTATCTAGCACACCG 4510
Db 18279 ATTTACATAAATCTTATTTCAAAATTTTCAAAAGGCCCCCAGGGGCTTAGTATCTAGCACACCG 18338
QY 4511 ACCGCGAACTAATAAAGCTTCACTGAAAGGAACTCCGGTTCCCGCCCGCGCGCATGGGT 4570
Db 18339 ACCGCGAACTAATAAAGCTTCACTGAAAGGAACTCCGGTTCCCGCCCGCGCGCATGGGT 18398
QY 4571 GAGATTCCTTGAAGTTGAGTATTTGGCCGCTTACCGGAAAGTTTACGGGCACTTCA 4630
Db 18399 GAGATTCCTTGAAGTTGAGTATTTGGCCGCTTACCGGAAAGTTTACGGGCACTTCA 18458
QY 4631 ACCCGGTCCAGCACGCGCGCGGTTAAACCGACTTGTCTCCCGCGAGAAATTTATGACATTT 4690
Db 18459 ACCCGGTCCAGCACGCGCGCGGTTAAACCGACTTGTCTCCCGCGAGAAATTTATGACATTT 18518
QY 4691 TTTTGTGTGTGTGGGCCCCAAATGAGTGCAGGTCAAACTTTGACAGTGCAGCAATTC 4750
Db 18519 TTTTGTGTGTGTGGGCCCCAAATGAGTGCAGGTCAAACTTTGACAGTGCAGCAATTC 18578
QY 4751 GTTGGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTCGAGGCTCAGCAGGACCTGCAGG 4810
Db 18579 GTTGGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTCGAGGCTCAGCAGGACCTGCAGG 18638
QY 4811 CATGCAAGCTAGCTTACTAGTGTATGATGATATTTCTATAGTGTCACTTAAATCTGC 4863
Db 18639 CATGCAAGCTAGCTTACTAGTGTATGATGATATTTCTATAGTGTCACTTAAATCTGC 18691

RESULT 7

US-10-055-001A-23/c

; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 33.8%; Score 1645; DB 15; Length 17862;
Best Local Similarity 65.2%; Pred. No. 6.9e-242;
Matches 2668; Conservative 0; Mismatches 1355; Indels 70; Gaps 14;

QY	27	GCTAGCATGGATCTCGGGCCCAAAATATGATTTTATTTGACTGATAGTACCTGCTGCG	86
DB	17083	GCTAGCATGGATCTCGGGCCCAAAATATGATTTTATTTGACTGATAGTACCTGCTGCG	17024
QY	87	TTGCAACAAATTGATGAGCAATGCTTTTATTAATGCCAATTTGTACAAAAAGCTGAA	146
DB	17023	TTGCAACAAATTGATGAGCAATGCTTTTATTAATGCCAATTTGTACAAAAAGCTGAA	16964
QY	147	CGAGAAACGTAATGATTAATATCAATATATTAATTTAGATTTTGCATAAAAAACAG	206
DB	16963	CGAGAAACGTAATGATTAATATCAATATATTAATTTAGATTTTGCATAAAAAACAG	16904
QY	207	ACTACATAATACGTGTAACACACACATATCCAGTCACTATGAATCAACTTATAGATGT	266
DB	16903	ACTACATAATACGTGTAACACACATATCCAGTCACTATGAATCAACTTATAGATGT	16844
QY	267	ATTAGTGACCTGTAGTCGACCGCAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACT	326
DB	16843	ATTAGTGACCTGTAGTCGACCGCAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACT	16784
QY	327	TAGTCGACGACGACCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACT	386
DB	16783	TAGTCGACGACGACCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACT	16724
QY	387	CGCTATTGCTCCTCAATCGCGTATTAAATCATAAAGAAATAAGAAAAAGAGGTGCGAGC	446
DB	16723	CGCTATTGCTCCTCAATCGCGTATTAAATCATAAAGAAATAAGAAAAAGAGGTGCGAGC	16664
QY	447	CTCTTTTGTGTGACAAAAATAAAAAATCTACTATTATATACGCTAGTGTATAGTC	506
DB	16663	CTCTTTTGTGTGACAAAAATAAAAAATCTACTATTATATACGCTAGTGTATAGTC	16604
QY	507	CTGAAATCATCTGCATCAGAACAAATTCACAACTCTTACTTTCTCTTCAAGTCG	566
DB	16603	CTGAAATCATCTGCATCAGAACAAATTCACAACTCTTACTTTCTCTTCAAGTCG	16544
QY	567	TTCCGGCTTCTCTGGATTTTCAGCTCTATACCTTCTAAACGCTGATAAAGTTTCTGTAAT	626
DB	16543	GTATTACAGTGACAGTTTCAGACGACAGCTATCAGTTGCTCAAGGCATATATGATGCAA	16484
QY	627	TTCTACTGTATCGACCTCGACGCTGGGTGTATTAAGGGAGCCTGACATTTATTTCCCC	686
DB	16483	TATCTCCGGTCTGTAAAGCACA---ACCATGCAGAAATGAAGCCGCTGCTGCGTGCC--	16429
QY	687	AGACATCAGGTTTAAATGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTT	746
DB	16428	-GAACGCTGGAAACGGGAAATTCAGGAAGGATGGCTGAGGTGCGCCCGGTTTATTGAAAT	16370

QY	747	CTTCCCGGATAACGAGACCGGCACACTGGCCATATCGTGGTCTCATATGCGCCAGCTTT	806
DB	16369	GAACGGCTCTTTTGTCTGACGAGAACAGGG-----ACTGGTGAAATGAGTTTAAAGTTT	16316
QY	807	CATCCCGCATATGCACACACCGGGTAAAGTTTCACGGGAGACTTTTATCTGACAGCAGCGT	866
DB	16315	ACACCTATAAAGAGAGAGCGGTATTCGTCTGTTTGTGATGTACAGAGTGATATTTTG	16256
QY	867	CACTGGCCAGGGGATACCACTCGCTCGCCCGGGGCTGTCAATAATATATCATCTCTGTACAT	926
DB	16255	ACACGCCCGGGCGACGAGTGTGTATCCCGCTGGCCAGTGCAGCTCTGTCTCAGATAAG	16196
QY	927	CCACAAACAGACGATAACGGCTCTCTCTTTATAGTGTAAACCTTAACTCACTTTTAC	986
DB	16195	TCCTCCGTAACCTTTACCGGTGGTGATATCGGGATGAAGCTGGCCCATGATGACCA	16136
QY	987	C-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAATTTCAATAAACCGGGGACC	1040
DB	16135	CGATATGGCCAGTGTGCGGTCTCCGTTATCGGGGAAGAGTGGCTGATCTTCAGCCACC	16076
QY	1041	TCAGCCATCCCTTCCTGATTTTCCGCTTTCAGCGCTC---GGCAGCAGACGAGGCT	1097
DB	16075	GGCAAAATGACATCAAAAACGCCATTAACCTGATGTCTGGGGAATATAAATGTGAGCT	16016
QY	1098	TCATTTCTGATGTTGTCTTACCCAGACCGGAGATATTGACATCATATATGCTTTGAGCA	1157
DB	16015	CCCTTATACAGCCAGCTTCGAGTTCGATACAGTAGAAATTTACAGAACTTTTATCACGT	15956
QY	1158	ACTGATAGCTGCGTGTCAACTGTCACTGTAAATAGC---CTGCTTTCATAGCACACTCT	1214
DB	15955	TTAGTAAGTATAGAGGCTGAAAATCCAGATGAAGCCGACACGACTTTGTAAGAGAAAGTAT	15896
QY	1215	TTTTGACATACCTTCGGGTAGTCCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCAG	1274
DB	15895	AAGAGTTGTGAATGGGTAGTCCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCAG	15836
QY	1275	GCTTCCCGGTATCAACAGGACACACAGGATTTTATTTATTTCTCGAAGTGATCTTCGTCA	1334
DB	15835	GCTTCCCGGTATCAACAGGACACACAGGATTTTATTTATTTCTCGAAGTGATCTTCGTCA	15776
QY	1335	CAGGTATTATTTCCGGCGAAAAGTGGTTCGGGTGATGCTGCCAACTTAGTCGACTACAGT	1394
DB	15775	CAGGTATTATTTCCGGCGAAAAGTGGTTCGGGTGATGCTGCCAACTTAGTCGACTACAGT	15716
QY	1395	CACTAATACATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGTGTTTACAGTATT	1454
DB	15715	CACATAACATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGTGTTTACAGTATT	15656
QY	1455	ATGATGCTCTGTTTTTATGCAAAAICTAAATTTAATAATATTTGATATTTATCATTTTACG	1514
DB	15655	ATGATGCTCTGTTTTTATGCAAAAICTAAATTTAATAATATTTGATATTTATCATTTTACG	15596
QY	1515	TTTCTGTTTCAGCTTTCTTGTAACAAAGTTGGCATTTATAGAGAGCACTTCTTATCAATTT	1574
DB	15595	TTTCTGTTTCAGCTTTCTTGTAACAAAGTTGGCATTTATAGAGAGCACTTCTTATCAATTT	15536
QY	1575	GTTGCAACGAAACAGGTCATCTCAGTCAAAAATAAATCAATTTTCCCATCCAGCTGCAG	1634
DB	15535	GTTGCAACGAAACAGGTCATCTCAGTCAAAAATAAATCAATTTTCCCATCCAGCTGCAG	15476
QY	1635	CTCCTCGAGGAATTCGGTACCCCGCTTGGTAAGGAA-----ATAATTATTTTC	1683
DB	15475	CTCCTCGAGGAATTCGGTACCCCGCTTGGTAAGGAA-----ATAATTATTTTC	15416
QY	1684	TTTTTTTCTTTTAGTATAAATAGTTTAAAGTGTAAATAGTATGATGATATATAATATA	1743
DB	15415	AATGTAAGATCAATGATATAACAAATGACATGATCTATCATGTTACCTTGTATTTCATGT	15356
QY	1744	GTTGTTTAAATTCGAAAAATAATTTATAAATAATATTTGTTTACATAAAAAACAATAGTAA	1803
DB	15355	TCGACTAATTCATTTTAAATTAAGTCAATCCATTTAGAGAGTTAATAAAACTACAGTATT	15296
QY	1804	TGTAATAAATAATGACAAAGTGTGTGTAAGACGAAGATAAAAGTTGAGAGTAAAGTAT	1863

Db	15295	ATTAGAAATTAATAAGAAATGTTGATGAAAATAATACTATATAAAATGAATAGATCTTGC	15236	Db	14226	AAGTATGTCAAAAGAGGCTGCTATGAA---GCAGGTATATACAGTGACAGTTGACAGC	14170
Qy	1864	ATTATTTTAAATGAATTTGATCGAATGTAAGATGATATACATAGCAATTAATTTGTTT	1923	Qy	2944	CTATACCTTAATAACAGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGG	3003
Db	15235	GCTTGTATATTAGCAATTAGATTATGTTTGTACATAGATTACTGTTTCTATTAGTT	15176	Db	14169	GACAGCTATCAGTTTGTCTCAAGGCATATATGATGTCAATATCTCCGGTCTGTGTAAGCAAA	14110
Qy	1924	TAATCATATAGTAATCTAGCTGTTTGAAGAAATTAATCAATGATTAATAACTATTA	1983	Qy	3004	CTGTGTATTAAGGGAGCTGACATTTATATCCCCAGAAACATCAGGTTAATCGCGCTTTTGTG	3063
Db	15175	TGATATATTTTACTTACTTGTATTTTAAATTTTGTATTTATTTGTTATTTGATTAATCAAGC	15116	Db	14109	CAATGCAATGAAGACCGCTGCTCTCGGTGCC---GAACGCTGGAAGCGGAATCAGG	14053
Qy	1984	GTAATAAATGAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2043	Qy	3064	ATGTCAITTTTCGGCTGCTGAGATCAGCCACTTTCTTCCCGATAACGAGAACCGGCACA	3123
Db	15115	AGATTGGAATTTCTCAACAAAATATTATTAACCTTTTAAACTAAATATTAGTAAATAGTTA	15056	Db	14052	AAGGATGGCTGAGTGCCTGGCTTTTATGAAATGAACGGCTCTTTTGTCTGACGAGAACA	13993
Qy	2044	AAATTAATATCTATACCATCTACTAATAATTTTAGTTTAAAGTTAATAAATTTTGTGA	2103	Qy	3124	CTGGCCATATCGGTGGTGCATCATGGCCAGCTTTTATCCCGATATGACACACCGGTTAA	3183
Db	15055	TAGATATTAAATTAATAATAAATAATTAATCAATAAATAAATAATTAATTTAATTTATTTA	14996	Db	13992	GGGA-----CTGTGAAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTAT	13939
Qy	2104	GAAATCCAAATCTGTTGTAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTA	2163	Qy	3184	AGTTTCAAGGAGACTTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGATCACCATCCGT	3243
Db	14995	TTCTTATTTTACTATAGTATTTTATCATTTGATTTTAAATCATCAACCGCTAGAATT	14936	Db	13938	CGTCTGTTTGTGGATGTACAGAGTGATATTATGACACGCCCGGCGAGGATGGTGATC	13879
Qy	2164	ACAAATAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGCT	2223	Qy	3244	CGCCGGCGGTGTCAATAATATCTCTGTACATCCACAAACAGACGATTAAGGCTCTCT	3303
Db	14935	ACTATTTATGATTAACAATAATTAATGCTAGTATATCATCTTACATGTTTCGATCAAAAT	14876	Db	13878	CCCTGGCCAGTGCACGCTCTGCTGTCTAGATAAAGTCTCCCGTGAACCTTTTACCGGTGGT	13819
Qy	2224	AAATTAACAAAGCGCAAGATCTATCAATTTATATAGTATATTTTCAATCAACATCTTAA	2283	Qy	3304	CTTTTATAGGTGTAACCTTAAACTTAACTGCAATTTTACCAGT-----CCCTGTTCTCGTCAGC	3357
Db	14875	CATTAAAAATAATATCTTACTCTCAACTTTTATCTTCTGCTTACACATCAGCTTGTCT	14816	Db	13818	CATATCGGGATGAAGCTGGCGCATGATGACACCGGATATGGCCAGTGTCCGCTCTCC	13759
Qy	2284	TTAATTTCTAAATAATCTGTTGATTTTATTAATCTTAAGTGGATGACTATTAATTA	2343	Qy	3358	AAAAAGAGCGTTTCAPTTCAATAAACCAGGCGCACTCAGCCATCCCTTCTGATTTTCGCG	3417
Db	14815	ATATTTTTTTACATTAATCTATGTTGTTTATGTAACAATAATTAATAAATTTTCTTCA	14756	Db	13758	GTATTCGGGGAAGAAGTGGCTGATCTCAGCCACCGCAAAATGACATCAAAAACCCCAT	13699
Qy	2344	ATGAAATAGTCGAACATGATAAACAAGGTAAACATGATAGATCATGCTCAATTTGTTTATCA	2403	Qy	3418	TTTCCAGCGTTC---GGCAGCAGCAGCAGCGGCTTCATCTGTCATGG---TTGTGCTTAC	3471
Db	14755	CAATTAACAACTATATTAATTAATATCACTAAATTAACATCACTTAACTATTATTATAC	14696	Db	13698	AACCTGATGTTCTGGGGAATATAAATGTGAGGCTCCCTTATACACAGCCAGTCTGCAAGT	13639
Qy	2404	TTGATCTTACATTTGGATGATTACAGTTGGGAGCTGGGTTGGAATCGATAGCTTGG	2463	Qy	3472	CAGACCGGAGATTTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTGCAACT	3531
Db	14695	TAAAAAGAAAAGAAATAATTA-----TTTCTTACCAGCTGGGGTACCGA	14647	Db	13638	CGATACAGTAGAANAATTACAGAACTTTATCAGTTTAGTATAGAGGCTGGAATCC	13579
Qy	2464	ATCCTCTAGAGAGCTGAGCTGCAATTAATGATTTTATTTTGTGACTGATGAGTACC	2523	Qy	3532	GTCACTGTAAATACGCTGCTCTATAGCACACCTCTTTTGTGACATATCTTCTTCTTGTATGC	3591
Db	14646	ATTCTCGAGAGCTGAGCTGGAATGCAATTAATGATTTTATTTTGTGCTGATGAGTACC	14587	Db	13578	AGATGAAGCCGAACGACTTGTGAAGAGAAAGTATAAGAGTTGTGAAATTTGTTCTTGTATGC	13519
Qy	2524	TGTTCTGTGCAAAATTTGATAAGCAATGCTTCTTATAATGCCAATTTTGTACAAGAA	2583	Qy	3592	AGATGATTTTACGACTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTCT	3651
Db	14586	TGTTCTGTGCAACAAATTTGATAAGCAATGCTTCTTATAATGCCAATTTTGTACAAGAA	14527	Db	13518	AGATGATTTTACGAGTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTCT	13459
Qy	2584	GCTGAACGAGAAAGTAAATGATATAAATATCAATATTAATTAATTAATTAATTAATTA	2643	Qy	3652	ACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAATACCGCAAT	3711
Db	14526	GCTGAACGAGAAAGTAAATGATATAAATATCAATATTAATTAATTAATTAATTAATTA	14467	Db	13458	ACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAATACCGCAAT	13399
Qy	2644	AAACAGACTACATAATCTGTAACAAACAAACATATCCAGTCACTATGAATCAACTACTTA	2703	Qy	3712	GAGGCAATAGCGAGTGGCTGGATACGACGATTCGTTTTGAGAGAAACATTTTGGAGGC	3771
Db	14466	AAACAGACTACATAATCTGTAACAAACAAACATATCCAGTCACTATGAATCAACTACTTA	14407	Db	13398	GAGGCAATAGCGAGTGGCTGGATACGACGATTCGTTTTGAGAGAAACATTTTGGAGGC	13339
Qy	2704	GATGGTATTAGTACCTGTAGTGCAGTAAAGTTGGCAGCATCACCCGAGCACTTTGGCC	2763	Qy	3772	TGTGGCTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTTGGAGGCTGTCCGTGCACT	3831
Db	14406	GATGGTATTAGTACCTGTAGTGCAGTAAAGTTGGCAGCATCACCCGAGCACTTTGGCC	14347	Db	13338	TGTGGCTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTTGGAGGCTGTCCGTGCACT	13279
Qy	2764	GAATTAATACCTGTGACGGAAGATCACTTCCAGATATAAATAAATCTGGTGTCCCTGTT	2823	Qy	3832	ACAGGTCACTAATACCATCTAAGTAGTGTGATTTAATTAATTAATTAATTAATTAATTA	3891
Db	14346	GAATTAATACCTGTGACGGAAGATCACTTCCAGATATAAATAAATAAATCTGGTGTCCCTGTT	14287	Db	13278	ACAGGTCACTAATACCATCTAAGTAGTGTGATTTAATTAATTAATTAATTAATTAATTA	13219
Qy	2824	GATACCGGAAGCCTGGGCCAACTTTTGGGAAAAATGAGAGCTTGTATCGGCATACCCA	2883	Qy	3892	AGTATTATGATGAGTCTGTTTTTANGCAAAATCTAATTAATTAATTAATTAATTAATTAAT	3951
Db	14286	GATACCGGAAGCCTGGGCCAACTTTTGGGAAAAATGAGAGCTTGTATCGGCATACCCA	14227	Db	13218	AGTATTATGATGAGTCTGTTTTTANGCAAAATCTAATTAATTAATTAATTAATTAATTAAT	13159
Qy	2884	TTTCAACACTCTTATACCTTTTCTCTTACAGTCTGCTTCTCATCTCGAATTTTCAAGCT	2943	Qy	3952	TTTACGTTCTCTGTTTCTGCTTTTGTACAAAGTTGGCATTTATAAAGGCAATTTGCTCAT	4011
				Db	13158	TTTACGTTCTCTGTTTCTGCTTTTGTACAAAGTTGGCATTTATAAAGGCAATTTGCTCAT	13099

QY 4012 CAATTGTGTGCAACGAAACAGGTCACTATCAGTCAAAATAAAATCAATTATTTGGGGCCCGA 4071
DB 13098 CAATTGTGTGCAACGAAACAGGTCACTATCAGTCAAAATAAAATCAATTATTTGGGGCCCGA 13039
QY 4072 GATCCATGCTAGC 4084
DB 13038 GATCCATGCTAGC 13026

RESULT 8

US-10-151-690-21
/ Sequence 21, Application US/10151690
/ Publication No. US2003012455A1
/ GENERAL INFORMATION:
/ APPLICANT: BRASCH, MICHAEL A.
/ APPLICANT: CHEO, DAVID
/ APPLICANT: LI, XIAO
/ APPLICANT: ESPOSITO, DOMINIC
/ APPLICANT: BYRD, DEVON R.N.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
/ FILE REFERENCE: 0942.5120001
/ CURRENT APPLICATION NUMBER: US/10/151,690
/ CURRENT FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 10/151,690
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/291,973
/ PRIOR FILING DATE: 2001-05-21
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 21
/ LENGTH: 4470
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: plasmid pDONR201
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (29)..(260)
/ OTHER INFORMATION: attcpl
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (656)..(961)
/ OTHER INFORMATION: ccdb
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1099)..(1184)
/ OTHER INFORMATION: ccda
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1303)..(1962)
/ OTHER INFORMATION: cmr
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2210)..(2442)
/ OTHER INFORMATION: attbp2
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2565)..(3374)
/ OTHER INFORMATION: kmr
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (3495)..(4134)
/ OTHER INFORMATION: ori
US-10-151-690-21

Query Match 24.8%; Score 1207.4; DB 15; Length 4470;
Best Local Similarity 99.9%; Pred. No. 3.9e-175;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGGTAGCATGATCTCGGGCCCAATAATGATTTTATTTGACTGATAGTACCTGTT 84
DB 5 ACGTAGCATGATCTCGGGCCCAATAATGATTTTATTTTGGACTGATAGTACCTGTT 64

QY 85 CGTTGCAACAAATTTGATGAGCAATGCCTTTTATAAATGCCAACTTTGTACAAAAAGCTG 144
DB 65 CGTTGCAACAAATTTGATGAGCAATGCCTTTTATAAATGCCAACTTTGTACAAAAAGCTG 124
QY 145 AACGAGAAACCGTAAATATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAC 204
DB 125 AACGAGAAACCGTAAATATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAC 184
QY 205 AGACTACATAATATCTGTAAAAACACAAATATCCAGTCACTATGAATCAACTACTTAGATG 264
DB 185 AGACTACATAATATCTGTAAAAACACAAATATCCAGTCACTATGAATCAACTACTTAGATG 244
QY 265 GTATTAGTACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGGTGATGCTGCCAA 324
DB 245 GTATTAGTACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGGTGATGCTGCCAA 304
QY 325 CTTAGTCGACCGACAGCCTTCCAAATGTTCTTCCTCAACCGGAATCGTGTATCCAGCCTA 384
DB 305 CTTAGTCGACCGACAGCCTTCCAAATGTTCTTCCTCAACCGGAATCGTGTATCCAGCCTA 364
QY 385 CTCGCTATTGCTCAATGCGGTATTAAATCATAAAAAGAAATAGAAAAAGAGTGGCA 444
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DB 545 CGTTGGGCTTCATCTGGGATTTTCAGCCTCTACTTACTTAAACGATAGATTTCTGTA 604
QY 625 ATTTCTACTGTATCGACCTGACAGACTGGCTGTGTATAAGGGAGCCTGCATTTATTTCC 684
DB 605 ATTTCTACTGTATCGACCTGACAGACTGGCTGTGTATAAGGGAGCCTGCATTTATTTCC 664
QY 685 CCAGAAATCATAGTTAATGGCGTTTTTGTATGATCTTTTCGCGGTGCTGTAGATCAGCCAC 744
DB 665 CCAGAAATCATAGTTAATGGCGTTTTTGTATGATCTTTTCGCGGTGCTGTAGATCAGCCAC 724
QY 745 TTCTTCCCGATAACGAGACCGGACACCTGCCATATCGTGGTCACTCATCGCCAGCT 804
DB 725 TTCTTCCCGATAACGAGACCGGACACCTGCCATATCGTGGTCACTCATCGCCAGCT 784
QY 805 TTTCATCCCCGATATGCACACCGGGTAAAGTTTACGGGAGACTTTTATCTGACAGCAGCG 864
DB 785 TTTCATCCCCGATATGCACACCGGGTAAAGTTTACGGGAGACTTTTATCTGACAGCAGCG 844
QY 865 TGACCTGGCCAGGGGATCACCATCGTCCCGGGCGTGTCAATAATATCTCTGTAC 924
DB 845 TGACCTGGCCAGGGGATCACCATCGTCCCGGGCGTGTCAATAATATCTCTGTAC 904
QY 925 ATCCCAAAACAGACGATTAACGGCTCTCTTTTATAGGTGTAAACCTTAAACCTGATTTTC 984
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QY 985 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAATTTCAATAAACCAGGAGCCTCAG 1044
DB 965 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAATTTCAATAAACCAGGAGCCTCAG 1024
QY 1045 CCATCCCTCTCTGATTTTCCGGCTTTCCAGCGTTCGACGACGACCGGGCTTCATTTCT 1104
DB 1025 CCATCCCTCTCTGATTTTCCGGCTTTCCAGCGTTCGACGACGACCGGGCTTCATTTCT 1084
QY 1105 GCATGGTGTGCTTACAGACCGGAGATATGACATCATATATGCTTTCAGCAACTGATA 1164
DB 1085 GCATGGTGTGCTTACAGACCGGAGATATGACATCATATATGCTTTCAGCAACTGATA 1144


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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match      24.7%; Score 1201; DB 15; Length 4428;
Best Local Similarity 99.6%; Pred. No. 3.7e-174;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGGCCCCCAATAATAGATTTTATTTGACGTAGTAGCACTGTT 84
Db 842 ACCTAGCATGATCTCGGGCCCCCAATAATAGATTTTATTTGACGTAGTAGCACTGTT 901
QY 85 CGTTGCAACAAATGTAGTACGATGCTTTTATATATGCAACTTTTGTACAAAAGCTG 144
Db 902 CGTTGCAACAAATGTAGTACGATGCTTTTATATATGCAACTTTTGTACAAAAGCTG 961
QY 145 AACGAAACGTAATAATGATATATCAATATATTAATTAATTAATTAATTAATTAATTA 204
Db 962 ATATCGAAACGTAATAATGATATATCAATATATTAATTAATTAATTAATTAATTAATTA 1021
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Db 1622 TTATCTCCCGATATGACACCGGGTAAAGTTCAAGGAGCTTTATCTGACAGCAGCG 1681
QY 865 TGCACTGGCCGAGGGGATCACCATTCGTCGCGCGGGGCTGCAATATATCACTCTGTAC 924
Db 1682 TGCACTGGCCGAGGGGATCACCATTCGTCGCGCGGGGCTGCAATATATCACTCTGTAC 1741
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RESULT 12
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942 5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63
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Query Match      24.6%; Score 1194.6; DB 15; Length 4627;
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 ATGGATCTCGGGCCCCCAATAATAGATTTTATTTGACGTAGTAGCACTGTTGTCGAA 92
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QY 93 CAAATTTGATGAGCAATGCTTTTATATATGCAACTTTTGTACAAAAGAGCTGAACGAA 152
Db 61 CAAATTTGATGAGCAATGCTTTTATATATGCAACTTTTGTACAAAAGAGCTGAATCGAA 120
QY 153 ACGTAAATGATATATAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTA 212
Db 121 ACGTAAATGATATATAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTA 180
QY 213 TAATCTGTAAACACACATATCCAGTCACTATGAATCAACTACTTATAGATGTTAGT 272
Db 181 TAATCTGTAAACACACATATCCAGTCACTATGAATCAACTACTTATAGATGTTAGT 240
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Db 661 TCAGGTTAATGGCGTTTTCATGTCAATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCC 720
QY 753 CGATAACGGAGACCGGCACACTCGGCATATCGGTGTCATCATGCGCCAGCTTTCATCCC 812
Db 721 CGATAACGGAGACCGGCACACTCGGCATATCGGTGTCATCATGCGCCAGCTTTCATCCC 780
QY 813 CGATATGCACACCGGTTAAAGTTTCAAGGAGACTTTATCTGACAGCAGAGCTGCACTGG 872
Db 781 CGATATGCACACCGGTTAAAGTTTCAAGGAGACTTTATCTGACAGCAGAGCTGCACTGG 840
QY 873 CCGAGGGGATCACCATCCGTCGCGCGCGGTGTCATATATCACTCTGTACATCCACAA 932
Db 841 CCGAGGGGATCACCATCCGTCGCGCGCGGTGTCATATATCACTCTGTACATCCACAA 900
QY 933 ACAGACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACCACTCC 992
Db 901 ACAGACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACCACTCC 960
QY 993 CTGTTCTGTCAGCAAAAGCGGTTTCATTTCAATAAACCGGCGACCTCAGCCATCCCT 1052
Db 961 CTGTTCTGTCAGCAAAAGCGGTTTCATTTCAATAAACCGGCGACCTCAGCCATCCCT 1020
QY 1053 TCCTGATTTTCGGTTTCCAGCGTTCCGACGCGTCCGACGAGCGGCTTCATTTCTCATGGTT 1112
Db 1021 TCCTGATTTTCGGTTTCCAGCGTTCCGACGCGTCCGACGAGCGGCTTCATTTCTCATGGTT 1080
QY 1113 GTGCTTACACGACCGGAGATATTGACATCATATATGCTTTGAGCACTGATAGCTGCGC 1172
Db 1081 GTGCTTACACGACCGGAGATATTGACATCATATATGCTTTGAGCACTGATAGCTGCGC 1140
QY 1173 TGTCACCTGTCATGTAATGCTGCTTCTATAGCACAACCTCTTTTGTGACATCTTCGGGT 1232
Db 1141 TGTCACCTGTCATGTAATGCTGCTTCTATAGCACAACCTCTTTTGTGACATCTTCGGGT 1200
QY 1233 A 1233
Db 1201 A 1201

RESULT 14
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 24.1%; Score 1174.2; DB 15; Length 17681;
Best Local Similarity 59.5%; Pred. No. 8e-170;
Matches 2327; Conservative 0; Mismatches 1508; Indels 78; Gaps 17;

QY 122 GCCAACTTGTACAAAAGCTGAACGAGAAACGTAATGATATATATCAATATTT 181
Db 16904 GACAGTTTGTACAAAAGCTGAACGAGAAACGTAATGATATATATCAATATTT 16845

QY 182 AAATTAGATTTCATATAAAACAGACTACATATACTGTAAACACACATATCCAGTC 241

Db 16844 AAATTAGATTTCATATAAAACAGACTACATATACTGTAAACACACATATCCAGTC 16785
QY 242 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACCGACGAGCTTCCAAA 301
Db 16784 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACCGACGAGCTTCCAAA 16725
QY 302 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTCTTCTCAA 361
Db 16724 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTCTTCTCAA 16665
QY 362 ACGGATCGTCATCCAGCTTACTCGGTATGTCCTCAATGCGGTATTAAATCATATAAA 421
Db 16664 ACGGATCGTCATCCAGCTTACTCGGTATGTCCTCAATGCGGTATTAAATCATATAAA 16605
QY 422 AGAAATAAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATCTACCT 481
Db 16604 AGAAATAAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATCTACCT 16545
QY 482 ATTATATACGCTAGTGTCTGTAATCATCTGCAATCATCTGCAATCAAGAAATTTCAAAAC 541
Db 16544 ATTATATACGCTAGTGTCTGTAATCATCTGCAATCATCTGCAATCAAGAAATTTCAAAAC 16485
QY 542 TCTTATACCTTTCTCTTACAAGTCTGTCGGCTTCTGGAATTTTCAGCCTCTATATCTTA 601
Db 16484 AAAAAGAGGTGCTGTAAGAA---GCAGCCTATTAAGTGAAGTGAACAGCAGCTAT 16428
QY 602 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 661
Db 16427 CAGTTGCTCAAGGCATATATGATGTCATATCTCGGTCTGTGTAAGCAACACCTGCGA 16368
QY 662 AGGAGCCTGACATTTATATCCCGACAGAAATCAGGTTAATGCGGTTTGTGATGATTT 721
Db 16367 ATGAAGCCCGTCTGTCGGTGC---GAAAGCTGAAAAGCGGAAATCAGGAAGGATGG 16311
QY 722 TCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGAGACCGGACACTGCGCCATA 781
Db 16310 CTGAGGTGCGCGGTTTATGAAATGAAAGGCTCTTTTGTGACGAGAACAGGG----- 16257
QY 782 TCGGTGTCATATGCGCGAGCTTTTATCCCGATATGACCCAGGTTAAAGTTTCAAGG 841
Db 16256 ACTGGTGAATGCAAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTTATGCTGTGTT 16197
QY 842 GAGACTTTATCTGACAGCAGACGTCGACCTGGCCAGGGGATCACCATCGTCGCCCGGG 901
Db 16196 GTGGATGTACAGAGTATATTAATGACAGCCCGGCGGACCGGATGGTATGCCCTGGCC 16137
QY 902 GTGTCAATAATATCACTCTGTATACATCCACAAACAGACGATACGGCTCTCTCTTTATAG 961
Db 16136 AGTGACGCTGCTGTGACATAAAGTCTCCCGTGAACCTTTACCCGGTGTGTCATATCGG 16077
QY 962 GTGTAAACCTTAACTGCAATTTACG-----AGTCCCTGTTCTGTCAGCAAAAGAGCC 1015
Db 16076 GATGAAGCTGGCGCATGATGACCCAGGATATGGCCAGTGTGCGGTCTCCGTTATCGG 16017
QY 1016 GTTCTATTTCAATAAACCGGCGACCTCAGCCATCCCTCTGATTTTCCGCTTTCCAGCG 1075
Db 16016 GAAGAAGTGGCTGATCTGAGCCACCGGAAATGACATCAAAACGCCATTAACCTGATG 15957
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Db 15956 TTCGGGGAATATAAATGTACAGGCTCCCTTATACAG-----CCAGTCTGAGGT 15906
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QY	3757	GAACTTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAAGACATTTGGAA	3816
Db	13257	GAACTTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAAGACATTTGGAA	13198
QY	3817	GGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTACTGGA	3876
Db	13197	GGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTACTGGA	13138
QY	3877	TATGTTGTGTTTTACAGTATATGATAGTCTGTTTTTATGCAAAATCTAATTAATATAT	3936
Db	13137	TATGTTGTGTTTTACAGTATATGATAGTCTGTTTTTATGCAAAATCTAATTAATATAT	13078
QY	3937	TGATATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTGTGTAAGTTGGC	3989
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Job time : 1354.69 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7543.25 Seconds
(without alignments)
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Title: US-10-055-001B-23_COPY_13000_17862

Perfect score: 4863

Sequence: 1 ttctattggagaggacacg.....atagtgtaacataatcgc 4863

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:**

3: em_estin:**

4: em_estmu:**

5: em_estrov:**

6: em_estpl:**

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9: gb_est1:**

10: gb_est2:**

11: gb_hic:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pin:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gsl1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	518.4	10.7	698	29	AG012840 Homo sapi
C 2	496.6	10.2	713	29	AG000762 Homo sapi
3	437.2	9.0	542	14	CD109790 AGNCOURT
C 4	411.8	8.5	723	29	AG000761 Homo sapi

C	5	408.4	8.4	725	29	AG013450
	6	404	8.3	522	14	CB997937
C	7	398.4	8.2	722	29	AG000763
C	8	357	7.3	487	14	CB395230
C	9	347.4	7.1	487	14	CB395230
C	10	340.2	7.0	384	12	BI174407
C	11	325.4	6.7	384	12	BI174407
C	12	301.4	6.2	337	12	BJ555980
C	13	273.2	5.6	1068	14	CF469981
C	14	271.8	5.6	1037	14	CF469119
C	15	264.4	5.4	724	29	AG000791
C	16	262.4	5.4	816	14	CF469496
C	17	257.4	5.3	557	12	BG220129
C	18	255.8	5.3	656	14	CK291800
C	19	254	5.2	569	14	CF469084
C	20	252.4	5.2	819	14	CF469247
C	21	247.4	5.1	320	29	CG206516
C	22	246	5.1	329	28	BH739300
C	23	245.4	5.0	1041	14	CF468941
C	24	243.6	5.0	1035	14	CF470036
C	25	242.8	5.0	1017	14	CF470004
C	26	239.2	4.9	659	14	CK287298
C	27	235.6	4.8	859	14	CF468865
C	28	234.8	4.8	506	14	CF468964
C	29	234.8	4.8	657	14	CF468948
C	30	230.2	4.7	712	28	AQ990809
C	31	230.2	4.7	712	28	AQ990809
C	32	229	4.7	628	14	CF469215
C	33	227.2	4.7	968	14	CF469474
C	34	220	4.5	583	14	CB403882
C	35	220	4.5	583	14	CB403882
C	36	215.2	4.4	393	14	CB403984
C	37	215.2	4.4	393	14	CB403984
C	38	215.2	4.4	1020	14	CF469337
C	39	214.6	4.4	1017	14	CF468787
C	40	214.2	4.4	1042	14	CF468958
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.
ACCESSION AG012840
VERSION AG012840.1 GI:3435047
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

698 bp DNA linear GSS 08-FEB-1999
f65H12X16, genomic

Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="21"
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ORIGIN

Query Match 10.7%; Score 518.4; DB 29; Length 698;
Best Local Similarity 98.9%; Pred. No. 1.1e-81;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 675 TTTATATATCCCGAGACATCAGGTTAAATGGCGTTTTGATGTCATTTTCGGCGTGGCTGA 734
Db 34 TTTATATATCCCGAGACATCAGGTTAAATGGCGTTTTGATGTCATTTTCGGCGTGGCTGA 93
QY 735 GATCAGCCACTTCTTCCCGGATAACGGAGACGGGACACTGGCCATATCGGTGTCATCA 794
Db 94 GATCAGCCACTTCTTCCCGGATAACGGAGACGGGACACTGGCCATATCGGTGTCATCA 153
QY 795 TCGCGCAGCTTTTCATCCCGGATATGACCCACCGGGTAAAGTTTCAAGGGAGACTTTATCTG 854
Db 154 TCGGCCA-NTTTCATCCCGGATATGACCCACCGGGTAAAGTTTCAAGGGAGACTTTATCTG 212
QY 855 ACAGCAGCGTGCATGGCCAGGGGATCAACATCGTCCCGCGGCGGTGTCATTAATAT 914
Db 213 ACAGCAGCGTGCATGGCCAGGGGATCAACATCGTCCCGCGGCGGTGTCATTAATAT 272
QY 915 CACTCTGTATACCCACACACAGCATACGGCTCTCTCTTTTATAGGTGTAACCTTAA 974
Db 273 CACTCTGTATACCCACACACAGCATACGGCTCTCTCTTTTATAGGTGTAACCTTAA 332
QY 975 ACTGCATTTTCAACGAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAATTAACCGG 1034
Db 333 ACTGCATTTTCAACGAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAATTAACCGG 392
QY 1035 GCGACTCAGCATCCCTTCTGATTTTCGCTTTCAGCGTTCGCGACGACGACGAG 1094
Db 393 GCGACTCAGCATCCCTTCTGATTTTCGCTTTCAGCGTTCGCGACGACGACGAG 452
QY 1095 GCTTCAATCTGATGTTGCTGTACACGACGGGATATGACATCATATATGCTTGA 1154
Db 453 GCTTCAATCTGATGTTGCTGTACACGACGGGATATGACATCATATATGCTTGA 510
QY 1155 GCAACTGATAGCTGCTGTCACTGTCACTGTATACGCTGCTTCAATAGCACCTCT 1214
Db 511 GCAACTGATAGC-GTCCGTCACTGTCACTGTATACGCTGCTTCAATAGCACCTCT 569
QY 1215 TTTTGACATCTCCGGTA 1233
Db 570 TTTTGACATCTCCGGTA 588

RESULT 2
AG000762/c 713 bp DNA linear GSS 06-FEB-1999
LOCUS AG000762.1 GI:2579570
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.

ACCESSION AG000762

VERSION AG000762.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in Database (1997)

2 (bases 1 to 713)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Direct Submission

Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@sc.ims.u-tokyo.ac.jp)

Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
source

Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="64E11X4"

ORIGIN

Query Match 10.2%; Score 496.6; DB 29; Length 713;
Best Local Similarity 94.2%; Pred. No. 7.9e-78;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

QY 679 TATTCCCGAGAACATCAGGTTAAATGGCGTTTTGATGTCATTTTCGGCGTGGCTGAGATC 738
Db 599 TATATCCCGGANCATCNGTTAAATGGCGTTTTTGAAGGNATTTTCGGCGTGGCTGAGAA 540
QY 739 AGCCACTTCTTCCCGGATAACGGAGACGGGACACTGSCCATATCGGTGTCATCATCGC 798
Db 539 CACCAACTTTTCCGATTACGNAGACGGGACACTGNCATATCGGTGTCATCATCGC 480
QY 799 CCAGCTTTTATCCCGGATATGACCCACCGGGTAAAGTTTCAAGGGAGACTTTTATCTGAC 858
Db 479 CCAGCTTTTATCCCGGATATGACCCACCGGGTAAAGTTTCAAGGGAGACTTTTATCTGAC 420
QY 859 CAGAGTGCTACGCGGCGGATCACCATCGTCCCGCGGCGGTGTCATTAATATCACT 918
Db 419 CAGAGTGCTACGCGGCGGATCACCATCGTCCCGCGGCGGTGTCATTAATATCACT 360
QY 919 CTGTACATCCCAACACAGCATAAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTG 978
Db 359 CTGTACATCCCAACACAGCATAAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTG 300
QY 979 CATTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCAATTAACCGGGCGA 1038
Db 299 CATTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCAATTAACCGGGCGA 240
QY 1039 CCTCAGCATCCCTTCCGATTTTCCGCTTTCAGCGTTCGCGACGACGACGCGGCT 1098
Db 239 CCTCAGCATCCCTTCCGATTTTCCGCTTTCAGCGTTCGCGACGACGACGCGGCT 180
QY 1099 CATTCGATGTTGTTGTTTACACGACGGAGATTTGACATCATATATGCTTGGAGCAA 1158
Db 179 CATTCGATGTTGTTTACACGACGGAGATTTGACATC--ATATGCTTGGAGCAA 122
QY 1159 CTGATAGCTGCGTGTCACTGTCACTGTAAATAGCTGCTTCAAGCACACTCTTTT 1218
Db 121 CTGAATANTGTGCTGTCACTGTCACTGTAAATAGCTGCTTCAAGCACACTCTTTT 62
QY 1219 GACATCTTCGGGTA 1233
Db 61 GACATCTTCGGGTA 47

RESULT 3

CD109790

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

CD109790 542 bp mRNA linear EST 15-MAY-2003
AGENCOURT_13988518 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30346919 5', mRNA sequence.

CD109790

CD109790.1

GI:30753999

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:
 http://image.llnl.gov
 Plate: NDAM387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.
 Location/Qualifiers
 1. 542
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 /clone="IMAGE:30346919"
 /tissue_type="Human Placenta"
 /lab_host="PH108 TonA"
 /clone_lib="NIH MGC 147"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
 ali-XhoI; Site_2: BamH; Oligo-dr primed using primer
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 insert size 2.3 kb and normalized to R07 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

ORIGIN

Query Match 9.0%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 2.7e-67;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

QY 642 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 701
 Db 23 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGTAA 82
 QY 702 TGGCGTTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCATCTTCCCGATAACGG 761
 Db 83 TGGCGTTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCATCTTCCCGATAACGG 142
 QY 762 AGACGGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGCA 821
 Db 143 AGACGGGCACACTGGCCATATCGGTGGTCATCATGCGTCAGCTTTTCATCCCGATATGCA 202
 QY 822 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 881
 Db 203 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 262
 QY 882 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGACGAT 941
 Db 263 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGACGAT 322
 QY 942 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCACTTTACCAAGTCCCTGTCTCG 1001
 Db 323 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCACTTTACCAAGTCCCTGTCTCG 382
 QY 1002 TCAGCAAAAGAGCCGTTCAATTAACACCGGGGACCTCAGCCATCCCTTCCTGATT 1061
 Db 383 TCAGCAAAAGAGCCGTTCAATTAACACCGGGGACCTCAGCCATCCCTTCCTGATT 442
 QY 1062 TCGCTTTTCCA-GCGTTCGGCAGCAGAGC-ACGGGCTTCATTC--TGCATGTTGTGCT 1117
 Db 443 TCCCTTTCCACGTTTTTCGGCAGCAGAGCAGCGGCTTCATTCCTGCAAGGTTGTGCT 502
 QY 1118 TACCAGACCGG-AGATATTGACATCATATATGCTT 1152
 Db 503 TACCAGACCGGAGATATTGACATCATATATGCTT 538

RESULT 4

AG000761/c
 LOCUS AG000761 Homo sapiens genomic DNA, 723 bp DNA linear GSS 06-FEB-1999
 DEFINITION survey sequence.
 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Homo sapiens genomic DNA, chromosome 21q
 Published Only in Database (1997)
 2 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Direct Submission
 Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
 Location/Qualifiers
 1. 723
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="64B11X4"

ORIGIN

Query Match 8.5%; Score 411.8; DB 29; Length 723;
 Best Local Similarity 98.1%; Pred. No. 7.7e-63;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 642 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 701
 Db 450 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 391
 QY 702 TGGCGTTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCATCTTCCCGATAACGG 761
 Db 390 TGGCGTTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCATCTTCCCGATAACGG 331
 QY 762 AGACGGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGCA 821
 Db 330 AGACGGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATATGCA 271
 QY 822 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 881
 Db 270 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 211
 QY 882 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGACGAT 941
 Db 210 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGACGAT 151
 QY 942 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCACTTTACCAAGTCCCTGTCTCG 1001
 Db 150 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCACTTTACCAAGTCCCTGTCTCG 91
 QY 1002 TCAGCAAAAGAGCCGTTCAATTAACACCGGGGACCTCAGCCATCCCTTCCTGATT 1061
 Db 90 TCAGCAAAAGAGCCGTTCAATTAACACCGGGGACCTCAGCCATCCCTTCCTGATA 31
 QY 1062 TCCG 1065
 Db 30 TCAG 27

RESULT 5

AG013450/c
 LOCUS AG013450 Homo sapiens genomic DNA, 725 bp DNA linear GSS 14-APR-1999

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999, this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
FEATURES             Location/Qualifiers
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Query Match      8.4%; Score 408.4; DB 29; Length 725;
Best Local Similarity 90.2%; Pred. No. 3.1e-62;
Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;

QY 676 TTATATTCCTCCAGAAACATCAGGTTAATGGGTTTTTGGTGTCTCTCTTTTATGTCATTTTCGGGTGGCTGAG 735
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QY 736 ATCAGGCATCTTCTCCCGATACGAGACCGGCACACTGGGCCATATCGTGGTGTATCAT 795
DB 663 ATCAGCNANTTTTCCCGAATANGNAGACGGCACANTGCCNATATFCNGTGTTCATCAT 604
QY 796 GGCACAGCTTTCATCCCGATATGCACACCGGGTAAGTTCACGGAG-ACCTTATCTG 854
DB 603 GGCACAGCTTTCATCCCAATA-GCACACGGGGTAANGTTTCAGGGAGAACTTTATCTG 545
QY 855 ACAGCAGACGTGCATCGGCC-AGGGGGATCACCATCCGTGCGCCGGCGGTGCAATAATA 913
DB 544 ACAGCAGACGTGCATCGGCCAAGGGGGATCACCATCCGTGCGCGGTGTC-ATANTA 486
QY 914 TCACCTGTGACATCCGCAACACAGACATACGGCTCTCTCTTTATAGGTGTAACCTTA 973
DB 485 TCACCTGTGACATCCGCAACACAGACATACGGCTCTCTCTTTATAGGTGTAACCTTA 427
QY 974 AACTGCATTTACACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCG 1033
DB 426 AACTGCATTTACACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCG 367
QY 1034 GGCAGCTCAGGCATCCCTTCTGTATTTTCCGTTTCCAGCGGTTCGCGACGCGAGACG 1093
DB 366 GGCAGCTCAGGCATCCCTTCTGTATTTTCCGTTTCCAGCGGTTCGCGACGCGAGACG 307
QY 1094 GGCTTCATCTGATGGTTGTGCTTACGACCGGAGATATTGACATCATATATGCTTG 1153
DB 306 GGCTTCATCTGATGGTTGTGCTTACGACCGGAGATATTGACATC--ATATGCTTG 249
QY 1154 AGCAACTGATAGTGTGCTGTCAACTGTCTGTAATAGCTGTCTTCATAGCACACCTTC 1213
DB 248 AGCAACTGATA-NGTGCTGTCTCAACTGTCTGTAATAGCTGTCTTCATAGCACACCTTC 190
QY 1214 TTTTGGACATACTTCGGGTA 1233

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Db 189 TTTTGGACATACTTCGGGTA 170
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CB997937 522 bp mRNA linear EST 01-MAY-2003
AGENCOURT 13894516 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
CB997937.1 GI:30292457
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.
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                     /lab_host="DH10B Tona"
                     /clone_lib="NIH_MGC_148"
                     /note="Organ: placenta; Vector: pBluescriptR; Site 1:
                     ali-XhoI; Site 2: BamHI; Library is oligo-dT primed and
                     directionally cloned using primer
                     5'-TTTGTGTTTGTGTTT-3', size-selected for average insert
                     size 2.3 kb and normalized to 5x. This is a primary
                     library enriched for full-length clones and constructed
                     using the Cap-trapper method (Carninci, in preparation).
                     Library constructed by M. Brownstein (NIH/NHGRI,
                     National Institutes of Health). Note: this is a NIH_MGC
                     Library."

ORIGIN
Query Match      8.3%; Score 404; DB 14; Length 522;
Best Local Similarity 96.2%; Pred. No. 2.1e-61;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 642 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGACATCATGTTAA 701
DB 23 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGACATCATGTTAA 82
QY 702 TGGCGTTTTCATGTCATTTTCGGGTGGCTGAGATCAGCACATTTCTTCCCGATAACGG 761
DB 83 TGGCGTTTTCATGTCATTTTCGGGTGGCTGAGATCAGCACATTTCTTCCCGATAACGG 142
QY 762 AGACCGGCACACTGCCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCGATATGCA 821
DB 143 AGACCGGCACACTGCCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCGATATGCA 202
QY 822 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGACAGACGTGACATGCGCCAGGGGA 881
DB 203 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGACAGACGTGACATGCGCCAGGGGA 262

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QY 882 TCACCATCGTCGCGCGCGGTGTCATTAATATCACTCTGTACATCCACAAACAGCAT 941
Db 263 TCACCATCGTCGCGCGCGGTGTCATTAATATCACTCTGTACATCCACAAACAGCAT 322
QY 942 AACGGCTCTCTCTTTATAGGTGTAACACTTAAAGTTCATTTTCCAGGTCCCTGTTCTCG 1001
Db 323 AACGGCTCTCTCTTTATAGGTGTAACACTTAAAGTTCATTTTCCAGGTCCCTGTTCTCG 381
QY 1002 TCAGCAAAAGACCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCC-TTCTGATT 1060
Db 382 TCAGCAAAAGACCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCC-TTCTGATT 441
QY 1061 TTCCGCTTTCCAGCGTTCGCGACGAGACGAC 1092
Db 442 TTTCGCTTTCCAGCGTTCGCGACGAGAC 473

RESULT 7
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LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
DEFINITION AG000763
ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLES Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLES Direct Submission
JOURNAL Submitted (31-OCT-1997) Maehira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagami-hara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES
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        /mol_type="genomic DNA"
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        /map="21q"
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ORIGIN
    Query Match 8.2%; Score 398.4; DB 29; Length 722;
    Best Local Similarity 92.2%; Pred. No. 1.8e-60;
    Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 697 GTTAATGGCGTTTGTGATGTCATTTTCGCGGTGGTGGATCAGGCACATTCCTCCCGAT 756
Db 722 GTTAAGGCTTTTGGANGCAATTTGCGGTGGC---GAGATCCCAATTTTCCCGA 667
QY 757 AACGAGACCGGCACACTCGGCATATTCGGTGGTGTATCATGCGCGACGTTTCATCCCGAT 816
Db 666 TAAGGAGACCGGCACA-TGGCCATAACGGTGGTGTATCA-CGCGCAGCTTCA-CCCGCAT 610
QY 817 ATGCACACCGGTAAAGTTCAGGAGACTTTATCTGTACACAGACGNGCACTGGCCAG 876
Db 609 ATGCACACCGGNTAAAGTTCAGGAGACTTTAACGACAGACGAGTGCATGCCCGAG 550
QY 877 GGGGATCACCATCCGTCGCGCGGGCGTGTCAATAATATCACTGTGTACATCCACAAACAG 936
Db 549 GGAATCACCATCCGTCGCGCGGGCGTGTCAATAATATCACTGTGTACATCCACAAACAG 490
QY 937 ACGATAACGGCTCTCTCTTTATAGGTGTAACCTTAAACCTGATTTACACGATCCCTGTT 996

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Db 489 ACGATAACGGCTCTCTCTTTATAGGTGTAACCTTAAACCTGATTTTACCAGTCCCTGTT 430
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Db 429 TCTCGTCAAGC-AAAGACGCGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCT 371
QY 1057 GATTTTCCGCTTCCAGGTTCCGCGACGACGACGACGCGCTTCATTCGCAATGGTGGC 1116
Db 370 GATTTTCCGCTTCCAGGTTCCGCGACGACGACGACGCGCTTCATTCGCAATGGTGGC 311
QY 1117 TTACCAGACCGGAGATATTGACATCATATATGCTTTCAGCAACTGATAGCTGTCTGCTGC 1176
Db 310 TTACCAGACCGGAGATATTGACATC--ATATGCTTTCAGCAACTGATAG-TGTGCTGTC 254
QY 1177 AACTGTCTCTGTATATACGCTGCTTCATAGCAACCTCTTTTTCAGCATCTTCGGGTA 1233
Db 253 AACTGTCTCTGTATATACGCTGCTTCATAGCAACCTCTTTTTCAGCATCTTCGGGTA 197

RESULT 8
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LOCUS CB395230
DEFINITION OSTR151B2_1 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lanesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
TITLES C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
    Marc Vidal Laboratory
    Dana Farber Cancer Institute
    1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
    Tel: 617 632 5180
    Fax: 617 632 5739
    Email: Marc.Vidal@dfci.harvard.edu
    Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project; Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
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FEATURES
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        /tissue type="whole animal"
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        /clone lib="AD-wrmCDNA"
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ORIGIN
    Query Match 7.3%; Score 357; DB 14; Length 487;
    Best Local Similarity 93.6%; Pred. No. 4.3e-53;
    Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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156 TAAATGATATATATCAATATATATAATTTGATTTTGCATATAAAACAGACTACATA 215
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216 TACTGTAACACACACATATCCAGTCACATGATGAATCAACTACTAGATGTTATAGTAC 275
Db      TACTGTAACACACACATATCCAGTCACATGATGAATCAACTACTAGATGTTATAGTAC 368
276 CTGTAGTCGACGACGACGCTTCCAAATGTTCTTCGAGGATCGTCTACTCGCTATTGT 395
Db      CTGTAGTCGACGACGACGCTTCCAAATGTTCTTCGAGGATCGTCTACTCGCTATTGT 428
336 GACAGCCTTCCAAATGTTCTTCGAGGATCGTCTACTCGCTATTGT 395
Db      GACAGCCTTCCAAATGTTCTTCGAGGATCGTCTACTCGCTATTGT 428
396 CCTCAATGCGGTATTAATCATATAAAAGAAATGAAGAGAGGTCGAGCCTCTTTTTT 455
Db      CCTCAATGCGGTATTAATCATATAAAAGAAATGAAGAGAGGTCGAGCCTCTTTTTT 488
456 GTGTGACAAATAAAACATCTAC-CTATTTCATATAGCTAGTCTCATAGTCTGAAAT 514
Db      GTGTGACAAATAAAAGCATCTACATATTCATATCTTTAGTGTTCATAGTCCCGAGTAT 128
515 CATCTGCATCAAGAACAAATTTCAACTCTTATACCTTTTCTTTTCAAG 563
Db      CTTCGCGCATCAAGAACAAAGCCCTTTTATTAATGCTATCTTGCAAG 79

RESULT 9
CB395230
LOCUS      OSTR151B2_1 AD-wrmCDNA 487 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR151B2_1 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION    CB395230.1 GI:30736941
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 487)
AUTHORS    Reiboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
            Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
            Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
            Endress, G.A., Jenna, S., Chevret, E., Papasotiropoulos, V.,
            Tollas, P.P., Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
            Doucette-Stamm, L., Hill, D.E. and Vidal, M.
            C. elegans ORFome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
            Nat. Genet. (2003) In press
            Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way, Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc.Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFome
            cloning project : Contact david.hill@dfci.harvard.edu or
            marc.vidal@dfci.harvard.edu
            POLYA=No.
FEATURES
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            /db_xref="taxon:6239"
            /sex="Hermaphrodite and male"
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/clone.lib="AD-wrmCDNA"

/note="The AD-wrmCDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

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Query Match      7.1%; Score 347.4; DB 14; Length 487;
Best Local Similarity 96.8%; Pred. No. 2.1e-51;
Matches 365; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 3580 TGTTCCTGATGAGATGATTTTCAGGACTATGACACTAGCTATATGAATAG-GTAGATG 3638
Db      TGTTCCTGATGAGATGATTTTCAGGACTATGACACTAGCTATATGAATAG-GTAGATG 170
QY 3639 TTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 3698
Db      TTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 230
QY 3699 TTAATACGGCATTGGACCAATAGCGAGTAGCTGATACGAGATTCGGTTTGAGAAGA 3758
Db      TTAATACGGCATTGGACCAATAGCGAGTAGCTGATACGAGATTCGGTTTGAGAAGA 290
QY 3759 ACATTTGGAAGGCTCGGTGCACTAAGTTGGCAGCATCACCCGAAGAACATTTTGGAAAG 3818
Db      ACATTTGGAAGGCTCGGTGCACTAAGTTGGCAGCATCACCCGAAGAACATTTTGGAAAG 350
QY 3819 CTGTGCGTGCAGTACAGGTCACTAATACATCAAGTAGTGTGATTCATAGTACATGATG 3878
Db      CTGTGCGTGCAGTACAGGTCACTAATACATCAAGTAGTGTGATTCATAGTACATGATG 410
QY 3879 TGTTCGTGTTTACAGTATTATGTCGTTTCTTTTATGCAAAATCTAATTTAATATATG 3938
Db      TGTTCGTGTTTACAGTATTATGTCGTTTCTTTTATGCAAAATCTAATTTAATATATG 470
QY 3939 ATATTATATCATTTT 3955
Db      ATATTATATCATTTT 487

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RESULT 10

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BI174407
LOCUS      OSTR043E11_1 AD-wrmCDNA 384 bp mRNA linear EST 09-JUL-2001
DEFINITION OSTR043E11_1 AD-wrmCDNA Caenorhabditis elegans cDNA similar to
            F11F1.5, mRNA sequence.
ACCESSION BI174407
VERSION    BI174407.1 GI:14640210
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans
REFERENCE  1 (bases 1 to 384)
AUTHORS    Reiboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
            Jackson, C., Shin, I., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
            Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
            Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
            Open-reading-frame sequence tags (OSTs) support the existence of at
            least 17,300 genes in C. elegans
            Nat. Genet. 27 (3), 332-336 (2001)
            21135099
            11242119
            Contact: Reiboul J, Vaglio P
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            44 Binney Street, Boston, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 2425
            Email: Jerome.Reiboul@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFome
            cloning project : Contact jerome_reiboul@dfci.harvard.edu or

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FEATURES

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            /sex="Hermaphrodite and male"
            /tissue_type="whole animal"
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philippe_vaglio@dfci.harvard.edu
POLYA-No_ Location/Qualifiers
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
ORIGIN
Query Match 7.0%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 4.4e-50;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 197 TAAAAACAGACTACATATCTGTAAAAACACACATATCCAGTCACTATGAATCAACTA 256
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QY 257 CTTTAGATGGTATTAGTACCTGTAGTCGCGGACGCTTCCAAATGTTCTTCAACGGGAATCGTGTAT 316
Db 92 CTTTAGATGGTATTAGTACCTGTAGTCGCGGACGCTTCCAAATGTTCTTCCGGGTGAT 151
QY 317 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCAACGGGAATCGTGTAT 376
Db 152 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCAACGGGAATCGTGTAT 211
QY 377 CGAGCCTACTCGGTATTGTCTCAATGCGGTATTAATCAATAAAGAAATAAGAAAG 436
Db 212 CCAACCTACTCGGTATTGTCTCAATGCGGTATTAATCAATAAAGAAATAAGAAAG 271
QY 437 AGTGGCGAGGCTCTTTTGTGACAAATAAATCAATCTACTTATCAATACCGCTAG 496
Db 272 AGTGGCGAGGCTCTTTTGTGACAAATAAATCAATCTACTTATCAATACCGCTAG 331
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Db 332 TGTCTAGTCTGAAATCATCTGCATCAAGAAATTTTCAACACTCTTTATAC 384

RESULT 11
BI174407/c
LOCUS
DEFINITION
  OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
  Fl1F1.5, mRNA sequence.
ACCESSION
  BI174407.1 GI:14640210
VERSION
  BI174407
KEYWORDS
  EST.
ORGANISM
  Caenorhabditis elegans
  Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida;
  Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
  1 (bases 1 to 384)
REFERENCE
  Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
  Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
  Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
  Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
  Open-reading-frame sequence tags (OSTs) support the existence of at
  least 17,300 genes in C. elegans
  Nat. Genet. 27 (3), 332-336 (2001)
  21135099
  11242119
  COMMENT
  Contact: Reboul J, Vaglio P
  Marc Vidal Laboratory
  Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA-No_ Location/Qualifiers
FEATURES
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      /note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
ORIGIN
Query Match 6.7%; Score 325.4; DB 12; Length 384;
Best Local Similarity 98.2%; Pred. No. 1.8e-47;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3580 TGTCTCTGATCGAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATCT 3639
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QY 3640 TTTTATTTTGTGCACAAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATT 3699
Db 306 TTTTATTTTGTGCACAAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATT 247
QY 3700 TAATACGGCATTCAGGACAAATAGCGTAGGCTGGATAGCAGATTCCTTTTGAGAGAA 3759
Db 246 TAATACGGCATTCAGGACAAATAGCGTAGGCTGGATAGCAGATTCCTTTTGAGAGAA 187
QY 3760 CATTTTGAAGGCTGTGCGTCACTAAGTTGGCAGCATCACCCGAAGAACATTTGAAGGC 3819
Db 186 CATTTTGAAGGCTGTGCGTCACTAAGTTGGCAGCATCACCCGAAGAACATTTGAAGGC 127
QY 3820 TGTCTGCTGACTACAGGCTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGGATAT 3879
Db 126 TGTCTGCTGACTACAGGCTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGGATAT 67
QY 3880 GTTGTGTTTTTACAGTATTATGATGCTGTTTTTTA 3914
Db 66 GTTGTGTTTTTACAGTATTATGATGCTGTTTTTTA 32

RESULT 12
BJ555980
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DEFINITION
  BJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil
  cDNA clone jmi8n08 5', mRNA sequence.
ACCESSION
  BJ555980
VERSION
  BJ555980
KEYWORDS
  EST.
SOURCE
  Ipomoea nil (Japanese morning glory)
  Ipomoea nil
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Convolvulaceae; Ipomoea.
  1 (bases 1 to 337)
REFERENCE
  Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,
  Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.
  ESTs of Japanese morning glory
  Unpublished (2002)

```

COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.		Location/Qualifiers 1..337 /organism="Ipomoea nil" /mol_type="mrna" /cultivar="Tokyo-kokei standard" /db_xref="taxon:35883" /clone="jmi9n08" /tissue_type="mixture of flower and flower bud" /clone_lib="Ipomoea nil mixture of flower and flower bud"		FEATURES	source	Location/Qualifiers 1..1068 /organism="Plasmodium yoelii yoelii" /mol_type="mrna" /strain="17X" /sub_species="yoelii" /db_xref="taxon:73239" /dev_stage="axenic hepatic stages" /lab_host="E. coli TOP10" /clone_lib="Plasmodium yoelii 17X axenic hepatic stages" /note="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii 17X sporozoites were isolated from salivary glands of infected Anopheles stephensi mosquitoes and purified over a DE52 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in 'Transformation of sporozoites into early exoerythrocytic malaria parasites does not require host cells', (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BD Biosciences SMART cDNA synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."	
ORIGIN	Query Match 6.2%; Score 301.4; DB 12; Length 337; Best Local Similarity 99.4%; Pred. No. 3.3e-43; Matches 313; Conservative 0; Mismatches 1; Indels 1; Gaps 1;				ORIGIN	Query Match 5.6%; Score 273.2; DB 14; Length 1068; Best Local Similarity 90.0%; Pred. No. 2.2e-38; Matches 278; Conservative 0; Mismatches 31; Indels 0; Gaps 0;		
QY	642	CTGCAGACTGGCTGTATTAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA	701		QY	667	GCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTTTTCATGTCATTTTCGGG	726
DB	24	CTGCAGACTGGCTGTATTAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA	83		DB	562	GCTGNCATTTATATCCCGAGAACATCAGGTTAATGCGGTTTTTNGATGTCATTTTCGGG	503
QY	702	TGCGGTTTTGATGTCATTTCCCGTGGTGAGATCAGCCACTTCTCCCGATAACGG	761		QY	727	GTGGCTGAGATCAGCCACTTCTCCCGATAAACGGAGACCGCACATCGGTCATTCGGT	786
DB	84	TGGC-TTTTGTATGCCATTTTCCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG	142		DB	502	GTGGCTGAGATCAGCCACTTCTCCCGATAAACGGAGACCGCACATCGGTCATTCGGT	443
QY	762	AGACCGGACACTGGCCATATCGTGGTGCATATGCGCCAGCTTTTCATCCCGATATGCA	821		QY	787	GCTCATCATGCGCCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCACGGGAGAC	846
DB	143	AGACCGGACACTGGCCATATCGTGGTGCATATGCGCCAGCTTTTCATCCCGATATGCA	202		DB	442	GGNCATCATGCGCCAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCACGGGAGAC	383
QY	822	CCACCGGTAAGTTCAAGGAGACTTTATCTGACAGCAGCTGACATCGGCGAGGGGA	881		QY	847	TTTATCTGACAGCAGCTGACATCGGCGAGGATCACCATCCGTCGCGGGCGTCTC	906
DB	203	CCACCGGTAAGTTCAAGGAGACTTTATCTGACAGCAGCTGACATCGGCGAGGGGA	262		DB	382	TTTATCTGACAGCAGCTGACATCGGCGAGGATCACCATCCGTCGCGGGCGTCTC	323
QY	882	TCACCATCGTCCCGGGGCTGCAATATATCTCTGTATATCTCTGTATATCAACAGACGAT	941		QY	907	AATAATATCACTCTGTATATCAACAGACAGATTAAGGCTCTCTCTTTATAGGTGTA	966
DB	263	TCACCATCGTCCCGGGGCTGCAATATATCTCTGTATATCACTCTGTATATCAACAGACGAT	322		DB	322	AANAATATCGTCCGNNCATCCACNANNCNANGNANGGCTNTNTNTTTCACAGGTGNA	263
QY	942	AACGGCTCTCTCTTT 956			QY	967	AACCTTTAA 975	
DB	323	AACGGCTCTCTCTTT 337			DB	262	AACNTTGAA 254	
RESULT 13	CF469981/c		1068 bp		RESULT 14			
LOCUS	P7-E11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium		yoelii cDNA, mRNA sequence.		CF469119/c			
DEFINITION	Yoelii yoelii cDNA, mRNA sequence.				LOCUS			
ACCESSION	CF469981				DEFINITION			
VERSION	CF469981.1		GI:34487353		Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii			
KEYWORDS	EST.				Yoelii cDNA, mRNA sequence.			
SOURCE	Plasmodium yoelii yoelii				CF469119			
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				CF469119.1			
REFERENCE	Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V., and Bhanot, P.				EST.			
AUTHORS	Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V., and Bhanot, P.				Plasmodium yoelii yoelii			
TITLE	Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture				Plasmodium yoelii yoelii			
JOURNAL	Unpublished (2003)				Plasmodium yoelii yoelii			
COMMENT	Contact: Bhanot P Department of Pathology New York University School of Medicine 550 First Avenue, MSB 131, New York, NY 10016, USA Tel: 212 263 5346 Fax: 212 263 8179 Email: bhanop1@med.nyu.edu similar to NR GI-23483806 hypothetical protein [Plasmodium yoelii yoelii] (e-108).				Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 1037) Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V., and Bhanot, P. Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture Unpublished (2003) Contact: Bhanot P Department of Pathology			

New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
No Blast Hits ().

FEATURES
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/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii 17X sporozoites were isolated from salivary glands of infected Anopheles stephensi mosquitoes and purified over a DE52 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in 'Transformation of sporozoites into early exoerythrocytic malaria parasites does not require host cells' (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BDBiosciences SMART cDNA synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."

ORIGIN

Query Match 5.6%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 3.9e-38;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
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QY 727 GTGGCTGAGATGAGCAGCTTCTCCCGGATACGGAGACGGGACACACTGGCCATATCGGT 786
Db 436 GTGGCTGAGATGAGCAGCTTCTCCCGGATACGGAGACGGGACACACTGGCCATATCGGT 377
QY 787 GGTCAATCATGCGCAGCTTCTATCCCGGATATCAGCAGCGGTAAGTTACGGGAGAC 846
Db 376 GGTCAATCATGCGCAGCTTCTATCCCGGATATCAGCAGCGGTAAGTTACGGGAGAC 317
QY 847 TTTATCTGACAGCAGCGTGCATCGCCAGGGGATCAGCATCCGTCGCCCGGGCGGTGC 906
Db 316 TTTATCTGACAGCAGCGTGCATCGCCAGGGGATCAGCATCCGTCGCCCGGGCGGTGC 257
QY 907 AATAATCACTCTGTACATCCACACAG--ACGATAAGGCTCTCTCTTTTATAGGTG 964
Db 256 AATAATCACTCTGTACATCCACACAG--ACGATAAGGCTCTCTCTTTTATAGGTG 197
QY 965 TAAACCTTAACTGCATTTC 984
Db 196 AAACCTTNNACNCCGTTTC 177

RESULT 15
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LOCUS AG000791
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 724)
AUTHORS
TITLE
JOURNAL

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1997)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
Location/Qualifiers

source

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Best Local Similarity 98.6%; Pred. No. 8.9e-37;
Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 943 ACGGCTCTCTCTTTTATAGGTGTAACCC-TTAAACTGCAATTTACCACTCCCTGTTCTCG 1001
Db 27 AGGGCTCTCTCTTTTATAGGTGTAACCCCTTTAAACTGCAATTTACCACTCCCTGTTCTCG 86
QY 1002 TCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCTGATTT 1061
Db 87 TCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCTGATTT 146
QY 1062 TCCGCTTTCCAGCGTTTCGGCAGCAGAGCGGGCTTCATTTCTGCATGGTTGTGTTACC 1121
Db 147 TCCGCTTTCCAGCGTTTCGGCAGCAGAGCGGGCTTCATTTCTGCATGGTTGTGTTACC 206
QY 1122 AGACCGGAGATATTGACATCATATATATGCTTGAGCAACTGATGCTGCTGCTCAACTG 1181
Db 207 AGACCGGAGATATTGACATC--ATATGCTTTGAGCAACTGATGCTGCTGCTCAACTG 264
QY 1182 TCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTTCGACATACCTTCGCGTA 1233
Db 265 TCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTTCGACATACCTTCGCGTA 316

Search completed: May 9, 2004, 21:55:50

Job time : 7547.45 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11140.1 Seconds
(without alignments)
17418.703 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LOCUS
DEFINITION
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ACCESSION
AJ311874
VERSION
AJ311874.1 GI:15982218
KEYWORDS
kanomycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; spec gene; spectinomycin resistance protein;
transposon In7.
SOURCE
Cloning vector pHELLSGATE
ORGANISM
artificial sequences; vectors.
REFERENCE
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.N., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,
circular SYN 09-JUL-2002

Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
JOURNAL MEDLINE
21461301
PUBMED
11576441
REFERENCE
2 (bases 1 to 18691)
Waterhouse, P.M.
Direct Submission
TITLE
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
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JOURNAL
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RESULT 2
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LOCUS BD263377 4470 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263377
VERSION BD263377.1 GI:33073145
KEYWORDS JP 2002537790-A/155.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 4470)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 155 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/155
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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LOCUS									
DEFINITION		BD263381	Compositions and methods for use in recombinational cloning of nucleic acids.						
ACCESSION		BD263381							
VERSION		BD263381.1	GI:33073149						
KEYWORDS		JP 2002537790-A/159							
SOURCE		synthetic construct							
ORGANISM		synthetic construct							
REFERENCE		artificial sequences.							
AUTHORS		1 (bases 1 to 4939)							
TITLE		Hartley, J.L., Brasch, M.A., Temple, G.F. and Chao, D.							
JOURNAL		Compositions and methods for use in recombinational cloning of nucleic acids							
		Patent: JP 2002537790-A	159	12-NOV-2002:					

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INSTRUMENT COMMENT
OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PF 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
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FEATURES
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Db	3996	ATTCAATATACGCTAGTGTGCATAGTCCTGAAAAATCATCTGCATCAAGAAACAAATTTACAAC	4055
Qy	446	TCATTATCTTTTCTCTTTACAAGTCGTTTCGGCTTCATCTGGATTTTTCAAGCCTCTATCTTA	505
Db	4056	TCATTATCTTTTCTCTTTACAAGTCGTTTCGGCTTCATCTGGATTTTTCAAGCCTCTATCTTA	4115
Qy	506	CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACCTGGCTGTGTATA	565
Db	4116	CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACCTGGCTGTGTATA	4175
Qy	566	AGGAGCGCTGACATTTATATTTCCCGAAACATCAGGTTAATGCGTTTTTGTATGTCAATT	625
Db	4176	AGGAGCGCTGACATTTATATTTCCCGAAACATCAGGTTAATGCGTTTTTGTATGTCAATT	4235
Qy	626	TCGCGGTGGCTGAGATCAGCACCTTCTTCCCGATAACGGAGACCGGCACACTGGGCATA	685
Db	4236	TCGCGGTGGCTGAGATCAGCACCTTCTTCCCGATAACGGAGACCGGCACACTGGGCATA	4295
Qy	686	TCGGTGGTCATCATGCGCGACGTTTCACTCCCGATATGCACACCGGGTAAAGTTTCACGG	745
Db	4296	TCGGTGGTCATCATGCGCGACGTTTCACTCCCGATATGCACACCGGGTAAAGTTTCACGG	4355
Qy	746	GAGACTTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGATACCATCCGTCGCGCGGGC	805
Db	4356	GAGACTTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGATACCATCCGTCGCGCGGGC	4415
Qy	806	GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAAAGGCTCTCTCTTTTATAG	865
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Qy	866	GTGTAAACCTTAAACTGCATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCAT	925
Db	4476	GTGTAAACCTTAAACTGCATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCAT	4535
Qy	926	TTCAATAAACCGGGCGACCTCAGACCATCCCTTCTCTGTATTTTCCGCTTTTCCAGCGTTCGGC	985
Db	4536	TTCAATAAACCGGGCGACCTCAGACCATCCCTTCTCTGTATTTTCCGCTTTTCCAGCGTTCGGC	4595
Qy	986	ACGCAGACGACGGGCTTCATTCTCGATGGTTGTGCTTACCAAGACCGGAGATATTGACATC	1045
Db	4596	ACGCAGACGACGGGCTTCATTCTCGATGGTTGTGCTTACCAAGACCGGAGATATTGACATC	4655
Qy	1046	ATATATGCGCTTGAGCAACTGATAGCTGTGCGTGTCAACTGTCTAATACGCTGTCTTC	1105
Db	4656	ATATATGCGCTTGAGCAACTGATAGCTGTGCGTGTCAACTGTCTAATACGCTGTCTTC	4715

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QY 1106 ATAGACACACCTCTTTTTCACATCTTCGGGTA 1137
Db 4716 ATAGACACACCTCTTTTTCACATCTTCGGGTA 4747

RESULT 4
BD263402/c 5594 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for use in recombinational cloning of
DEFINITION nucleic acids.
ACCESSION BD263402
VERSION BD263402.1 GI:33073170
KEYWORDS JP 2002537790-A/180.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 5594)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/180
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
00, C12N5/00
CC pDONR207
PH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
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ORIGIN
Query Match 24.8%; Score 1108.8; DB 6; Length 5594;
Best Local Similarity 99.8%; Pred. No. 6.9e-151;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAGTTGTACAAAAGAGCTGAACGAGAAACGTAATAATGATATTAATCAATATATT 85
Db 5483 GCCAAGTTGTACAAAAGAGCTGAACGAGAAACGTAATAATGATATTAATCAATATATT 5424

QY 86 AAATTAGATTTTGCATATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 145
Db 5423 AAATTAGATTTTGCATATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCGCTTCCAAA 205
Db 5363 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCGCTTCCAAA 5304

QY 206 TGTTCTTCGGGTGATGCTGCCAACTAGTACCGACGACGCTTCCAAATGTTCTCTCAA 265
Db 5303 TGTTCTTCGGGTGATGCTGCCAACTAGTACCGACGACGCTTCCAAATGTTCTCTCAA 5244

QY 266 ACCGAATCGTCGATCCAGCTACTCGCTATTGCTCTCAATGCGGTATTAATCAATAAAA 325
Db 5243 ACCGAATCGTCGATCCAGCTACTCGCTATTGCTCTCAATGCGGTATTAATCAATAAAA 5184

QY 326 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGCACAAATAAAAAACATCTACCT 385
Db 5183 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGCACAAATAAAAAACATCTACCT 5124

QY 386 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 445
Db 5123 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 5064

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QY 446 TCTTATACCTTTTCTCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 505
Db 5063 TCTTATACCTTTTCTCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 5004

QY 506 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCGAGACTGGCTGTGTATA 565
Db 5003 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCGAGACTGGCTGTGTATA 4944

QY 566 AGGAGAGCTGACATTTATATTTCCCGAACAATCAGGTTAATGGGTTTTTGATGTCATTT 625
Db 4943 AGGAGAGCTGACATTTATATTTCCCGAACAATCAGGTTAATGGGTTTTTGATGTCATTT 4884

QY 626 TCGCGGTGGCTGAGATCAGGCACCTTTCTTCCCGATAACGGAGACCGGCACATCGGCCATA 685
Db 4883 TCGCGGTGGCTGAGATCAGGCACCTTTCTTCCCGATAACGGAGACCGGCACATCGGCCATA 4824

QY 686 TCGGTGTCATCATCGCGCAGCTTTTCATCCCGATGATGCACCACCGGGTAAAGTTCAGG 745
Db 4823 TCGGTGTCATCATCGCGCAGCTTTTCATCCCGATGATGCACCACCGGGTAAAGTTCAGG 4764

QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGAGGGGATCACCATCCGTCGCCCGGGC 805
Db 4763 GAGACTTTATCTGACAGCAGCTGCTGCTGCGAGGGGATCACCATCCGTCGCCCGGGC 4704

QY 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTTATAG 865
Db 4703 GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTTATAG 4644

QY 866 GTGTAAACCTTAAACTGATTTTACAGCTGCTGCTGCTGTCAGCAAAAGACCGGTTTCAT 925
Db 4643 GTGTAAACCTTAAACTGATTTTACAGCTGCTGCTGCTGTCAGCAAAAGACCGGTTTCAT 4584

QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCAGCGTTCGGC 985
Db 4583 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCAGCGTTCGGC 4524

QY 986 ACGCAGACGACGGGCTTCATTTCTGCATGGTGTGTGTTACCGAGACCGGAGATTTGACATC 1045
Db 4523 ACGCAGACGACGGGCTTCATTTCTGCATGGTGTGTGTTACCGAGACCGGAGATTTGACATC 4464

QY 1046 ATATATGCTTGTAGCAACTGATAGTGTGCTGTGCTCAACTGTCACTGTAATAGCTGCTTC 1105
Db 4463 ATATATGCTTGTAGCAACTGATAGTGTGCTGTGCTCAACTGTCACTGTAATAGCTGCTTC 4404

QY 1106 ATAGCACACCTCTTTTTCACATCTTCGGGTA 1137
Db 4403 ATAGCACACCTCTTTTTCACATCTTCGGGTA 4372

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RESULT 5
BD263380 4165 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for use in recombinational cloning of
DEFINITION nucleic acids.
ACCESSION BD263380
VERSION BD263380.1 GI:33073148
KEYWORDS JP 2002537790-A/158.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4165)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 158 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/158
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744

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Query Match	22.1%	Score 989.6	DB 6	Length 4165
Best Local Similarity	98.0%	Pred. No. 1.2e-133		
Matches 1008	Conservative 0	Mismatches 9	Indels 3	Gaps 1
QY	2284	GACCACCTTTGTCACAGAAAGCTGAACGAGAAACGTAATAATGATATAAAATATCAATATATTT	2343	
DB	2184	GCCAACTTTGTACAAGAAAGCTGACGAGNAAAGTAATGATATAAAATATCAATATATTT	2243	
QY	2344	AAATATGATTTTGCATAAAAAAAGACACTACATAATCTGTAAAAACAACACATATCCAGTC	2403	
DB	2244	AAATATGATTTTGCATAAAAAAAGACACTACATAATCTGTAAAAACAACACATATCCAGTC	2303	
QY	2404	ACTATGAATCAACTACTTACATGGTATTAGTGACCTGTAGTCGCACTAAGTTGCGACATC	2463	
DB	2304	ACTATGATTTCAACTACTTACATGGTATTAGTGACCTGTAGTCGCACTAAGTTGCGACATC	2363	
QY	2464	ACCCGACGCACTTTGCGCCGAATAAATACCTGTGACGGAAGATCACTTGCAGAAATAAT	2523	
DB	2364	ACCCGACGCACTTTGCGCCGAATAAATACCTGTGACGGAAGATCACTTGCAGAAATAAT	2423	
QY	2524	AAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCAACCTTTTGGCGAAAAATGAGA	2583	
DB	2424	AAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCAACCTTTTGGCGAAAAATGAGA	2483	
QY	2584	CGTGTGATCGG---ATTTCACAACCTCTTATATCTTTCTCTTACAAGTCGTTGGGCTTCATC	2640	
DB	2484	CGTGTGATCGGCACATTTTCAACCTCTTATATCTTTCTCTTACAAGTCGTTGGGCTTCATC	2543	
QY	2641	TGGATTTTCAGCCTCTATATCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC	2700	
DB	2544	TGGATTTTCAGCCTCTATATCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC	2603	
QY	2701	GACCTGCAGACTGGCTGTGTATAGGAGAGCTGCACATTTATTTCCGCCAGAAACATCAGGT	2760	
DB	2604	GACCTGCAGACTGGCTGTGTATAGGAGAGCTGCACATTTATTTCCGCCAGAAACATCAGGT	2663	
QY	2761	TATATGGCGTTTTTGATGTCAATTTTTCGGGTGGCTGTGATCAGCGCACTTTCTTCCCGATAA	2820	
DB	2664	TATATGGCGTTTTTGATGTCAATTTTTCGGGTGGCTGTGATCAGCGCACTTTCTTCCCGATAA	2723	
QY	2821	CGGAGACGGCACACTGGCCATATTCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGATAT	2880	
DB	2724	CGGAGACGGCACACTGGCCATATTCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGATAT	2783	
QY	2881	GCACACCGGGTAAAGTTTCACGGAGAGACTTTATCTGACAGCAGACGTGCACCTGGCCACGG	2940	
DB	2784	GCACACCGGGTAAAGTTTCACGGAGAGACTTTATCTGACAGCAGACGTGCACCTGGCCACGG	2843	
QY	2941	GGATCACCATCCGTGCGCCGGCGTGTGCATATATATCTCTGTACATTCACAAACAGAC	3000	
DB	2844	GGATCACCATCCGTGCGCCGGCGTGTGCATATATATCTCTGTACATTCACAAACAGAC	2903	
QY	3001	GATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTTACCAGTCCCTGTC	3060	
DB	2904	GATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTTACCAGTCCCTGTC	2963	
QY	3061	TCGTACGAAAGAGCCGTTTCATTTCAATAAACCGGGCGACCTCAGGCATCCCTTCTCTGA	3120	
DB	2964	TCGTACGAAAGAGCCGTTTCATTTCAATAAACCGGGCGACCTCAGGCATCCCTTCTCTGA	3023	

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Db	3318	AAATTAGATTTTCGATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGTC	3377
QY	146	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA	205
Db	3378	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA	3437
QY	206	TGTTCTTCGGGTGATGCTGCCAATTAGTTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA	265
Db	3438	TGTTCTTCGGGTGATGCTGCCAATTAGTTCGACCGACAGCCTTCCAAAATGTTCTTCTCAA	3497
QY	266	ACGGAATCGTCGTATCCAGCTACTCGCTATTCGCTCAATGCCGTATTAAATCATAAAA	325
Db	3498	ACGGAATCGTCGTATCCAGCTACTCGCTATTCGCTCAATGCCGTATTAAATCATAAAA	3557
QY	326	AGAAATAGAAAAAGAGGGTGGAGCCTCTTTTTTGTGTGACAAAAATAAAAACATCTACCT	385
Db	3558	AGAAATAGAAAAAGAGGGTGGAGCCTCTTTTTTGTGTGACAAAAATAAAAACATCTACCT	3617
QY	386	ATTTCATATACGTAGTCTCATAGTCCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC	445
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QY	446	TCCTTATACTTTTTCTTCAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA	505
Db	3678	TCCTTATACTTTTTCTTCAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA	3737
QY	506	CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTCGACACTGGCTGTGTATA	565
Db	3738	CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTCGACACTGGCTGTGTATA	3797
QY	566	AGGAGCGCTGACATTTATATATTTCCCGAGAACATCAGGTTAATGGCGTTTTTGATGCAATTT	625
Db	3798	AGGAGCGCTGACATTTATATATTTCCCGAGAACATCAGGTTAATGGCGTTTTTGATGCAATTT	3857
QY	626	TCGCGGTGGCTGAGATCAGGCACATTTCTTCCCGATAACGGAGACCGGCACACTGGCCATA	685
Db	3858	TCGCGGTGGCTGAGATCAGGCACATTTCTTCCCGATAACGGAGACCGGCACACTGGCCATA	3917
QY	686	TCGGTGGTCATCATCGCGCCAGCTTTCATCCCGATATGCAACCAGCGGTAAAGTTCACGG	745
Db	3918	TCGGTGGTCATCATCGCGCCAGCTTTCATCCCGATATGCAACCAGCGGTAAAGTTCACGG	3977
QY	746	GAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGGGGATCACAATCGGTGCGCCGGCC	805
Db	3978	GAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGGGGATCACAATCGGTGCGCCGGCC	4037
QY	806	GTGTCAATAAATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTTATAG	865
Db	4038	GTGTCAATAAATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTTATAG	4097
QY	866	GTGTAAACCTTTAAACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCA	925
Db	4098	GTGTAAACCTTTAAACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCA	4157
QY	926	TTCAATAAACCGGGGGAAGCTGAGCAATCCCTCTCTGTATTTCCCGCTTTCCA	976
Db	4158	TTCAATAAACCGGGGGAAGCTGAGCAATCCCTCTCTGTATTTCCCGCTTTCCA	4208

RESULT	7
BD263378/c	
LOCUS	BD263378
DEFINITION	Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION	BD263378
VERSION	BD263378.1 GI:33073146
KEYWORDS	JP 2002537790-A/156.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences.
REFERENCE	1 (bases 1 to 4204)
AUTHORS	Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE	Compositions and methods for use in recombinational cloning of


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Db 4785 AATCTAATGCTAATATAAACAAGCCGACGATCTATCATTTTATATAGTATATTTTCAAT 4844
QY 2085 CAACATCTTATTAATATCTTAATAATATCTTGTAGTTTATTAATTAATTAATGAATGA 2144
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QY 2145 CTATTAATTAATGAATAGTAGTCGAACATGAATAACAAGGTAACATGATAGTATCATGTCA 2204
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QY 2205 TTGTGTTATCATGATCTTACATTTGGATTTGATTTACAGTTGGGAAGCTGGGTTCCAAATC 2264
Db 4965 TTGTGTTATCATGATCTTACATTTGGATTTGATTTACAGTTGGGAATTTGGGTTCCAAATC 5024
QY 2265 GATAGCTTGGATCTCTAGACACATTTGTGCAAGAAGCTGAACAGAGAAAGTAAATG 2324
Db 5025 GATAGCTTGGATCTCTAGACATCTGCTTTAATGAGATATCGAGAGCCCTATGATGCGC 5084
QY 2325 ATATAAATATCAATATATTAATTAATAGATTTTGCATAAAAAC 2366
Db 5085 ATGATATTGCTTCAATCTCTGTTGTGCAGCTGTGTAATAAAC 5126

RESULT 9
LOCUS CVE311873 6063 bp DNA circular SYN 09-JUL-2002
DEFINITION Cloning vector pKANNBIBAL.
ACCESSION AJ311873
VERSION AJ311873.1 GI:15982216
KEYWORDS kan gene; kanamycin resistance protein; pdk gene; promoter.
SOURCE Cloning vector pKANNBIBAL
ORGANISM Cloning vector pKANNBIBAL
artificial sequences; vectors.
REFERENCE 1
AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,
Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
JOURNAL Plant J. 27 (6), 581-590 (2001)
MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 6063)
AUTHORS Waterhouse, P.M.
TITLE Direct Submision
JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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Query Match 18.4%; Score 824.4; DB 12; Length 6063;
Best Local Similarity 92.9%; Pred. No. 8.6e-110;
Matches 875; Conservative 0; Mismatches 66; Indels 1; Gaps 1;
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QY 1665 AGAGTAAGTATATATTTTATTAATGAAATTTGATCGAACAATGTAAGATGATATACTAGCATTT 1724
Db 4664 AGAGTAAGTATATATTTTATTAATGAAATTTGATCGAACAATGTAAGATGATATACTAGCATTT 4723
QY 1725 AATATTTGTTTAAATCATATATATAGTAATTTCTAGCTGGTTTGAATTAATAATATCAATCAT 1784
Db 4724 AATATTTGTTTAAATCATATATATAGTAATTTCTAGCTGGTTTGAATTAATAATATCAATCAT 4783
QY 1785 AAAATACATATAGTAATAATAAGTAATAATTAATTAATAATAATATTTTATTTATGATTAATA 1844
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QY 1845 GTTTATTTATATAATTAATAATATCTATACATTTACTATAATTTTATAGTTTAAAGTTTATAATA 1904
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Db 4964 AAGCTAAGTAACAATAATAATATCAACTAATAGAAACAGTAATCTAATGTGAACAAACAT 5023
QY 2025 AATCTAATGCTAATATAACAAGGCAAGATCTATCTATTTTATATAGTATTTTATTTTCAAT 2084
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Db	5024	AATCTAATGCTAAATATATACCAAGCGCAAGATCTCATTTTATATAGTATTAATTTTCAAT	5083
Qy	2085	CAACATTTCTTAAATTTCTAAATAAATACCTTGATGTTTTTATTAACTTCTTAATGGATTGA	2144
Db	5084	CAACATTTCTTAAATTTCTAAATAAATACCTTGATGTTTTTATTAACTTCTTAATGGATTGA	5143
Qy	2145	CTATTAATTTAAATGAATTAAGTCGAACATGAATAAACAAGGTAACATGATAGATCATGTCA	2204
Db	5144	CTATTAATTTAAATGAATTAAGTCGAACATGAATAAACAAGGTAACATGATAGATCATGTCA	5203
Qy	2205	TTTGGTTATCATTTGATCTTACATTTTGATTTGATTTACAGTTGGAGCTGGTTCGAAATC	2264
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Qy	2325	ATATAATATCAATATATTAATTAATTTAGATTTTGCATAAAAAAC	2366
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RESULT	10		
BD263382/c			
LOCUS		5156 bp DNA linear	PAT 17-JUL-2003
DEFINITION		Compositions and methods for use in recombinational cloning of nucleic acids.	
ACCESSION	BD263382		
VERSION	BD263382.1	GI.33073150	
KEYWORDS	JP 2002537790-A/160.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 5156)		
AUTHORS	Hartley J.L., Brasch, M.A., Temple, G.F. and Cheo, D.		
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids		
JOURNAL	Patent: JP 2002537790-A 160 12-NOV-2002;		
COMMENT	INVITROGEN CORP		
OS	Artificial Sequence		
PN	JP 2002537790-A/160		
PD	12-NOV-2002		
PF	02-MAR-2000 JP 2000602252		
PR	02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049	PR	
PI	28-MAY-1999 US 60/136744		
PC	PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO		
CL	C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/00		
CC	pDONR206		
CC	May be any nucleotide		
CC	May be any nucleotide		
FH	Key	Location/Qualifiers	
FT	misc feature	(1102).. (1102)	
FT	misc feature	(3080).. (3080).	
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Best Local Similarity	99.8%;	Pred. No. 1.1e-109;	
Matches	825; Conservative	0; Mismatches	2; Indels 0; Gaps 0;
Qy	311	TATTAATCATAAAAAGAAATAGAAAAAGAGTGGAGCCTCTTTTTTTGTGTGACAAA	370
Db	5156	TATTAATCATAAAAAGAAATAGAAAAAGAGTGGAGCCTCTTTTTTTGTGTGACAAA	5097
Qy	371	TAAAAACATCTCACTATTTCATATACGCTAGTGTTCATAGTCCCTGAAATCATCTGCATCAA	430

AUTHORS Kardailsky, I. and Weigel, D.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES Location/Qualifiers
source 1..10138
/organism="Activation-tagging vector pSKI015"
/mol_type="genomic DNA"
/db_xref="taxon:109189"
misc_feature 12..31
/notes="T7 RNA polymerase promoter"
misc_feature 36..2204
/notes="derived from pUC19"
misc_feature 2205..2662
/notes="derived from phage f1"
misc_feature 2663..2829
/notes="derived from pUC19"
misc_feature 2830..2849
/notes="T7 RNA polymerase promoter"
misc_feature 2894..4178
/notes="cauliflower mosaic virus 35S gene promoter enhancer
sequences (tetramer)"
misc_feature 4270..4294
/notes="T-DNA right border"
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/notes="T-DNA left border"
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/product="octopine synthase"
/notes="3' end"
mRNA complement(8785..93420)
/product="mannopine synthase"
CDS complement(8791..9342)
/notes="promotes resistance to glutamine synthetase
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/db_xref="GI:6537290"
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Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3880 CCGTTCATTTACTGATGTGACCTACTCTATATATGTAATTAATAATGAACAAT 3939
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QY 3940 ATATTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATAACAACAAT 3999
DB 8532 ATATTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATAACAACAAT 8473
QY 4000 TGGTTTTATTATCAAAATCCAAATTTTAAAAAGGGCAGAACCGGTCAAACTTAAAA 4059
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Db 8412 GACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCGCCAGGGCTAGTATCTACGACA 8353
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RESULT 15
A24783
LOCUS A24783 7566 bp DNA linear PAT 24-FEB-1995
DEFINITION plasmid pPS0212 replicable en E.coli.
ACCESSION A24783
VERSION A24783.1 GI:833505
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 7566)
AUTHORS
TITLE MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS
JOURNAL Patent: WO 9309218-A 23-13-MAY-1993;
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 16.3%; Score 728.8; DB 6; Length 7566;
Best Local Similarity 99.7%; Pred. No. 5.4e-96;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 3758 CAATTCTGTGTGCGCTTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3817
DB 3752 CAATTCTGTGTGCGCTTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3811
QY 3818 GTTTCGGTTCATCTAAGATATATACCGGTTACTATCGTATTTTATGAATAATAT 3877
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QY 3878 CTCCTGTTCAATTTACTGATGTGACCTACTATGATAGTCAATATTAATAATGAACA 3937
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3932	ATATATTGTGCTGAATAGGTTTATAGCGACAATCTATGATAGAGCGGCACAATAACAAACA	3991
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4058	AAGACTGATTACATAAAATCTTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4117
4052	AAGACTGATTACATAAAATCTTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4111
4118	CACACCGAGCGCGCAACTTAATAACGTTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGG	4177
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4178	CATGGGTGAGATTCTTGAAGTTCAGATTATGGCGCTCCGCTCTTACCGAAAGTTTACGGCA	4237
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4238	CCATTCAACCCGGTCCAGCACGGCGCGCGGGTAAACCGACTTGTGTGCCCGCAGAAATTATGC	4297
4232	CCATTCAACCCGGTCCAGCACGGCGCGCGGGTAAACCGACTTGTGTGCCCGCAGAAATTATGC	4291
4298	AGCAATTTTGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACTTGCAGTGACG	4357
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4358	ACAAATCGTTCGGCGGGTCCAGGCGCGAATTTTGGCGACAAATGTCGAGGGCTCAGCAGGAC	4417
4352	ACAAATCGTTCGGCGGGTCCAGGCGCGAATTTTGGCGACAAATGTCGAGGGCTCAGCAGGAC	4411
4418	CTGCAGGCATGC	4429
4412	CTGCAGGAATTC	4423

Search completed: May 9, 2004, 11:28:34
Job time : 11161.1 secs

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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1031.31 Seconds
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18441.778 Million cell updates/sec

Title: US-10-055-001b-24_COPY_13000_17476

Perfect score: 4477

Sequence: 1 ttctcattgagagacacg.....atagtgacacctaatactgc 4477

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4477	100.0	17476	6	ABQ82141 Acceptor
2	4406.6	98.4	17458	6	ABQ82142 Acceptor
3	4262	95.2	17681	6	ABQ82143 Acceptor
4	3234.8	72.3	18691	6	ABQ82130 Acceptor
5	1277.8	28.5	17458	6	ABQ82142 Acceptor
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7	1108.8	24.8	4470	3	AAC55521 Donor pla
8	1108.8	24.8	4470	3	ABZ58767 Destinati
9	1108.8	24.8	4892	8	ADA50329 Plasmid v
10	1108.8	24.8	4939	3	AAC55525 Donor pla
11	1108.8	24.8	5584	3	AAC55632 Donor pla
12	1108.8	24.8	5584	7	ABZ58766 Donor pla
13	1102.4	24.6	4428	7	ABZ58768 Destinati
14	1102.4	24.6	4627	7	ABZ58769 Destinati
15	1102.4	24.6	4627	7	ABZ58770 Destinati
16	1074.8	24.0	17681	6	ABQ82143 Acceptor
17	969.6	22.1	4185	3	AAC55524 Donor pla
18	947.8	21.2	4208	3	AAC55523 Donor pla
19	827	18.5	4204	3	AAC55522 Donor pla
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22	780	17.4	786	9	AAZ38603 Flavaria
23	747	16.7	7050	2	AAQ40419 Sequence

24	728.8	16.3	7566	2	AAQ42160	AaQ42160 Plasmid p
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26	713	15.9	4947	3	AAZ60627	AaZ60627 Nucleotid
27	711.4	15.9	3435	8	ACC85049	Acc85049 Nucleotid
28	710.2	15.9	7599	4	AAF25320	Aaf25320 Nucleotid
29	709.8	15.9	5399	2	AAQ25706	AaQ25706 pDE108. 3
30	709.8	15.9	6555	2	AAQ53874	AaQ53874 Plasmid p
31	709.8	15.9	14194	4	AAC66932	Aac66932 Plant sig
32	707	15.8	24596	1	AAU50182	Aau50182 Complete
33	703.8	15.7	24593	1	AAU50226	Aau50226 Sequence
34	703	15.7	2867	7	ABZ68391	Abz68391 Nucleotid
35	617.6	13.8	18691	6	ABQ82130	AbQ82130 Acceptor
36	597	13.3	1846	6	AAD44626	Aad44626 Gateway t
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39	597	13.3	5957	3	AAC55464	Aac55464 Destinati
40	597	13.3	6025	3	AAC55469	Aac55469 Destinati
41	597	13.3	6264	3	AAC55507	Aac55507 Destinati
42	597	13.3	6354	3	AAC55491	Aac55491 Destinati
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44	597	13.3	6464	3	AAC55454	Aac55454 Destinati
45	597	13.3	6526	3	AAC55471	Aac55471 Destinati

ALIGNMENTS

RESULT 1

ABQ82141
ID ABQ82141 standard; DNA; 17476 BP.

XX
AC ABQ82141;

XX
DT 11-DEC-2002 (first entry)

XX
DE Acceptor vector PHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.

XX
OS Synthetic.

XX
PN WO200259294-A1.

XX
PD 01-AUG-2002.

XX
PF 24-JAN-2002; 2002WO-AU0000073.

XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.

XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;

XX
XX WPI; 2002-682659/73.

XX
XX New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

XX
XX Claim 15; Page 74-83; 104pp; English.

XX
XX The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
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SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
Query Match 100.0%; Score 4477; DB 6; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 13120 ACTGTAAACACACATATCCAGTCATGATGAATCACTATAGATGATAGTAC 13179
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QY 181 TGTAGTCGACGACGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 240
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DB |||||
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DB |||||
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DB |||||
QY 13300 CTCATGCGGTATTAATCATTAATAAGAAATTAAGAAAGAGGTGGAGCCTCTTTTGTG 13359
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QY 361 TGTGACAAAATAAAACATCTACCTATTTCATATACGCTAGTGTCTAGTCTGAAAATCA 420
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QY 541 TCGACCTCGAGACTGGCTGTGTATAGGAGCCTGACATTTATTTCCCGCAAGAACATCAG 600
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QY 13540 TCGACCTCGAGACTGGCTGTGTATAGGAGCCTGACATTTATTTCCCGCAAGAACATCAG 13599
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DB |||||
QY 13600 GTTAATGGGTTTTTGTATGATCAATTTTCGGGTGGCTGGAGATCAAGCCTTTCTCCCGAT 13659
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QY 661 AACGAGACCGGCACACTGGCCATATCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGAT 720
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QY 13660 AACGAGACCGGCACACTGGCCATATCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGAT 13719
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QY 13720 ATGCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACGACGACGTCGACCTGCCAG 13779
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QY 781 GGGGATCACCATCCGTCGCGCGCGCGGTGTCAATPAATATCACTCTGTACATCCCAACACAG 840
DB |||||

DB 13780 GGGGATCACCATCCGTGCGCGCGCGGTGTCAATPAATATCACTCTGTATATCCCAACACAG 13839
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QY 13840 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTCAACAGTCCCTGT 13899
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QY 1081 AACTGTCACTTAATAGCTGCTTTCTAGACACACTCTTTTTCGACATCTTCGGGTAGT 1140
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QY 14080 AACTGTCACTTAATAGCTGCTTTCTAGACACACTCTTTTTCGACATCTTCGGGTAGT 14139
DB |||||
QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCGGGTATCAACAGGAC 1200
DB |||||
QY 14140 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCGGGTATCAACAGGAC 14199
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QY 1201 ACCAGGATTTTATTTATTCGCGAAGTATCTTCGCTCACAGGTATTTATTCGGCGCAAG 1260
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QY 14200 ACCAGGATTTTATTTATTCGCGAAGTATCTTCGCTCACAGGTATTTATTCGGCGCAAG 14259
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QY 14260 TGGCTCGGGTGATGCTGCCAACTTAGTCGACTACAGTCTACTAATACCATCTAAGTAGT 14319
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QY 1321 GATTCATAGTCACTGGATATGTTGTTTACAGTATATGTTAGTCTGTTTTTTATGCAA 1380
DB |||||
QY 14320 GATTCATAGTCACTGGATATGTTGTTTACAGTATATGTTAGTCTGTTTTTTATGCAA 14379
DB |||||
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QY 14380 AATCTAATTTAATATTTATGATATTTATATATTTTACGTTCTCTGTCAGCTTTCTTGTA 14439
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QY 1441 CAAAGTGTCTCGAGGAATTCGTAACCCAGCTTTGGTAAGGAAATAATTTCTTTT 1500
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QY 14440 CAAAGTGTCTCGAGGAATTCGTAACCCAGCTTTGGTAAGGAAATAATTTCTTTT 14499
DB |||||
QY 1501 TCCTTTTATGATATAAATAGTTAAGTGTATTAATAGTATTAATATAATAGTTGT 1560
DB |||||
QY 14500 TCCTTTTATGATATAAATAGTTAAGTGTATTAATAGTATTAATATAATAGTTGT 14559
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DB |||||
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QY 14620 AAAAATATGACAGATGATGTGTAAGACGAGAGATAAAAGTTCAGAGTAAGTATTTAT 14679
DB |||||
QY 1681 TTTTAAATGAAATTCGATCGAACATGTAGATCATATCTAGCATTAATTTGTTTAAATC 1740
DB |||||
QY 14680 TTTTAAATGAAATTCGATCGAACATGTAGATCATATCTAGCATTAATTTGTTTAAATC 14739
DB |||||
QY 1741 ATAAATAGTAATTTCTAGCTGGTTTGTATGAAATTAATAATCAATGATAAAATCTATAGTAA 1800
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QY 14740 ATAAATAGTAATTTCTAGCTGGTTTGTATGAAATTAATAATCAATGATAAAATCTATAGTAA 14799
DB |||||
QY 1801 AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860
DB |||||
QY 14800 AATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 14859
DB |||||
QY 1861 AATATCTATACCATTTACTTAATATTTTATAGTTTAAAGTTTAAATATATTTTGTAGAAAT 1920
DB |||||

Db 14860 AATATCTATACCACTTACTAATAATTTTAGTTTAAAGTTAATAATATTTTGTAGAAAT 14919
Qy 1921 TCCAACTCGCTGTGTAATTTATCAATAAACAATAATTAATAATAACAGCTTAAAGTAAACAA 1980
Db 14920 TCCAACTCGCTGTGTAATTTATCAATAAACAATAATTTAAATAACAAGCTTAAAGTAAACAA 14979
Qy 1981 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGTCTAATAT 2040
Db 14980 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGTCTAATAT 15039
Qy 2041 AACAAAGCGCAAGTCTATCAATTTTATATAGTATATTTTCAATCAACATCTTATTAAT 2100
Db 15040 AACAAAGCGCAAGTCTATCAATTTTATATAGTATATTTTCAATCAACATCTTATTAAT 15099
Qy 2101 TTCTAAATTAATCTGTGTAGTTTATTAATCTTAACTCTAAATGCAATGACTTAAATTAAGTAA 2160
Db 15100 TTCTAAATTAATCTGTGTAGTTTATTAATCTTAAATGCAATGACTTAAATTAAGTAA 15159
Qy 2161 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTATCATTTGAT 2220
Db 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTATCATTTGAT 15219
Qy 2221 CTTACATTTGGATTCATTAAGTTGGAAAGCTGGGTTCCGAATCGATGAAGCTTGATCCT 2280
Db 15220 CTTACATTTGGATTCATTAAGTTGGAAAGCTGGGTTCCGAATCGATGAAGCTTGATCCT 15279
Qy 2281 CTAGACCACTTTGTACAAAGAACTGAACGAAACGTAAGTAAATGATATTAATATCAATAT 2340
Db 15280 CTAGACCACTTTGTACAAAGAACTGAACGAAACGTAAGTAAATGATATTAATATCAATAT 15339
Qy 2341 ATTAATTTAGATTTTGGCAATAAACAAGACTACATAATACCTGTAAACACAACTATCCA 2400
Db 15340 ATTAATTTAGATTTTGGCAATAAACAAGACTACATAATACCTGTAAACACAACTATCCA 15399
Qy 2401 GTCATATGAATCAACTCTATAGATGGTATAGTGAACCTGTAGTGCATTAAGTTGGCAGC 2460
Db 15400 GTCATATGAATCAACTCTATAGATGGTATAGTGAACCTGTAGTGCATTAAGTTGGCAGC 15459
Qy 2461 ATCACCACGACCTTTGGCGGATTAATACCTGTGAGGAAAGTCACTTCGCAAGRATA 2520
Db 15460 ATCACCACGACCTTTGGCGGATTAATACCTGTGAGGAAAGTCACTTCGCAAGRATA 15519
Qy 2521 AATAAATCCTGGTGTCCCTGTGTATACCGGGAAGCCCTGGGCAACTTTTGGCGGAAATG 2580
Db 15520 AATAAATCCTGGTGTCCCTGTGTATACCGGGAAGCCCTGGGCAACTTTTGGCGGAAATG 15579
Qy 2581 AGACGTTGATCGGATTCACAACTCTTATACCTTTCTCTTACAGTGGTTCGGCTTCATC 2640
Db 15580 AGACGTTGATCGGATTCACAACTCTTATACCTTTCTCTTACAGTGGTTCGGCTTCATC 15639
Qy 2641 TGGATTTTTCAGGCTCTATACCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC 2700
Db 15640 TGGATTTTTCAGGCTCTATACCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC 15699
Qy 2701 GACCTGCAGACTGGCTGTGTATAAGGAGCCCTGACATTTATATCCCGAAGACATCAGGT 2760
Db 15700 GACCTGCAGACTGGCTGTGTATAAGGAGCCCTGACATTTATATCCCGAAGACATCAGGT 15759
Qy 2761 TAAATGGCGTTTGTATGTCATTTTGGCGGTGGCTGAGTACAGCACTTCTCCCGATAA 2820
Db 15760 TAAATGGCGTTTGTATGTCATTTTGGCGGTGGCTGAGTACAGCACTTCTCCCGATAA 15819
Qy 2821 CGGAGACCGGACACCTGGCCATATCGGTGGTCAATGCGCCAGCTTTTCATCCCGATAT 2880
Db 15820 CGGAGACCGGACACCTGGCCATATCGGTGGTCAATGCGCCAGCTTTTCATCCCGATAT 15879
Qy 2881 GCACCAACCGGTTAAAGTTTCAACGGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGG 2940
Db 15880 GCACCAACCGGTTAAAGTTTCAACGGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGG 15939
Qy 2941 GGAATCAACATTCGCTCGCCGGCGGTCAATTAATATCACTGTGATATCAACAAACAGAC 3000
Db 15940 GGAATCAACATTCGCTCGCCGGCGGTCAATTAATATCACTGTGATATCAACAAACAGAC 15999

Qy 3001 GATAACGGCTCTCTCTTTTATAGGTAAACCTTAAACCTCATTTACCAGTCCCTCTTC 3060
Db 16000 GATAACGGCTCTCTCTTTTATAGGTAAACCTTAAACCTCATTTACCAGTCCCTCTTC 16059
Qy 3061 TCGTCAGCAAAAAGAGCGGTTTCAATTTCAATAAAACGGGCGACCTCAGCCATCCCTTCTCTGA 3120
Db 16060 TCGTCAGCAAAAAGAGCGGTTTCAATTTCAATAAAACGGGCGACCTCAGCCATCCCTTCTCTGA 16119
Qy 3121 TTTTTCGGCTTTCCAGCGTTCCGGCAGCAGAGCGGCTTCATTTCTGCATGGTGTGCTT 3180
Db 16120 TTTTTCGGCTTTCCAGCGTTCCGGCAGCAGAGCGGCTTCATTTCTGCATGGTGTGCTT 16179
Qy 3181 ACCAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAA 3240
Db 16180 ACCAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAA 16239
Qy 3241 CTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTGTGACATATCTCTGTCTTGTAT 3300
Db 16240 CTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTGTGACATATCTCTGTCTTGTAT 16299
Qy 3301 GCAGATGATTTTCAGGACTATGACACTAGCTAGCTATATGAATAGGTAGATTTTATTTT 3360
Db 16300 GCAGATGATTTTCAGGACTATGACACTAGCTAGCTATATGAATAGGTAGATTTTATTTT 16359
Qy 3361 TCACAAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCA 3420
Db 16360 TCACAAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCA 16419
Qy 3421 TTGAGGCAATPAGCGAGTAGGCTGGATACGACGATCCGTTTGTGAGAGAACATTTGGAAG 3480
Db 16420 TTGAGGCAATPAGCGAGTAGGCTGGATACGACGATCCGTTTGTGAGAGAACATTTGGAAG 16479
Qy 3481 GCTGTCCGTGCACTTAAGTTGCGACATCACCGAAGAACATTTGGAAGGCTGTCCGTGCA 3540
Db 16480 GCTGTCCGTGCACTTAAGTTGCGACATCACCGAAGAACATTTGGAAGGCTGTCCGTGCA 16539
Qy 3541 CTACAGGTCACATAATACCTCTAAGTAGTTGATTCATAGTGCATGGATATGTTGTGTTTT 3600
Db 16540 CTACAGGTCACATAATACCTCTAAGTAGTTGATTCATAGTGCATGGATATGTTGTGTTTT 16599
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Db 16600 ACAGTATATGATGCTGTGTTTTTATGCAAAATCAATCTAATTTAATATATGATTTATATC 16659
Qy 3661 ATTTTACGTTTCTGCTTCAGCTTTTTTGTACAACTTGTCTAGAGTCCCTGCTTTAATGAG 3720
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Qy 3721 ATATGCGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCTGTGTGCAAGTTGTAA 3780
Db 16720 ATATGCGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCTGTGTGCAAGTTGTAA 16779
Qy 3781 AAAACCTGAGCATGTGATGCTAGCTCCTTACCGCCGGTTTCCGTTCAATCTTAATGATA 3840
Db 16780 AAAACCTGAGCATGTGATGCTAGCTCCTTACCGCCGGTTTCCGTTCAATCTTAATGATA 16839
Qy 3841 TATCACCGGTTACTATCTGATTTTATGAATAAATATCTCCGTTCAATTTACTGATTTGTA 3900
Db 16840 TATCACCGGTTACTATCTGATTTTATGAATAAATATCTCCGTTCAATTTACTGATTTGTA 16899
Qy 3901 CCTACTACTTATATGTAACAATATTAATAAGAAAACAATATTTGTGCTGAATAGTTTAA 3960
Db 16900 CCTACTACTTATATGTAACAATATTAATAAGAAAACAATATTTGTGCTGAATAGTTTAA 16959
Qy 3961 TAGGACATCTATGATAGAGCGGCAACAATAACAACAATTTCCGTTTATTTATTAACAATC 4020
Db 16960 TAGGACATCTATGATAGAGCGGCAACAATAACAACAATTTCCGTTTATTTATTAACAATC 17019
Qy 4021 CAATTTTAAAAAAGCGGCGAGAACCGGTCAAAACCTTAAAGACTGATTAATCAATAATCTTAT 4080
Db 17020 CAATTTTAAAAAAGCGGCGAGAACCGGTCAAAACCTTAAAGACTGATTAATCAATAATCTTAT 17079

QY 4081 TCATATTTTCAAAAGCCCGGCTAGTCTATCGACACACCGCGGCACTAATAA 4140
DB |||||||
QY 17080 TCATATTTTCAAAAGCCCGGCTAGTCTATCGACACACCGCGGCACTAATAA 17139
DB |||||||
QY 4141 CGTTCACTGAAGGGAACCTCGGTTCCCGCCGCGCATGGGTGAGATTCTTTGAAATT 4200
DB |||||||
QY 17140 CGTTCACTGAAGGGAACCTCGGTTCCCGCCGCGCATGGGTGAGATTCTTTGAAATT 17199
DB |||||||
QY 4201 GAGTATGGCTCGCTCTACCGAAAGTTACGGGACCAATTAACCGGTCACGACGG 4260
DB |||||||
QY 17200 GAGTATGGCTCGCTCTACCGAAAGTTACGGGACCAATTAACCGGTCACGACGG 17259
DB |||||||
QY 4261 CGGCGGGTAACCGACTTCTGCGCGGAAATTATGAGCAATTTTGGTGTATGGG 4320
DB |||||||
QY 17260 CGGCGGGTAACCGACTTCTGCGCGGAAATTATGAGCAATTTTGGTGTATGGG 17319
DB |||||||
QY 4321 CCCCAATGAAGTGAGGTCAGGTCACCACTTGACAGTACGACAAATCGTTGGCGGGTCCAGG 4380
DB |||||||
QY 17320 CCCCAATGAAGTGAGGTCAGGTCACCACTTGACAGTACGACAAATCGTTGGCGGGTCCAGG 17379
DB |||||||
QY 4381 GCGAATTTTGGCAACATGTCAGGCTCAGAGACCTGCGAGCATGCAAGCTAGCTTA 4440
DB |||||||
QY 17380 GCGAATTTTGGCAACATGTCAGGCTCAGAGACCTGCGAGCATGCAAGCTAGCTTA 17439
DB |||||||
QY 4441 CTAGTGATGCATATCTATAGTGTCACTTAATCTGC 4477
DB |||||||
QY 17440 CTAGTGATGCATATCTATAGTGTCACTTAATCTGC 17476
DB |||||||

RESULT 2

ABQ82142
ID ABQ82142 standard; DNA; 17458 BP.
XX
AC ABQ82142;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX
XW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN W0200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
XX
PR 29-NOV-2001; 2001US-0333743P.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 16; Page 83-93; 104pp; English.

XX
XX The present invention describes a vector (1) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and

CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX

SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;

Query Match 98.4%; Score 4406.6; DB 6; Length 17458;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;

QY 1 TTTCAATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAAGCTGAAACGAGAAAGCT 60

DB TTTCAATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAAGCTGAAACGAGAAAGCT 13059

QY 61 AAAATGATATAAATCAATATATTAATTTAGATTTTGCATAAAAAAGCTGAAACGAGAAAGCT 120

DB AAAATGATATAAATCAATATATTAATTTAGATTTTGCATAAAAAAGCTGAAACGAGAAAGCT 13119

QY 121 ACTGTAAAAACAACATATCCAGTCACATGAATCAACTACTTAGATGGTATTAGTACC 180

DB ACTGTAAAAACAACATATCCAGTCACATGAATCAACTACTTAGATGGTATTAGTACC 13179

QY 181 TGTAGTCACCGACGAGCCTTCCAAATGTTCTCGGGTGTGTCGCAACTAGTCGACCG 240

DB TGTAGTCACCGACGAGCCTTCCAAATGTTCTCGGGTGTGTCGCAACTAGTCGACCG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGTCGTATCCAGCTACTCGCTATTGTC 300

DB ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGTCGTATCCAGCTACTCGCTATTGTC 13299

QY 301 CTCATATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGGTCGAGCCTCTTTTTCG 360

DB CTCATATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGGTCGAGCCTCTTTTTCG 13359

QY 361 TGTGCAAAATAAACAACATCTACCTATTATATATAGTGTATAGTCTGCAAAATCA 420

DB TGTGCAAAATAAACAACATCTACCTATTATATATAGTGTATAGTCTGCAAAATCA 13419

QY 421 TCTGCATCAAGAACAAATTTCAAACTCTTATATCTTTCTTTTACAGTCGTTCCGCTTCA 480

DB TCTGCATCAAGAACAAATTTCAAACTCTTATATCTTTCTTTTACAGTCGTTCCGCTTCA 13479

QY 481 TCTGGAATTTTCAAGCCTTATATCTTAACTGATATAAGTTTCTGTAATTTCTACTGTA 540

DB TCTGGAATTTTCAAGCCTTATATCTTAACTGATATAAGTTTCTGTAATTTCTACTGTA 13539

QY 541 TCGACCTGCGACTGCTGTATAGGAGCCTGACATTTATATTTCCCAAGAAATCAATCAG 600

DB TCGACCTGCGACTGCTGTATAGGAGCCTGACATTTATATTTCCCAAGAAATCAATCAG 13599

QY 601 GTTAATGGCGTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGAT 660

DB GTTAATGGCGTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGAT 13659

QY 661 AACGAGACCGGCACTGCGGCATATCGGTGTATCATGCGCCAGCTTTCATCCCGAT 720

DB AACGAGACCGGCACTGCGGCATATCGGTGTATCATGCGCCAGCTTTCATCCCGAT 13719

QY 721 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACGACGACGTCGACTGGCCAG 780

DB ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACGACGACGTCGACTGGCCAG 13779

QY 781 GGGGATCAACATCCGTCGCGCGCGGTGTCAATAATATACACTCTGTACATCCAGAACAG 840
DB 13780 GGGGATCAACATCCGTCGCGCGCGGTGTCAATAATATACACTCTGTACATCCAGAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTCACCAAGTCCCTGT 900
DB 13840 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTCACCAAGTCCCTGT 13899
QY 901 TCTGTCAGCAAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCT 960
DB 13900 TCTGTCAGCAAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCT 13959
QY 961 GATTTTCGCTTTCAGCGGTCGCGACGAGAGCGGCTTCATTTCTGCAAGTGTGTC 1020
DB 13960 GATTTTCGCTTTCAGCGGTCGCGACGAGAGCGGCTTCATTTCTGCAAGTGTGTC 14019
QY 1021 TTACAGACCGGAGATTAATGACATCATATATATGCTTTGAGCAACTGATAGCTGTCGCTGTC 1080
DB 14020 TTACAGACCGGAGATTAATGACATCATATATGCTTTGAGCAACTGATAGCTGTCGCTGTC 14079
QY 1081 AACTGTCACTGTAAATACGCTGCTTATAGCACACCTCTTTTGTGACANACTCGGGTAGTG 1140
DB 14080 AACTGTCACTGTAAATACGCTGCTTATAGCACACCTCTTTTGTGACANACTCGGGTAGTG 14139
QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAGTTGGCCAGGGCTTCCGGTATCAACAGGAC 1200
DB 14140 CCGATCAACGCTCTCATTTTCGCCAAAGTTGGCCAGGGCTTCCGGTATCAACAGGAC 14199
QY 1201 ACCAGGATTTATTTCTGCGAAGTGTCTTCGTCACAGGTATTTATTCGGCGCAAG 1260
DB 14200 ACCAGGATTTATTTCTGCGAAGTGTCTTCGTCACAGGTATTTATTCGGCGCAAG 14259
QY 1261 TGGCTGGGTGATGCTGCCAACTTGTGCTGACAGCTGCTCAATATACCATCTAAGTAGTT 1320
DB 14260 TGGCTGGGTGATGCTGCCAACTTGTGCTGACAGCTGCTCAATATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTACTGGATATGTTGCTTTTACAGTATTAATGATGCTGTTTTTATGCAA 1380
DB 14320 GATTCATAGTACTGGATATGTTGCTTTTACAGTATTAATGATGCTGTTTTTATGCAA 14379
QY 1381 AATCTAATTTAATATATGATATTTATATATTTATATTTTACGTTTCGCTTACGTTCTGTGA 1440
DB 14380 AATCTAATTTAATATATGATATTTATATATTTATATTTTACGTTTCGCTTACGTTCTGTGA 14439
QY 1441 CAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAATTAATTTCTTTT 1500
DB 14440 CAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAATTAATTTCTTTT 14495
QY 1501 TCCTTTTAGTATAAAATAGTAAAGTGTATTAATGATGATTAATAATAATAGTTGT 1560
DB 14496 TCCTTTTAGTATAAAATAGTAAAGTGTATTAATGATGATTAATAATAATAGTTGT 14555
QY 1561 TATAATGTGAAAAATTAATTAATAATATATTTGTTTACATAAACAACATAGTAAGTAA 1620
DB 14556 TATAATGTGAAAAATTAATTAATAATATATTTGTTTACATAAACAACATAGTAAGTAA 14615
QY 1621 AAAAATATGACAGTGTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1680
DB 14616 AAAAATATGACAGTGTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 14675
QY 1681 TTTTAAATGAAATTTGATCGAACATGTAGATGATATAGTATGATTAATAATAATAGTTTAAATC 1740
DB 14676 TTTTAAATGAAATTTGATCGAACATGTAGATGATATAGTATGATTAATAATAATAGTTTAAATC 14735
QY 1741 ATAAATAGTAATTCAGCTGGTTGATGATTAATAATATATATATATATATATATATAT 1800
DB 14736 ATAAATAGTAATTCAGCTGGTTGATGATTAATAATATATATATATATATATATATAT 14795
QY 1801 AATAAGAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1860
DB 14796 AATAAGAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 14855

QY 1861 AATATCTATACATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 1920
DB 14856 AATATCTATACATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 14915
QY 1921 TCCAATCTGCTGTAAATTTATCAATAAACAATAATAATAATAATAATAATAATAATAATA 1980
DB 14916 TCCAATCTGCTGTAAATTTATCAATAAACAATAATAATAATAATAATAATAATAATAATA 14975
QY 1981 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAAT 2040
DB 14976 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAAT 15035
QY 2041 AACAAAGCGCAAGATCTATCAITTTATATAGTATTTATTTTCAATCAACATCTTATTAAT 2100
DB 15036 AACAAAGCGCAAGATCTATCAITTTATATAGTATTTATTTTCAATCAACATCTTATTAAT 15095
QY 2101 TTCTAAATTAATACCTGTAGTTTATTAACCTTCTAATAGGATGACTATTAATTAATGA 2160
DB 15096 TTCTAAATTAATACCTGTAGTTTATTAACCTTCTAATAGGATGACTATTAATTAATGA 15155
QY 2161 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGTTGTTTATCAATTCAT 2220
DB 15156 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGTTGTTTATCAATTCAT 15215
QY 2221 CTTACATTTGGATTTACAGTTGGGAAGCTGGGTTGAAAATCGATAGCTTGGATCT 2280
DB 15216 CTTACATTTGGATTTACAGTTGGGTTGAAAATCGATAGCTTGGATCT 15261
QY 2281 CTAGACCACTTTGTACAAAGAACTGACGAGAAACGTAAATATGATATAATAATCAATAT 2340
DB 15262 CTAGACCACTTTGTACAAAGAACTGACGAGAAACGTAAATATGATATAATAATCAATAT 15321
QY 2341 ATTAAATTTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACACATATCCA 2400
DB 15322 ATTAAATTTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACACATATCCA 15381
QY 2401 GTCACTATGAATCAACTACTAGTAGTGTATTTAGTGACCTGTAGTGTAGTGTGGCAGC 2460
DB 15382 GTCACTATGAATCAACTACTAGTAGTGTATTTAGTGACCTGTAGTGTAGTGTGGCAGC 15441
QY 2461 ATCCCGGACGACCTTTCGCGGCAATAAATACCTGTGCGGAAGATCACTTCGCGAATA 2520
DB 15442 ATCCCGGACGACCTTTCGCGGCAATAAATACCTGTGCGGAAGATCACTTCGCGAATA 15501
QY 2521 AATAAATCTGCTGCTCTGTTGATACCGGGAAGCCCTGGGCAACTTTTGGCGAAAATG 2580
DB 15502 AATAAATCTGCTGCTCTGTTGATACCGGGAAGCCCTGGGCAACTTTTGGCGAAAATG 15561
QY 2581 AGAGTTGATCGGATTTCAAACTCTTATATCTTTTCTTACAAAGTCTGCTGCTTCAATC 2640
DB 15562 AGAGTTGATCGGATTTCAAACTCTTATATCTTTTCTTACAAAGTCTGCTGCTTCAATC 15621
QY 2641 TGGATTTTCAGGCTCTATACCTTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATC 2700
DB 15622 TGGATTTTCAGGCTCTATACCTTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATC 15681
QY 2701 GACCTGACAGCTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGGT 2760
DB 15682 GACCTGACAGCTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGGT 15741
QY 2761 TAAATGGCGTTTGTAGTCTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAA 2820
DB 15742 TAAATGGCGTTTGTAGTCTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAA 15801
QY 2821 CGGAGACCGGACACCTGGCCATATCGGTGCTCATATGCGCCAGCTTTTCTATCCCGATAT 2880
DB 15802 CGGAGACCGGACACCTGGCCATATCGGTGCTCATATGCGCCAGCTTTTCTATCCCGATAT 15861
QY 2881 GCACCAACCGGTAAGTTTCAACGGAGACTTTTATCTGACAGCAGACGTCGACCTGGCCAGG 2940
DB 15862 GCACCAACCGGTAAGTTTCAACGGAGACTTTTATCTGACAGCAGACGTCGACCTGGCCAGG 15921
QY 2941 GGATCACCATCCGTCGCGCGGCGTGTCAATTAATATCACTCTGTATATCCACAAAACAGAC 3000

Db 15922 GGATCACCATCGTCCGCGGGCGTCAATAATATCACTCTGTATACATCCACAAACAGC 15981
QY 3001 GATAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCCACAGTCCCTGTTC 3060
Db 15982 GATACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCCACAGTCCCTGTTC 16041
QY 3061 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCTGA 3120
Db 16042 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCTGA 16101
QY 3121 TTTTCGGCTTTCCAGGTTCCGACGACGACGAGGCTTCAATCTGCAATGTTGTGCTT 3180
Db 16102 TTTTCGGCTTTCCAGGTTCCGACGACGACGAGGCTTCAATCTGCAATGTTGTGCTT 16161
QY 3181 ACCAGACCGGAGATATTGACATCATATATGCTTCCAGCAACTGATAGCTGCTGTCGA 3240
Db 16162 ACCAGACCGGAGATATTGACATCATATATGCTTCCAGCAACTGATAGCTGCTGTCGA 16221
QY 3241 CTGTACTGTATACGCTGCTTCATAGACACACTCTTTTGTGACATCTCTGTTCTTGAT 3300
Db 16222 CTGTACTGTATACGCTGCTTCATAGACACACTCTTTTGTGACATCTCTGTTCTTGAT 16281
QY 3301 GCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATGTTTATTTTG 3360
Db 16282 GCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATGTTTATTTG 16341
QY 3361 TCACACAAAAGAGCGCTCGACCTCTTTTCTTATCTCTTTTATGATTTAATACGGCA 3420
Db 16342 TCACACAAAAGAGCGCTCGACCTCTTTTCTTATCTCTTTTATGATTTAATACGGCA 16401
QY 3421 TTGAGACAAATAGCGAGTGGTGGATACGAGATTCGGTTTCAGAGAACATTTGGGAAG 3480
Db 16402 TTGAGACAAATAGCGAGTGGTGGATACGAGATTCGGTTTCAGAGAACATTTGGGAAG 16461
QY 3481 GCTGTCGGTCGACTAAGTTGGCAGCATCACCGAAGAAATTTGGAGGCTGTCCGTGGA 3540
Db 16462 GCTGTCGGTCGACTAAGTTGGCAGCATCACCGAAGAAATTTGGAGGCTGTCCGTGGA 16521
QY 3541 CTACAGGTCACTAATACATCAAGTAGTGTGATTCATAGTACGATGATGTTGTTTT 3600
Db 16522 CTACAGGTCACTAATACATCAAGTAGTGTGATTCATAGTACGATGATGTTGTTTT 16581
QY 3601 ACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTAATATGATTTATATATC 3660
Db 16582 ACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTAATATGATTTATATATC 16641
QY 3661 ATTTTACGTTTCTCGTTACGTTTTTTGTACAAACTTGTCTAGAGTCCCTGTTTAAGAG 3720
Db 16642 ATTTTACGTTTCTCGTTACGTTTTTTGTACAAACTTGTCTAGAGTCCCTGTTTAAGAG 16701
QY 3721 ATATGAGACGCTATGATCGCATGATTTCTTTCAATTCGTTGTGTCAGTTGTAA 3780
Db 16702 ATATGAGACGCTATGATCGCATGATTTCTTTCAATTCGTTGTGTCAGTTGTAA 16761
QY 3781 AAAACCTGAGCATGTAGTCTAGATCTCTTACCGCGGTTTCGGTTTCATTTCAATGAATA 3840
Db 16762 AAAACCTGAGCATGTAGTCTAGATCTCTTACCGCGGTTTCGGTTTCATTTCAATGAATA 16821
QY 3841 TATCACCGTTTATGATGATTTTATGATTAATAATTTCTCCGTTCAATTTACGATGTA 3900
Db 16822 TATCACCGTTTATGATGATTTTATGATTAATAATTTCTCCGTTCAATTTACGATGTA 16881
QY 3901 CCTTACTACTTATATGATGATTAATAATAAGAAACAAATATTTGCTGAATAGTTTA 3960
Db 16882 CCTTACTACTTATATGATGATTAATAATAAGAAACAAATATTTGCTGAATAGTTTA 16941
QY 3961 TAGCGACATCTATGATAGCGCCACAAATAACAAATTTGCGTTTATTTATTTACAAATC 4020
Db 16942 TAGCGACATCTATGATAGCGCCACAAATAACAAATTTGCGTTTATTTATTTACAAATC 17001
QY 4021 CAATTTTAAAGAGCGGACCGGTGCAACCTTAAAGACGTATTTACATTAATCTTAT 4080

Db 17002 CAATTTTAAAGAGCGGACGACCCGGTCAAAACCTTAAAGACTGATTACATAAATCTTAT 17061
QY 4081 TCAATTTTAAAGAGCGGACGACCCGGTCAATTTCTAGACACACCCAGCGGGAATATAA 4140
Db 17062 TCAATTTTAAAGAGCGGACGACCCGGTCAATTTCTAGACACACCCAGCGGGAATATAA 17121
QY 4141 CGTTCACTGAAGGAACTCCGGTTCCCGCGGCGCATGGGTGAGATTCCTTTGAAGTT 4200
Db 17122 CGTTCACTGAAGGAACTCCGGTTCCCGCGGCGCATGGGTGAGATTCCTTTGAAGTT 17181
QY 4201 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCACCCGGTCCAGCAGG 4260
Db 17182 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGACCAATTCACCCGGTCCAGCAGG 17241
QY 4261 CGGCGGGTAAACCACTTGTCTGCGCGGAGATTTATGAGCAATTTTGGTGTATGTGG 4320
Db 17242 CGGCGGGTAAACCACTTGTCTGCGCGGAGATTTATGAGCAATTTTGGTGTATGTGG 17301
QY 4321 CCCCAATGAAGTGCAGGTCAAACTTGCACAGTACGACAAATCGTTGGGCGGTCACAGG 4380
Db 17302 CCCCAATGAAGTGCAGGTCAAACTTGCACAGTACGACAAATCGTTGGGCGGTCACAGG 17361
QY 4381 GCGAATTTTGGCAACAACTGTCAGGCTCAGCAGACCTGCGAGCATGCAAGCTAGCTTA 4440
Db 17362 GCGAATTTTGGCAACAACTGTCAGGCTCAGCAGACCTGCGAGCATGCAAGCTAGCTTA 17421
QY 4441 CTAGTGTAGCATATTTCTATAGTGTCACTAAATCTGC 4477
Db 17422 CTAGTGTAGCATATTTCTATAGTGTCACTAAATCTGC 17458

RESULT 3

ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.

XX ABQ82143;
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Wesley S, Waterhouse P, Helliwell C;

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 17; Page 93-102; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter

CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

Query Match 95.2%; Score 4262; DB 6; Length 17681;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 205; Gaps 1;

QY 1 TTTTCATTTGGAGAGACAGCTCGAGACAAAGTTTCTGACAAAAGCTGAACGAGAAACGT 60
Db TTTTCATTTGGAGAGACAGCTCGAGACAAAGTTTCTGACAAAAGCTGAACGAGAAACGT 13059

QY 61 AAAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db AAAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 13119

QY 121 ACTGTAAACACACATATCCAGTCACTATGAATCACTATGAATCACTATGAATCACTAT 180
Db ACTGTAAACACACATATCCAGTCACTATGAATCACTATGAATCACTATGAATCACTAT 13179

QY 181 TGTAGTCGACGACAGCCCTCCAAATGTTCTTTGGGTGATGCTGCCAACTTAGTCGACCG 240
Db TGTAGTCGACGACAGCCCTCCAAATGTTCTTTGGGTGATGCTGCCAACTTAGTCGACCG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCAACGGAAATGCTGATCCAGCTACTCGCTATGTGC 300
Db ACAGCCTTCCAAATGTTCTTCAACGGAAATGCTGATCCAGCTACTCGCTATGTGC 13299

QY 301 CTCATGCGGTATTAATCATAAAGAAATAGAAAGAGGTGCGAGCCCTCTTTTTCG 360
Db CTCATGCGGTATTAATCATAAAGAAATAGAAAGAGGTGCGAGCCCTCTTTTTCG 13359

QY 361 TGTGACAAAATAAAAACATCTACTATTCATATACGCTAGTGTCTAGTCTGAAATCA 420
Db TGTGACAAAATAAAAACATCTACTATTCATATACGCTAGTGTCTAGTCTGAAATCA 13419

QY 421 TCTGATCAAGAAACAAATTTTCAACACTCTTATACCTTTCTTCAACAGTCTGCGCTTCA 480
Db TCTGATCAAGAAACAAATTTTCAACACTCTTATACCTTTCTTCAACAGTCTGCGCTTCA 13479

QY 481 TCTGGATTTTTCAGCCTCTACTACTTACTTACTTCTTCTTCAACAGTCTGCGCTTCA 540
Db TCTGGATTTTTCAGCCTCTACTACTTACTTACTTCTTCTTCAACAGTCTGCGCTTCA 13539

QY 541 TCGACCTGACAGCTGGCTGTGTATAAGGGAGCCCTGACATTTATTTCCCGAACATCAG 600
Db TCGACCTGACAGCTGGCTGTGTATAAGGGAGCCCTGACATTTATTTCCCGAACATCAG 13599

QY 601 GTTAAATGGCGTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGAT 660
Db GTTAAATGGCGTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGAT 13659

QY 661 AACGGAGACCGGCACACTGCGCATATCGGTGGTTCATCATCGCCAGCTTTCATCCCGAT 720
Db AACGGAGACCGGCACACTGCGCATATCGGTGGTTCATCATCGCCAGCTTTCATCCCGAT 13719

QY 721 ATGCACCACCGGGTAAAGTTTACGGGAGACTTTTATCTGACGACAGCTGACCTGGCCAG 780

Db 13720 ATGCACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGACTGGCCAG 13779

QY 781 GGGGATACCATCGTCTGCCCGGGCGGTCAATAATATCACTGTACATCCCAACACAG 840

Db 13780 GGGGATACCATCGTCTGCCCGGGCGGTCAATAATATCACTGTACATCCCAACACAG 13839

QY 841 ACGATACCGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTAACTGCAATTTCAACAGTCCCTGT 900

Db 13840 ACGATACCGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTAACTGCAATTTCAACAGTCCCTGT 13899

QY 901 TCTCGTCAGCAAAAGAGCCGTTCAATTAATAAACCGGGGAGACCTCAGCCATCCCTTCT 960

Db 13900 TCTCGTCAGCAAAAGAGCCGTTCAATTAATAAACCGGGGAGACCTCAGCCATCCCTTCT 13959

QY 961 GATTTTCGGCTTCCAGCGGTTCGSCAGCAGACGAGCGGCTTCAATCTGATGTTGTGC 1020

Db 13960 GATTTTCGGCTTCCAGCGGTTCGSCAGCAGACGAGCGGCTTCAATCTGATGTTGTGC 14019

QY 1021 TTACGACGCGAGATATTGACATCATATATGCCCTTGAGCAACTGTAGCTGCTGCTC 1080

Db 14020 TTACGACGCGAGATATTGACATCATATATGCCCTTGAGCAACTGTAGCTGCTGCTC 14079

QY 1081 AACTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTAGTG 1140

Db 14080 AACTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTAGTG 14139

QY 1141 CCGATCAACGCTCTCATTTTCCGCAAAAGTTGSCCGAGCGCTTCCGGTATCAACAGGAC 1200

Db 14140 CCGATCAACGCTCTCATTTTCCGCAAAAGTTGSCCGAGCGCTTCCGGTATCAACAGGAC 14199

QY 1201 ACCAGGATTTTATTTCTGCGAAGTGATCTTCCGTACACAGTATTTTATCGGCGCAAG 1260

Db 14200 ACCAGGATTTTATTTCTGCGAAGTGATCTTCCGTACACAGTATTTTATCGGCGCAAG 14259

QY 1261 TCGCTCGGCTGATGCTGCCAACTTAGTCGACTACAGGTCACTATACCATCTAGTAGTT 1320

Db 14260 TCGCTCGGCTGATGCTGCCAACTTAGTCGACTACAGGTCACTATACCATCTAGTAGTT 14319

QY 1321 GATTCATAGTCACTCGATATGTTGTTTAAAGTATTTATGATGTTAGTCTGTTTTTATGCAA 1380

Db 14320 GATTCATAGTCACTCGATATGTTGTTTAAAGTATTTATGATGTTAGTCTGTTTTTATGCAA 14379

QY 1381 AATCTAAATTAATTAATTTATATATTTATATCAATTTTACGTTCTCGTTGAGCTTCTGTA 1440

Db 14380 AATCTAAATTAATTAATTTATATATTTATATCAATTTTACGTTCTCGTTGAGCTTCTGTA 14439

QY 1441 CAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTTCTTTT 1500

Db 14440 CAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTTCTTTT 14499

QY 1501 TCCTTTTAGTATAAAATAGTTAAAGTATGTTAAATAGTATGATTAATAATATATAGTTGT 1560

Db 14500 TCCTTTTAGTATAAAATAGTTAAAGTATGTTAAATAGTATGATTAATAATATATAGTTGT 14559

QY 1561 TATAATTTGAAAAAATAATTTATATAATATATTTGTTTACATAAACAACATAGTAATGTA 1620

Db 14560 TATAATTTGAAAAAATAATTTATATAATATATTTGTTTACATAAACAACATAGTAATGTA 14619

QY 1621 AAAAATATGCAAGTGTGTAAGCAGGAAGATATAAGTTGAGAGTAAGTATATAT 1680

Db 14620 AAAAATATGCAAGTGTGTAAGCAGGAAGATATAAGTTGAGAGTAAGTATATAT 14679

QY 1681 TTTTAAATGAATTTGATCGAAACATGTAAAGATGATATAGTACATTAATTTGTTTTAAATC 1740

Db 14680 TTTTAAATGAATTTGATCGAAACATGTAAAGATGATATAGTACATTAATTTGTTTTAAATC 14739

QY 1741 ATAATAGTAATTTCTAGCTGGTTTGTATGAATTAATTAATTAATTAATTAATTAATTA 1800

Db 14740 ATAATAGTAATTTCTAGCTGGTTTGTATGAATTAATTAATTAATTAATTAATTAATTA 14799

QY 1801 AATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860

|||||
15760 ATAGTAATCTAGCTGGTTGATGAATTAATATCAATGATAAATACTATAGTAAATAAT 15819
QY
1804 AAGATAAATAAATAAATAAATAATTTTTTANGATAATAGTTTTATTAATAATAAT 1863
Db
15820 AAGATAAATAAATAAATAAATAATTTTTTATGATAATAGTTTTATTAATAATAAT 15879
QY
1864 ATCTATACCAATACATAAATAATTTTAAAGTTAAAGTTAAATATTTTGTAGAAATTC 1923
Db
15880 ATCTATACCAATACATAAATAATTTTAAAGTTAAAGTTAAATATTTTGTAGAAATTC 15939
QY
1924 AATCTGCTGTAAATTTATCAATAAACAATAAATAAATAAAGCTAAAGTAAACAATAA 1983
Db
15940 AATCTGCTGTAAATTTATCAATAAACAATAAATAAATAAAGCTAAAGTAAACAATAA 15999
QY
1984 ATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAATTAAC 2043
Db
16000 TATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAATTAAC 16059
QY
2044 AAAGCGAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAATTC 2103
Db
16060 AAAGCGAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAATTC 16119
QY
2104 TAAATAATACTTGTAGTTTTTAACTTCTAATAGGATGACTATTTAATTAATAAGATTA 2163
Db
16120 TAAATAATACTTGTAGTTTTTAACTTCTAATAGGATGACTATTTAATTAATAAGATTA 16179
QY
2164 GTGCAACATGAATAAACAAGGTAAACATGATAGATCAATGTCATGTTGTATCATTTGATCTT 2223
Db
16180 GTGCAACATGAATAAACAAGGTAAACATGATGATCATGTCATTTGTATCATTTGATCTT 16239
QY
2224 ACATTTGGATTCATTAACAGTTCGGAGCTGGGTTTGGAAATCGATAAGCTTGGATCTCTA 2283
Db
16240 ACATTTGGATTCATTAACAGTTCGGAGTGGGTTTGGAAATCGATAAGCTTGGATCTCTA 16299
QY
2284 GA----- 2285
Db
16300 GAGAGCTGAGCTGGATGGCAATAATGATTTATTTGACTGATAGTGACCTGTTCTGTT 16359
QY
2286 -----CCACTTTGTACAAGAAAGCTGAACG 2310
Db
16360 GCAACAAATGTGAAGCAATGCTTTCTTATAATGCCAACTTTGTACAGAAAGCTGAACG 16419
QY
2311 AGAAACGTAAATGATATAAATAATCAATATATTAATTTAGATTTTGCATAAATAAACAAGAC 2370
Db
16420 AGAAACGTAAATGATATAAATAATCAATATATTAATTTAGATTTTGCATAAATAAACAAGAC 16479
QY
2371 TACATAAATCTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 2430
Db
16480 TACATAAATCTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 16539
QY
2431 TAGTGACCTGTAGTCGACTAAGTTGGCGCATCAACCGGAGCACTTTGGCCGGAATATAT 2490
Db
16540 TAGTGACCTGTAGTCGACTAAGTTGGCGCATCAACCGGAGCACTTTGGCCGGAATATAT 16599
QY
2491 ACCGTGACGGAGAGATCACTTCGAGATAAATAAATAATCCCTGGTGTCCCTGTTGATACCGG 2550
Db
16600 ACCGTGACGGAGAGATCACTTCGAGATAAATAAATAATCCCTGGTGTCCCTGTTGATACCGG 16659
QY
2551 GAAGCCCTGGGCCAACTTTTGGCGGAAAATGAGACGTTGATCGG-----ATTTCCACAA 2602
Db
16660 GAAGCCCTGGGCCAACTTTTGGCGGAAAATGAGACGTTGATCGG-----ATTTCCACAA 16719
QY
2603 CTCTTATACATTTCTCTTACAAGTTCGTTGCGGTTTCATCTGATTTTTCAGCCTCTATACTT 2662
Db
16720 CTCTTATACATTTCTCTTACAAGTTCGTTGCGGTTTCATCTGATTTTTCAGCCTCTATACTT 16779
QY
2663 ACTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTAT 2722
Db
16780 ACTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTAT 16839
QY
2723 AAGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTGTATGATTCAT 2782

16840 AAGGAGCCTGACATTTATATATCCAGAACATCAGGTTAATGCGTTTGTGATGTCATT 16899
QY
2783 TTCCGGTGGCTGATAGATCAGCACCTTTCTCCCGATAACGAGACCCGACACACTGGCCAT 2842
Db
16900 TTCCGGTGGCTGATAGATCAGCACCTTTCTCCCGATAACGAGACCCGACACACTGGCCAT 16959
QY
2843 ATCCGTGGTCAATCATGCGCCAGCTTTTCATCCCGCATATGACCAACCGGGTAAAGTTTCAG 2902
Db
16960 ATCCGTGGTCAATCATGCGCCAGCTTTTCATCCCGCATATGACCAACCGGGTAAAGTTTCAG 17019
QY
2903 GGAGACTTTATCTGACAGCAGACGTCGTCAGTCGGCCAGGGGATCACCATTCGTCGCCCGGG 2962
Db
17020 GGAGACTTTATCTGACAGCAGACGTCGTCAGTCGGCCAGGGGATCACCATTCGTCGCCCGGG 17079
QY
2963 CGTGTCAATATATCACTCTCTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATA 3022
Db
17080 CGTGTCAATATATCACTCTCTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATA 17139
QY
3023 GGTGTAAACCTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 3082
Db
17140 GGTGTAAACCTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 17199
QY
3083 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCG 3142
Db
17200 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCG 17259
QY
3143 CACGACAGACGCGGCTTCATTTCTGATGTTGTGCTTTACAGACCCGGAGATATTGACAT 3202
Db
17260 CACGACAGACGCGGCTTCATTTCTGATGTTGTGCTTTACAGACCCGGAGATATTGACAT 17319
QY
3203 CATATATGCTTTGAGCAACTGATAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 3262
Db
17320 CATATATGCTTTGAGCAACTGATAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 17379
QY
3263 CATACACACCTCTTTTGGACATCTCTGTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 3322
Db
17380 CATACACACCTCTTTTGGACATCTCTGTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 17439
QY
3323 ACACATAGCGTATATCAATAGGTAGATGTTTATTTTGTGTCACACAAAAGAGGCTCGCA 3382
Db
17440 ACACATAGCGTATATCAATAGGTAGATGTTTATTTTGTGTCACACAAAAGAGGCTCGCA 17499
QY
3383 CCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTTGAGGCAATAGCGAGTAGCG 3442
Db
17500 CCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTTGAGGCAATAGCGAGTAGCG 17559
QY
3443 TGGATACGACGATTCGCTTTGAGAGACATTTGGAAGCTGTCGGTCGACTAAGTTGCG 3502
Db
17560 TGGATACGACGATTCGCTTTGAGAGACATTTGGAAGCTGTCGGTCGACTAAGTTGCG 17619
QY
3503 AGCATCACCCGAAAGAACATTTGGAAGCTGTCGGTCGACTACAGGTCACTAATACCATCT 3562
Db
17620 AGCATCACCCGAAAGAACATTTGGAAGCTGTCGGTCGACTACAGGTCACTAATACCATCT 17679
QY
3563 AAGTATGATGATCATAGTACGATATGTTGTGTTTACAGTATATGATGTCGTTTT 3622
Db
17680 AAGTATGATGATCATAGTACGATATGTTGTGTTTACAGTATATGATGTCGTTTT 17739
QY
3623 TTATGCAAAATCTAATTAATATATGATTTATATATATATATATATATATATATATATATAT 3682
Db
17740 TTATGCAAAATCTAATTAATATATGATTTATATATATATATATATATATATATATATATAT 17799
QY
3683 TTTTGTACAAAACCTTG----- 3698
Db
17800 TTTTGTACAAAAGTTGGCATTTAAAAAGCATTTGCTCATCAATTTGTTGCAACGAACAG 17859
QY
3699 -----TCTAGAG 3705
Db
17860 GTCACTATCAGTCAAAAATAAATCATTTATTTGGGGCCCGAGATCCATGCTAGCTCTAGAG 17919
QY
3706 TCCTGCTTTAATGAGATATGCGAGACCGCTATGATGCGATGATATTTGCTTTCAATTCG 3765
Db
17920 TCCTGCTTTAATGAGATATGCGAGACCGCTATGATGCGATGATATTTGCTTTCAATTCG 17979

QY 3766 TTGTGACGCTGTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGT 3825
Db 17980 TTGTGACGCTGTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGT 18039
QY 3826 TCATTCTAATGAATATATACACCGGTTTACATCGTATTTTATGAATAATTTCTCGGTTTC 3885
Db 18040 TCATTCTAATGAATATATACACCGGTTTACATCGTATTTTATGAATAATTTCTCGGTTTC 18099
QY 3886 AATTACTGATTTGTTACCTTACTTATATGATGACAAATATTAATAAGAAACAAATATATTG 3945
Db 18100 AATTACTGATTTGTTACCTTACTTATATGATGACAAATATTAATAAGAAACAAATATATTG 18159
QY 3946 TCCTGAATAGGTTTATAGGACATCTATGATAGCGCCACAAATACAAACAAATTTGCGTT 4005
Db 18160 TCGTGAATAGGTTTATAGGACATCTATGATAGCGCCACAAATACAAACAAATTTGCGTT 18219
QY 4006 TTATTATTACAAATCCAAATTTTAAAAAGAGCGGAGAACCGGTCAAACTTAAAAAGACTGA 4065
Db 18220 TTATTATTACAAATCCAAATTTTAAAAAGAGCGGAGAACCGGTCAAACTTAAAAAGACTGA 18279
QY 4066 TTACATAAATCTTATTCAAAATTTTAAAAAGAGCGGAGAACCGGTCAAACTTAAAAAGACTGA 4125
Db 18280 TTACATAAATCTTATTCAAAATTTTAAAAAGAGCGGAGAACCGGTCAAACTTAAAAAGACTGA 18339
QY 4126 GCGGCGAACTTAATACGTTTCACTGAAGGAACTCCCGGTTCCCGCGCGGCGGCGATGGGTG 4185
Db 18340 GCGGCGAACTTAATACGTTTCACTGAAGGAACTCCCGGTTCCCGCGCGGCGGCGATGGGTG 18399
QY 4186 AGATTCCTTGAAGTTGAGTATTCGGGTCGCGTCTACCGAAAGTTACGGGCGACCATTCAA 4245
Db 18400 AGATTCCTTGAAGTTGAGTATTCGGGTCGCGTCTACCGAAAGTTACGGGCGACCATTCAA 18459
QY 4246 CCGGTCGACGCGGCGGCTAACCGACTTGTCCCGCGAGATTTATGAGCAATTTT 4305
Db 18460 CCGGTCGACGCGGCGGCTAACCGACTTGTCCCGCGAGATTTATGAGCAATTTT 18519
QY 4306 TTGTGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACTTGCACAGTGCACGCAAAATCG 4365
Db 18520 TTGTGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACTTGCACAGTGCACGCAAAATCG 18579
QY 4366 TTGGGCGGTCGAGGCGAATTTTGGCAACATGTGCGAGGCTCAGGAGACCTGCAGGC 4425
Db 18580 TTGGGCGGTCGAGGCGAATTTTGGCAACATGTGCGAGGCTCAGGAGACCTGCAGGC 18639
QY 4426 ATCAAGCTAGCTACTAGTGTGTCATATTTCTATAGTGTCACTTAATCTGC 4477
Db 18640 ATGCAAGCTAGCTACTAGTGTGTCATATTTCTATAGTGTCACTTAATCTGC 18691

RESULT 5
ABQ82142/c
ID ABQ82142 standard; DNA; 17458 BP.
XX AC ABQ82142;
XX AC ABQ82142;
DT 11-DEC-2002 (first entry)
XX DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX DE Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KW recombination site; double stranded RNA; plant; ds.
XX OS Synthetic.
XX OS
XX PN WO200259294-A1.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-AU000073.
XX PR 26-JAN-2001; 2001US-0264067P.
XX PR 29-NOV-2001; 2001US-0333743P.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX DR
XX PT New vectors comprising operably linked DNA fragments having an origin of
XX PT replication, a selectable marker and a chimeric DNA construct, useful for
XX PT silencing target nucleic acids and for producing large amounts of double-
XX PT stranded RNA.
XX PS Claim 16; Page 83-93; 104pp; English.
XX CC The present invention describes a vector (I) comprising operably linked
XX CC DNA fragments having: (a) origin of replication allowing replication in a
XX CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
XX CC selectable marker region capable of being expressed in the recipient cell
XX CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
XX CC region capable of being recognized by RNA polymerases of a eukaryotic
XX CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
XX CC fourth recombination sites; (iii) 3' transcription terminating and
XX CC polyadenylation region functional in the eukaryotic cell. The first and
XX CC fourth recombination sites, or the second and third recombination sites
XX CC are capable of reacting with a same recombination site, and preferably
XX CC are identical. The first and second recombination sites, or the third and
XX CC fourth recombination sites, do not recombine with each other or with a
XX CC same recombination site. The vector is useful for producing large amounts
XX CC of double-stranded RNA which can be used for silencing target nucleic
XX CC acid sequences. The vectors can also be used to convert a DNA fragment
XX CC into an inverted repeat structure. Plants transformed with a vector from
XX CC the present invention can be used in a conventional breeding scheme to
XX CC produce more plants with the same characteristics or to introduce a
XX CC chimeric gene for reduction of the phenotypic expression of nucleic
XX CC acids. The present sequence represents an acceptor vector nucleotide
XX CC sequence from the present invention
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 28.5%; Score 1277.8; DB 6; Length 17458;
Best Local Similarity 62.4%; Pred. No. 4.5e-173;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;
QY 21 CTCGACAGAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAAT 80
Db 16686 CTCGACAGAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAAT 16627
QY 81 ATATTAAATAGATTTTGCATAAAAACAGACTACATATACTGTAAAAACAAACATATC 140
Db 16626 ATATTAAATAGATTTTGCATAAAAACAGACTACATATACTGTAAAAACAAACATATC 16567
QY 141 CAGTCACATGAATCAACTTACTTAGATGGTATTAGTGACCTTAGTCGACAGCCCTT 200
Db 16566 CAGTCACATGAATCAACTTACTTAGATGGTATTAGTGACCTTAGTCGACAGCCCTT 16507
QY 201 CCAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAGCTTCCAAATGTTCTT 260
Db 16506 CCAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAGCTTCCAAATGTTCTT 16447
QY 261 CTCACACGGAATGCTGCTATCCAGCCTACTCGTATTGTTCCTCAATGCGGTATTAATCA 320
Db 16446 CTCACACGGAATGCTGCTATCCAGCCTACTCGTATTGTTCCTCAATGCGGTATTAATCA 16387
QY 321 TAAAAAGAAATAGAAAAAGAGTGCAGGCCTCTTTTGTGTGACAAATAAAAAACATC 380
Db 16386 TAAAAAGAAATAGAAAAAGAGTGCAGGCCTCTTTTGTGTGACAAATAAAAAACATC 16327
QY 381 TACCTATTATATACGCTAGTGTCTAGTCTCTGAAATCATCTGCAATCAAGAACATTTTC 440
Db 16326 TACCTATTATATACGCTAGTGTCTAGTCTCTGAAATCATCTGCAATCAAGAACATTTTC 16267
QY 441 ACAACTCTTATATCTTTTCTTCTTACAAGTCTGTCGGCTTCATCTGGATTTTTCAGCCTCTAT 500

Db 16266 ATGTCAAAAGAGGTGTCCTATGAA--GCAGCGTATTACAGTGACAGTTCGACAGCGACA 16210
Qy 501 ACTTACTAAGCGTGATAAAGTTTCGTAAATTTCTACTGTATCGACCTCGACACTGGCTGT 560
Db 16209 GCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGTGTAAGCACAAACAT 16150
Qy 561 GTATAAGGAGGCGCTGACATTTATATATCCCGAAGCATCAGGTTAATGGCGTTTGTGATG 620
Db 16149 GCAGAAATGAAGCCCGTGTCTCGTGGCC---GAACGCTGGAAAGCGGAAATCAGGAAG 16093
Qy 621 CATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGATTAACGGAGACCGGCACACTGG 680
Db 16092 GATGCTGAGGTGCGCCCGGTTTATTGAAATGAACGGCTCTTTTGTGTGACGAAACAGGG- 16034
Qy 681 CCAATATCGGTGTCAATCATGCGCCAGCTTTTCAATCCCGATATGACCAACCGGGTAAAGTT 740
Db 16033 -----ACTGGTGAATGTCAGTTTAAAGTTTACACCTATAAAAGAGAGAGCGGTTATCGTC 15979
Qy 741 CACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCCACATCCGTCGCC 800
Db 15978 TGTTTGTGATGTAAGAGTGATATTATGACACGCCCGGGCGACGGATGGTGATCCCCC 15919
Qy 801 CGGGCGTGTCAATATATCACTCTGTACATCCAAAACAGACGATAACGGCTCTCTCTTT 860
Db 15918 TGGCCAGTGCACTGTCTGTGTCAGATAAAGTCTCCCGTGAACCTTTACCGGGTGGTGCA 15859
Qy 861 TATAGGTGTAACCTTAACTGCATTTACCC-----AGTCCCTGTCTCGTCAGCAAAA 914
Db 15858 TCGGGGATGAAGCTGGCGCATGATGACCACCGATATGGCCAGTGGCCGGTCTCCGTGA 15799
Qy 915 GAGCGCGTTCATTTCAATAACCGGGCGACCTCAGCCATCCCTTCCTGTGATTTCCGCTTTC 974
Db 15798 TCGGGGAAGAGTGGCTGATCTCAGCCAACCGGAAATGACATCAAAAACGCCATTAAC 15739
Qy 975 CAGCGTTC---GGCAGCGAGACGACGGGCTTCACTCTGATGGTGTGCTTACGACACCG 1031
Db 15738 TGAATGTTTCGGGGAATATAAATGTCAAGGCTCCCTTATACACAG-----CGAGTCTG 15688
Qy 1032 GAGATATTCACATCATATATGCTTCAGCAACTGATAGCTGCTGCTCAACTGCTCACTG 1091
Db 15687 CAGTCTGATACAGTAAATACAGAACTTTATCAGTTTAGTAAATAGAGGTGAA 15628
Qy 1092 TAATAGCTGTCTTATAGACACCTCTTTTACATACACTTCGGGTAGTG---CGATCA 1147
Db 15627 AATCCAGATGAAGCCGAAACGCTGTGAAGAGAAAGTATAAAGAGTTGTGAATCCGATCA 15568
Qy 1148 AGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTCCCGGTATCAACAGGACACCCAGCA 1207
Db 15567 ACGTCTCATTTTGGCCAAAAGTTGGCCAGGGCTCCCGGTATCAACAGGGACACCCAGCA 15508
Qy 1208 TTTTATTTATCTCGAAGTATCTTCCTGTCAGAGTATTTATTCGGCGCAAAAGTGGCTG 1267
Db 15507 TTTTATTTATCTCGAAGTATCTTCCTGTCAGAGTATTTATTCGGCGCAAAAGTGGCTG 15448
Qy 1268 GTGATGCTGCCAACTTAGTGTGATACAGTCTAATAACCATCTAAGTAGTGTGATCAT 1327
Db 15447 GTGATGCTGCCAACTTAGTGTGATACAGTCTAATAACCATCTAAGTAGTGTGATCAT 15388
Qy 1328 AGTACTGCATATGTTGTGTTTACAGTATATGATGCTGTTTATTTATGCAAAATCTAA 1387
Db 15387 AGTACTGCATATGTTGTGTTTACAGTATATGATGCTGTTTATTTATGCAAAATCTAA 15328
Qy 1388 TTTTATATATTTAT 1447
Db 15327 TTTTAT 15268
Qy 1448 GTCTCGAGGAATTCGGTACCCCGAGCTTGGTAAAGAAATATATATATATATATATAT 1507
Db 15267 GTCTAGAGGA--TCCAAGCTTAAAGTAAAGTAACTG--TAATCAATCCAAATGTAAGATCA 15212
Qy 1508 AGTATAAATAGTTAGTGTATGTTTATGATGATATATATATATATATATATATATAT 1567
Db 15211 ATGATAACAATAGATGATCTATCATGTGTACCTGTTTATTCATGTTCGACTAATTC 15152

Qy 1568 GTGAAAAATAATTTATAATATATCTTTACATAAAACACATAGTAATGTAAAAAATA 1627
Db 15151 TTTTAAATTAATAGTCAATCCATTTAGAGTTTAAATAAAGTCAAGTATATTTAGAAATTA 15092
Qy 1628 TGACAAAGTGTGTGTAGAGACGAAGATAAAGTGTGAGAGTATATATATTTTAAAT 1687
Db 15091 ATAAGATGTTGATTTGAAATAATCTATATATAAATGATAGATCTTGGCGCTTGTATAT 15032
Qy 1688 GAATTTGATCGAATGATGATATCTAGCATTAATTTTGTTTTATCATATATAG 1747
Db 15031 TAGCATTAGATTTATGTTTGTTCATTAGATTTCTGTTCTTATTAGTTTGTATTTT 14972
Qy 1748 TAAATTTAGCTGGTTTGTAGTAATTAATATCAATGATAAAATCTATAGTAAAAATAGA 1807
Db 14971 TTAATTTAGCTGGTTTATTAATATTTTCTTTTATGATAAATCAAGCAGATTTGAAAT 14912
Qy 1808 ATAATAAATTAATAATATTTTATGATTAATAGTTTATTAATAATAATATCT 1867
Db 14911 CTAACAAAATATTTAATTAACCTTTTAAACTAAATATTTAGTAATGGTATAGATTTTAA 14852
Qy 1868 ATACCATTTACTAAATATTTTAAAGTTTAAATAATTTTGTAGAAATCCCAATC 1927
Db 14851 TATATAATAACTTATTAATCATATAAATAATATTTTAAATTTATTTATTTCTTTATTT 14792
Qy 1928 TGCCTGTAAATTTATCAATAAAACAAATATTAATAACAAAGCTAAAGTAAACAATAATC 1987
Db 14791 CTAATAGTATTTTATCATTTGATTTTAAATTCATCAACCCAGCTAGAAATTTATTTAT 14732
Qy 1988 AAACATAATAGAAACAGTAACTCTAATGTAACAAACATAATCTAATGCTTAATAACAAG 2047
Db 14731 AAAACAAAATATTAATGCTAGTATATATCATTTACATTTGATCAAAATTCATTTAA 14672
Qy 2048 CGCAGATCTCATTTTATATATAGTATTTTCAATCAACATCTCTTAAATTTCTAAA 2107
Db 14671 TATCTTACTCTCACTTTTATCTTCTGCTTACACATCACTGCTGATTTTCTTTTAC 14612
Qy 2108 TAATACTTTGTAGTTTATTAATCTCTAAATGGAATGACTATTAATAATGAATTAGTGC 2167
Db 14611 ATTACTATGTTGTTATGTAACAAATATATTTATAAATTTATTTTTCACAAATTAACA 14552
Qy 2168 AACATGAATAACAGGTAAACATGATAGATCATGTCATGTCATTTATTTATTTTACAT 2227
Db 14551 CTATATTTATTAATTCATTAATTAACATCACTTAATTTTATCTTAAAGGAAATA 14492
Qy 2228 TTGGATGATTTACAGTTGGGAAGCTGGGTTGGAATTCGATAGCTTGGATCTCTAGACC 2287
Db 14491 AGAAAATAATTTATTTCCCTTACAGTTGGTACCGAAT-----TCCTCGAGACC 14446
Qy 2288 ACTTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATTTAAT 2347
Db 14445 ACTTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATTTAAT 14386
Qy 2348 TAGATTTTGCATAAATAAAGACAGACTATAAATCTGTAATAACACATATCCAGTCACTA 2407
Db 14385 TAGATTTTGCATAAATAAAGACAGACTATAAATCTGTAATAAACAACATATCCAGTCACTA 14326
Qy 2408 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTTCGACTAAGTTGCGACATCAACC 2467
Db 14325 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTTCGACTAAGTTGCGACATCAACC 14266
Qy 2468 GACGCACTTTGGCGGATTAATATCTGTGACGGAAGATCACTTTCGAGAAATAAATAAT 2527
Db 14265 GACGCACTTTGGCGGATTAATATCTGTGACGGAAGATCACTTTCGAGAAATAAATAAT 14206
Qy 2528 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAATTTTGGCGAAAATGAGACGTT 2587
Db 14205 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAATTTTGGCGAAAATGAGACGTT 14146
Qy 2588 GATCGGATTTCAACTCTTATCTTTCTCTTACAAAGTGTTCGGCTTCATCTGATTT 2647
Db 14145 GATCGS-----CACTACCCGAAATGCTCAAAAGAGGTGTGCTATGAACGACGCTATTAC 14090

2648 TCAGCTCTTACTTACTTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACTGC 2707
14089 AGTGACAGTTGACGCGACGACGATACAGTTGCTCAAGGCAATATATGATGTCAATATCTCC 14030
2708 AGACTGG-----CTGTGTATAAGGAGGCTGACATTTATATTTCCCCAGAACATCAG 2758
14029 GGTCTGGTAAGACACAACCATGACAGATGAAGCCCGTCTGTCGGTGC---GAACGCTGG 13973
2759 GTTAATGGGTTTTTGTATGTCATTTTCGGGFGGTGATGATCAGCACTTCTTCCCGCAT 2818
13972 AAAGCGAAATCAGGAAGGATGCTGAGTGGCGCGGTTTATTGAAATGAACGGCTCT 13913
2819 AACGAGACCGGACACACTGGCCATATCGTGTGTCATGCGCCAGCTTTCATCCCGAT 2878
13912 TTTGCTGACGAAACAGGGA-----CTGCTGAATGCGATTTAAGTTTACACTATGA 13859
2879 ATGCACACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTCGCACTGGCCAG 2938
13858 AAGAGAGAGCCGTTATCGTCTGTTGTGGATGACAGAGTGATATTTATGACACGCCGG 13799
2939 GGGATACACATCCGTCGCGCGGGGTGTCATATATACACTCTGTACATCCACAAACAG 2998
13798 GCGAGGATGGTATCCCGCTGGCCAGTCACGCTCTGCTGTGATGATGATGATGATGATG 13739
2999 ACGATAAGCGCTCTCTCTTTTATAGTGTAAACCTTAAACCTGATTTACAC-----AGT 3052
13738 ACTTACCCGGTGTGCATATCGGGATGAAAGCTGGCCCATGATGACACCGATATGCG 13679
3053 CCCTGTTCTCGTCAGCAAAAGCCGTTTCATTTCAATAAACCGGGCGACTCAGCCATCC 3112
13678 CAGTGTGCGGCTCTCGGTTATCGGGAAGAGTGGCTGATCTCAGCCACCGGAAATGA 13619
3113 CTTCTGTATTTCCGTTTCCAGCTTC---GGCAGCAGACGACGGGTTTCTATCTGCA 3169
13618 CATCAAAAACGCCATTAACCTGATGTTCTGGGGAATATAATGTGAGGCTCCCTTATACA 13559
3170 TGG---TTGCTGTACAGACCGGAGATATTGACATCATATATGCTTGGACCACTGATA 3226
13558 CAGCAGCTCGAGGTCGATACAGTAGAATATACAGAACTTTATCAGTTAGTAGTA 13499
3227 GCTGTCGCTGCACTGTCTGATGATGATTTTCAGGACTATGACACTGATGATGATGATG 3286
13498 TAGAGGCTGAAATCCAGATGAAGCCGACGACTTGTAAAGAAAAAGTATAAGAGTTGTG 13439
3287 CTTCTCTTCTGATGATGATGATTTTCAGGACTATGACACTGATGATGATGATGATGATG 3346
13438 AATTTGTTCTGATGATGATGATTTTCAGGACTATGACACTGATGATGATGATGATGATG 13379
3347 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTCTTTTAT 3406
13378 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTCTTTTAT 13319
3407 GATTTATACGGATTGAGACAAATAGCGATAGGCTGGATGACAGATTCGTTTGTAGA 3466
13318 GATTTATACGGATTGAGACAAATAGCGATAGGCTGGATGACAGATTCGTTTGTAGA 13259
3467 AGAACATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3526
13258 AGAACATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13199
3527 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3586
13198 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13139
3587 ATATGTTGTTTACAGTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3646
13138 ATATGTTGTTTACAGTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13079
3647 TTGATATTTATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3705
13078 TTGATATTTATCATTTTACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13020

RESULT 6

ABQ82141/C
ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
OS Synthetic.
XX WO200259294-A1.
XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU0000073.
XX 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
DR
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 15; Page 74-83; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
Query Match 28.4%; Score 1273; DB 6; Length 17476;
Best Local Similarity 62.1%; Pred. No. 2.1e-172;
Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;
QY 21 CTCGACAGAGTTTGTACAAAAAGCTGACAGAAACGTTAAATGATATATCAAT 80
DB 16704 CTCACAGAGTTTGTACAAAAAGCTGACAGAAACGTTAAATGATATATCAAT 16645
QY 81 ATATTAAATAGATTTTGCATATAAAGACAGCTACATATATCTGTAACAAACATATC 140
DB 16644 ATATTAAATAGATTTTGCATATAAAGACAGCTACATATATCTGTAACAAACATATC 16585

141 CAGTCACATGATCAATCACTTAGATCGTATAGTACCTCTAGTCGACCGACAGCCCTT 200
16584 CAGTCACATGATCAATCACTTAGATCGTATAGTACCTCTAGTCGACCGACAGCCCTT 16525
201 CCAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTT 260
16524 CCAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTT 16465
261 CTCAAACGGATTCGTCGTATCCAGCCTACTCGCTATTTGTCCTCAATGCGGTATTAATCA 320
16464 CTCAAACGGATTCGTCGTATCCAGCCTACTCGCTATTTGTCCTCAATGCGGTATTAATCA 16405
321 TAAAAAGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGCAAAATAAAAAACATC 380
16404 TAAAAAGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGCAAAATAAAAAACATC 16345
381 TACCTATTCAATACCGCTAGTCATAGTCCTGAAATCATCTGCAATCAAGAACCAATTC 440
16344 TACCTATTCAATACCGCTAGTCATAGTCCTGAAATCATCTGCAATCAAGAACCAAGT 16285
441 ACAACTCTTATCTCTCTTACAGTGGTTCGCTTCATCTGCAATCTAGCTTTCAGCCCTCTAT 500
16284 ATGTCAAAAGAGGTGTGCTATGAA---GCAAGCTATTACAGTGACAGTGTGACGGACA 16228
501 ACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560
16227 GCTATCAGTTGCTCAAGGCATATATGATCTCAATCTCCGGTCTGGTAAGCACAAACAT 16168
561 GTATAGGAGGCTGACATTTATATPCCCGCAACATCAGGTTAATGGCGTTTTTGATGT 620
16167 GCAGAATGAAGCCGTCGTCGGTGCC---GAAAGCTGGAAGCGGAAAAATCAGGAAG 16111
621 CATTTTCGGGTGGCTGAGTACGACATCAGCACATCTTCCCGGATAAGGAGACCGCACACTGG 680
16110 GATGGCTGAGTGGCCCGGTTTATTGGAATGAACGGCTCTTTTGTGTCGAGAAAGGGG- 16052
681 CCATATCGGTGGTCAATCAGCGCAGCTTTCTPCCCGGATGATGCACACCGGGTAAAGTT 740
16051 -----ACTGGTGAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCCGTTATCGTC 15997
741 CACGGAGACTTTATCTGACAGCAGAGTGCACCTGGGCGAGGGGGATCACCATCCGTCGCC 800
15996 TGTGTTGTGATGTACAGAGTGATTTATTGACACGCGCCGGCGACGGATGGTGTATCCGCC 15937
801 CGGGCGTGTCAATAATCACTCTGTACATCCCAAAACAGACGATAAACGGCTCTCTCTTT 860
15936 TGGCCAGTGACGCTGCTGTGTGATAGTCTCCGCTGNACTTTACCGGTGGTGCATA 15877
861 TATAGGTGTAACCTTAACTGCAATTCACG-----AGTCCCTGTTCTGTCGACGCAAAA 914
15876 TCGGGGATGAAAGCTGGCGCATGATGACCAACCGATATGGCCAGTGTGCGGTCTCCGTTA 15817
915 GAGCCGTTCATTTCAATAACGGGCGACCTCAGCCATCCCTCCCTGATTTTCGGCTTTC 974
15816 TCGGGGAAGAAGTGGGTGATCTCAGCACCGCGGAAATGATCAAAAACGCCATTAAAC 15757
975 CAGCGTTC---GGCAGCAGACGACGGGCTTCATCTGCAATGTTGTGCTTACGACACCG 1031
15756 TGATGTTCTGGGAATATAATGTACAGCTCCCTTATACAG-----CCAGTCTG 15706
1032 GAGATATGTACATATATGCTGTCAGCACTGATAGTGTGCTGCTGCTCACTGTCACTG 1091
15705 CAGGTCGATACAGTAGAAATACAGAACTTTATCAGGTTTAGTATAGTAGGCTGAA 15646
1092 TATACGCTGTTTCATAGCACACCTCTTTTGTACATACCTTTCGGGTAGTG---CCGATCA 1147
15645 AATCCAGATGAAGCCGAAACGACTTGTGAAGAAAGATATAAGAGTTGTGAAATCCGATCA 15586
1148 ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGAACACCAAGGA 1207
15585 ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGGAACACCAAGGA 15526

1208 TTTATTATTCTCGAAAGTGATCTTCGGTCAACAGGTATTTATTTCGGGCAAAAGTCGCTG 1267
15525 TTTATTATTCTCGAAAGTGATCTTCGGTCAACAGGTATTTATTTCGGGCAAAAGTCGCTG 15466
1268 GGTGATGCTGCAACTTAGTCGACTACAGGTCACATTAATCACTCTAAGTAGTGTATTCAT 1327
15465 GGTGATGCTGCAACTTAGTCGACTACAGGTCACATTAATCACTCTAAGTAGTGTATTCAT 15406
1328 AGTCAGCTGATATGTTGTTTTTACAGTATTAATGATGTCGTTTTTTTATGCAAAATCTAA 1387
15405 AGTCAGCTGATATGTTGTTTTTACAGTATTAATGATGTCGTTTTTTTATGCAAAATCTAA 15346
1388 TTTAATATATTGATTTATATATCAATTTTACGTTTCTCGTTTCAGCTTCTCTGTACAAAGT 1447
15345 TTTAATATATTGATTTATATCAATTTTACGTTTCTCGTTTCAGCTTCTCTGTACAAAGT 15286
1448 GTCTCGAGGAATTCGGTACCCGACGCTTGTAAAGGAA-----TAAATATTTTCTT 1497
15285 GTCTAGAGGATCCAGCTTATCGATTTTGAACCCGAGCTTCCCACTGTAATCAATCCAAA 15226
1498 TTTTCCTTTTAGTATATAAATAGTTAAAGTGATGTTAAATAGTATGATTAATAATATAGT 1557
15225 TGTAGATCAATGATAACAAATGACATGATCTATCATGTTACCTGTTTATTCATGTTT 15166
1558 TGTATAATTTGAAAAAATAATTTTATAATAATTTGTTTACATAAAACACATAGTAATG 1617
15165 GACTAATTTCAATTTAATTAATAGTCAATCCATTTAGAAGTTAATAAACTACAAAGTATTAT 15106
1618 TAAAAAATATACAAAGTGATGTGAAGCAAGAGATATAAAGTTGAGAGTAAGTATAT 1677
15105 TTAGAAATTAATAGAAATGTTGATTTGAAATTAATTAATTAATTAATGATAGTCTTGGC 15046
1678 TATTTTAAATGAATTTGATCGAAACATGTAAGATGATATATAGCAATTAATTTGTTTAA 1737
15045 TTTGTTATATTAGCATTAGATTTATGTTTGTACATTAATGATTAATTTCTTCTATTAGTTG 14986
1738 ATCAATAATAGTAATTTCTAGCTGGTTTGAATTAATAATCAATGATAAAATACATAGT 1797
14985 ATATTATTGTTTACTTTAGCTTTGTTTAAATTTTGTGTTTATGATAAATTTACAGCAG 14926
1798 AAAAAATGAATAAATAAATAAATAATTTTATGATTAATAGTTTATATATAA 1857
14925 ATTGGAATTTCTACAAATAATTTATTAATTTTAACTTTTAACTAAATATTTAGTAATGGTATA 14866
1858 TTAATAATCTATPACCACTTACTAAATATTTAGTTTAAAGTTTAAATAATTTTGTGTTAA 1917
14865 GATAATTAATATAATAAATAATTAATTAATCAATAAATAAATAATTTTAAATTTATTTAT 14806
1918 AATTCCAATCTGCTGTTGATTTTATCAATAAACAATAATATAAATAAACAAGCTTAAAGTAA 1977
14805 CTATTTTACTATAGTATTTTATCATTTGATTAATTTAATTCATCAACACAGCTAGAAATTA 14746
1978 AATAATATCAAACTAATAAGAACAGTATTAATTAATGTAAACAAACATAATCTAATGCTAA 2037
14745 TATTATGATTAACAACAAATTTAATGCTAGTATATCATCTTACATGTTTCGATCAAAATCA 14686
2038 TATAACAAAGCGCAGATCTATCATTTTATATAGTATTAATTTTCAATCAACATTTCTATT 2097
14685 TTAATAAATAATATATCTCTCACTTTTATCTCTTCTGCTTACACATCATCTGTCAT 14626
2098 AATTTCTAATAATATCTCTGATTTTATTAATCTTCAATGATTTGATTTGATTTAATTAAT 2157
14625 ATTTTCTTACATTCATPATGTTGTTTATGTAACAAATATATTTTATAAATTTTTCACA 14566
2158 GAATTAGTCGAACATCAATAAACAAGGTAAACATGATGATGATCATGTCATTTGTTTATCAT 2217
14565 ATTATTAACATATATATTAATCACTACTAATTAACATCACTTAATCTATTTTATACATA 14506
2218 GATCTTACATTTGGATTTGATTCAGTTGGGAAGCTGGGTTCGAAATTCGATTAAGCTTGGAT 2277
14505 AAAGGAAAAAAGAAAAATAATTTATTT-----TCCTTACCAGGCTGGGTACCGAAT 14456
2278 CCTCTAGACCACTTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAA 2337

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 3; Length 4470;
Best Local Similarity 99.8%; Pred. No. 5.1e-149; Mismatches 0; Indels 0; Gaps 0;
Matches 1110; Conservative 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATATATATATATAT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATATATATATATAT 161

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAACACACATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCCAAA 281

QY 206 TGTCTTCGGGTGATGCTGCCAACTAGTCGACGAGCCTTCCAAAATGTTCTCTCAA 265
DB 282 TGTCTTCGGGTGATGCTGCCAACTAGTCGACGAGCCTTCCAAAATGTTCTCTCAA 341

QY 266 ACGGAATGCTGATGCCAGCCTACTCGCTATTGCTCTCAATGCCGTATTAATATCAATA 325
DB 342 ACGGAATGCTGATGCCAGCCTACTCGCTATTGCTCTCAATGCCGTATTAATATCAATA 401

QY 326 AGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAATCTACCT 385
DB 402 AGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAATCTACCT 461

QY 386 ATTATATACGTAGTGTATGATGCTGAAAATCATCTGCATCAAGAACAAATTTCAACAC 445
DB 462 ATTATATACGTAGTGTATGATGCTGAAAATCATCTGCATCAAGAACAAATTTCAACAC 521

QY 446 TCTTATACCTTTTCTTACAGTCGTTTCGGCTTCATCTCGAATTTTCAGCCTCTATACCTTA 505
DB 522 TCTTATACCTTTTCTTACAGTCGTTTCGGCTTCATCTCGAATTTTCAGCCTCTATACCTTA 581

QY 506 CTAACAGCTGATAAAGTTTCTGTAATTTTCTACTGTATCGACCTGCGACTGGCTGTATA 565
DB 582 CTAACAGCTGATAAAGTTTCTGTAATTTTCTACTGTATCGACCTGCGACTGGCTGTATA 641

QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGGCGTTTGTATGTCATTT 625
DB 642 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGGCGTTTGTATGTCATTT 701

QY 626 TCGCGTGGCTGAGTCAGCCTCTTCTCCGATACCGAGACCGGACACTGGCCATA 685
DB 702 TCGCGTGGCTGAGTCAGCCTCTTCTCCGATACCGAGACCGGACACTGGCCATA 761

QY 686 TCGGTGCTCATCATGCGCCAGCTTTTCATCCCCGATATGCACACCGGGTAAAGTTCCACGG 745
DB 762 TCGGTGCTCATCATGCGCCAGCTTTTCATCCCCGATATGCACACCGGGTAAAGTTCCACGG 821

QY 746 GAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGGATACCATTCGCTCCCGCGGC 805
DB 822 GAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGGATACCATTCGCTCCCGCGGC 881

806 GTGTCATATATATCACTCTGTACATCCACAAACAGACGATAAAGGCTCTCTCTTTTATAG 865
882 GTGTCATATATATCACTCTGTACATCCACAAACAGACGATAAAGGCTCTCTCTTTTATAG 941
866 GTGTAACACCTTAAATGTCATTTTACCAGTCCCTGTTTCTGTCAGCAAAAGAGCGGTTTCA 925
942 GTGTAACACCTTAAATGTCATTTTACCAGTCCCTGTTTCTGTCAGCAAAAGAGCGGTTTCA 1001
926 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCGGC 985
1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCGGC 1061
986 ACGCAGACGACGGGCTTTCATTTCTGATGTTTGTCTTACCAGACCGGAGATATTGACATC 1045
1062 ACGCAGACGACGGGCTTTCATTTCTGATGTTTGTCTTACCAGACCGGAGATATTGACATC 1121
1046 ATATATGCTTTGAGCAACTGATAGCTGTCTGTCTCAACTGTCTGTAATACGCTGCTTC 1105
1122 ATATATGCTTTGAGCAACTGATAGCTGTCTGTCTCAACTGTCTGTAATACGCTGCTTC 1181
1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
1182 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1213

RESULT 8
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR201 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 26B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

Db	1062	ACGAGACGACGGGCTTCATCTTCGATGGTGTGCTTACCAGACCGGAGATATTGACATC	112			
Qy	1046	ATATATGCGCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	1105			
Db	1122	ATATATGCGCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	1181			
Qy	1106	ATAGCACACCTCTTTTGACATACCTTCGGGTA	1137			
Db	1182	ATAGCACACCTCTTTTGACATACCTTCGGGTA	1213			
RESULT 9						
ADAS0329	ADA50329 standard; DNA; 4892 BP.					
XX	AC	ADA50329;				
DT	20-NOV-2003	(first entry)				
XX	Plasmid vector pMK2010 DNA sequence.					
DE	site-specific recombination; array construction; reporter gene fusion;					
XX	mutagenesis; protein production; protein characterisation;					
KW	plasmid pMK2010; ds.					
KW	Synthetic.					
OS	WO2003064623-A2.					
XX	07-AUG-2003.					
PN	31-JAN-2003; 2003WO-US003176.					
XX	31-JAN-2002; 2002US-0354063P.					
PR	(UNITW) UNIV WASHINGTON STATE RES FOUND.					
XX	Kahn ML, House BL, Mortimer MW;					
PI	WPI; 2003-679497/64.					
DR	Moving an insert nucleic acid between vectors using site-specific					
XX	recombination in vivo, useful for studying the biology of the organism,					
PT	including array construction, reporter gene fusions, mutagenesis and					
PT	protein production.					
XX	Claim 41; Page 47-51; 52pp; English.					
PS	The invention comprises a method for moving an insert nucleic acid					
XX	molecule between vectors, the method involves moving an insert nucleic					
CC	acid from one vector to another using site-specific recombination. The					
CC	method of the invention is useful for studying the biology of an					
CC	organism, including array construction, reporter gene fusions, and					
CC	mutagenesis, protein production and characterisation. The present DNA					
CC	sequence represents the plasmid vector pMK2010 of the invention.					
XX	Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;					
SQ						
Query Match						
Best Local Similarity 24.8%; Score 1108.8; DB 8; Length 4892;						
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0						
Qy	26	GACAGCTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATCAATATATT	85			
Db	102	GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATCAATATATT	151			
Qy	86	AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAATATCCAGTC	145			
Db	162	AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAATATCCAGTC	221			
Qy	146	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAA	205			
Db	222	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAA	281			

QY 206 TGTTCCTCGGTGATGCTCCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCTCAA 265
Db 282 TGTTCCTCGGTGATGCTCCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCTCAA 341
QY 266 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAA 325
Db 342 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAA 401
QY 326 AGAATAAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAAATCAATCACT 385
Db 402 AGAATAAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAAATCAATCACT 461
QY 386 ATTATATACGCTAGTGTATGCTGCTGAAATCATCTGCATCAAGAAATTTTCAAC 445
Db 462 ATTATATACGCTAGTGTATGCTGCTGAAATCATCTGCATCAAGAAATTTTCAAC 521
QY 446 TCTTATACCTTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGCTCTTATCTTA 505
Db 522 TCTTATACCTTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGCTCTTATCTTA 581
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTATCTGATCGACCTGCGGTGCTGATTA 565
Db 582 CTAAACGTGATAAAGTTTCTGTAATTTCTATCTGATCGACCTGCGGTGCTGATTA 641
QY 566 AGGAGCGCTGACATTTATATCCCGCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db 642 AGGAGCGCTGACATTTATATCCCGCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 701
QY 626 TCGCGTGGTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGCACACTGGCCATA 695
Db 702 TCGCGTGGTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGCACACTGGCCATA 761
QY 686 TCGGTGCTCATATGCGCAGCTTTCTATCCCGATATGACACACCGGTAAAGTTCAAGG 745
Db 762 TCGGTGCTCATATGCGCAGCTTTCTATCCCGATATGACACACCGGTAAAGTTCAAGG 821
QY 746 GAGACTTTATCTCAGCAGCAGCTGCACTGCGCAGGGGATACCATTCGTCGCCCGGGC 805
Db 822 GAGACTTTATCTCAGCAGCAGCTGCACTGCGCAGGGGATACCATTCGTCGCCCGGGC 881
QY 806 GTGTCAATAATATCACTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTATAG 865
Db 882 GTGTCAATAATATCACTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTATAG 941
QY 866 GTGTAAACCTTAACTGATTTTACAGTCCCTGTTCTGTCAGCAAAAGACGGTTTAT 925
Db 942 GTGTAAACCTTAACTGATTTTACAGTCCCTGTTCTGTCAGCAAAAGACGGTTTAT 1001
QY 926 TTCAATAAACCGGGCGACCTCAGCATCCCTTCTGATTTTCCGCTTTCCAGGTTCCGGC 985
Db 1002 TTCAATAAACCGGGCGACCTCAGCATCCCTTCTGATTTTCCGCTTTCCAGGTTCCGGC 1061
QY 986 ACGCAGACGAGCGGCTTCTATCTGATGTTGCTTTACAGACCGGAGATATGACATC 1045
Db 1062 ACGCAGACGAGCGGCTTCTATCTGATGTTGCTTTACAGACCGGAGATATGACATC 1121
QY 1046 ATATATGCTTGGACACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 1122 ATATATGCTTGGACACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
QY 1106 ATAGCACACCTCTTTTGGACATCTTCCGGTA 1137
Db 1182 ATAGCACACCTCTTTTGGACATCTTCCGGTA 1213

RESULT 10
ID AAC55525
XX AAC55525 standard; DNA; 4939 BP.
AC AAC55525;
XX 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
OS Synthetic.
XX WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US005432.
XX PR 02-MAR-1999; 99US-0122389P.
XX PR 23-MAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX DR WPI; 2000-543948/49.
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX Example 10; Fig 53; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention

XX SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 3; Length 4939;
Best Local Similarity 99.8%; Pred. No. 5.1e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAAAGTAAATGATATAATATCAATATAT 85
Db 3636 GCCAATCTTGTACAAAAAAGCTGAACGAGAAAAGTAAATGATATAATATCAATATAT 3695
QY 86 AAATTAGATTTTGCATATAAAAAACAGACTACATTAATCTGTAAACACACATATCCAGTC 145
Db 3696 AAATTAGATTTTGCATATAAAAAACAGACTACATTAATCTGTAAACACACATATCCAGTC 3755
QY 146 ACTATGAATCAACTACTTAGTGGTATTAGTGACCTGTAGTCACCGACGACGCTTCCAAA 205
Db 3756 ACTATGAATCAACTACTTAGTGGTATTAGTGACCTGTAGTGACCGACGACGCTTCCAAA 3815

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QY 206 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCA 265
D 3816 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCA 3875
QY 266 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGCTCAATCGCGTATTAAATCATAAAA 325
D 3876 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGCTCAATCGCGTATTAAATCATAAAA 3935
QY 326 AGAATAAGAAAAAGAGTGCAGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
D 3936 AGAATAAGAAAAAGAGTGCAGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 3995
QY 386 ATTCAATACGCTAGTGTCTATGCTGCTGAATCATCTGCATCAAGAAATTTTCAACAC 445
D 3996 ATTCAATACGCTAGTGTCTATGCTGCTGAATCATCTGCATCAAGAAATTTTCAACAC 4055
QY 446 TCTTATACCTTTCTCTTACAAGTCTGTCGGCTTCATCTGGATTTTTCAGCCTCTATACCTTA 4115
D 4056 TCTTATACCTTTCTCTTACAAGTCTGTCGGCTTCATCTGGATTTTTCAGCCTCTATACCTTA 4115
QY 506 CTAAAGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACCTGGCTGTGTATA 565
D 4116 CTAAAGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACCTGGCTGTGTATA 4175
QY 566 AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGCTTTTGTGATGTCATTT 625
D 4176 AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGCTTTTGTGATGTCATTT 4235
QY 626 TCGCGTGTCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACCTGGCCATA 685
D 4236 TCGCGTGTCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACCTGGCCATA 4295
QY 686 TCGGTGCTCATATGCGGACGCTTTCATCCCGATATGACACACCGGTAAGTTTCAACGG 745
D 4296 TCGGTGCTCATATGCGGACGCTTTCATCCCGATATGACACACCGGTAAGTTTCAACGG 4355
QY 746 GAGACTTTATCTGACAGACGCTGACCTGGCCAGGGGGATCACCATCCGTCGCGCGGGC 805
D 4356 GAGACTTTATCTGACAGACGCTGACCTGGCCAGGGGGATCACCATCCGTCGCGCGGGC 4415
QY 806 GTGTCAATATATCATCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 865
D 4416 GTGTCAATATATCATCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 4475
QY 866 GTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTGTCAGCAAAAGAGCGCTCAT 925
D 4476 GTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTGTCAGCAAAAGAGCGCTCAT 4535
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGCGTTCCGC 985
D 4536 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGCGTTCCGC 4595
QY 986 ACCGAGACGACGGGCTTCATCTGCGATGTTGCTTACAGACCGGAGATTTGACATC 1045
D 4596 ACCGAGACGACGGGCTTCATCTGCGATGTTGCTTACAGACCGGAGATTTGACATC 4655
QY 1046 ATATATGCTTGAAGCACTGATAGTCTGCTGCTGCTCACTGCTGTAATACGCTGCTTC 1105
D 4656 ATATATGCTTGAAGCACTGATAGTCTGCTGCTGCTCACTGCTGTAATACGCTGCTTC 4715
QY 1106 ATAGCACACCTCTTTTGTACATCTTCGGGTA 1137
D 4716 ATAGCACACCTCTTTTGTACATCTTCGGGTA 4747
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RESULT 11

AAC55632/c

ID AAC55632 standard; DNA; 5584 BP.

XX AC

XX AC

XX AC

XX AC

DT 11-JAN-2001

(first entry)

XX

Donor plasmid pDONR207 nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attP; attL; attR; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda.

Synthetic.

WO200052027-A1.

08-SEP-2000.

02-MAR-2000; 2000WO-US005432.

02-MAR-1999; 99US-0122389P.

23-MAR-1999; 99US-0126049P.

28-MAY-1999; 99US-0136744P.

(LIFE-) LIFE TECHNOLOGIES INC.

Hartley JL, Brasch MA, Temple GF, Cheo D; WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.

Disclosure; Fig 97; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 3; Length 5584; Best Local Similarity 99.8%; Pred. No. 5e-149; Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GCAAGTTTGTACAAAAAGCTGAACGAGAAACGTTAAATATGATATATCAATATATT 85

D 5483 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTTAAATATGATATATCAATATATT 5424

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAAATCTGTTAAACACACATATCCAGTC 145

D 5423 AAATTAGATTTTGCATAAAAACAGACTACATAAATCTGTTAAACACACATATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 205

D 5363 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 5304

QY 206 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265


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Db 5303 TGTTCCTCGGCTGATGCTGCCAACTTAGTCGACGACGACCTTCCAAATGTTCTTCTCAA 5244
Qy 266 ACGGAATCGTGTATCCAGACCTACTCGCTATTGTCCTCAATGCCGCTATTAAATCATAAAA 325
Db 5243 ACGGATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGCTATTAAATCATAAAA 5184
Qy 326 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAACATCTACT 385
Db 5183 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAACATCTACT 5124
Qy 386 ATTCAATATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAACAAATTTTCAACAC 445
Db 5123 ATTCAATATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAACAAATTTTCAACAC 5064
Qy 446 TCTTATACCTTTCTCTTACAGCTCGTTCGGCTTCACTCGAATTTTCAGCCTCTATACCTA 505
Db 5063 TCTTATACCTTTCTCTTACAGCTCGTTCGGCTTCACTCGAATTTTCAGCCTCTATACCTA 5004
Qy 506 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565
Db 5003 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 4944
Qy 566 AGGGAGCCTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGGTTTTTGATGTCAATT 625
Db 4943 AGGGAGCCTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGGTTTTTGATGTCAATT 4884
Qy 626 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGCACACTGGGCATA 685
Db 4883 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGCACACTGGGCATA 4824
Qy 686 TCGGTGCTCATCATGCGCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTTCAACG 745
Db 4823 TCGGTGCTCATCATGCGCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTTCAACG 4764
Qy 746 GAGACTTTTATCTGACAGCAGCTGACCTGGCCAGGGGGATCACCATCCGTCGCCCGCGGC 805
Db 4763 GAGACTTTTATCTGACAGCAGCTGACCTGGCCAGGGGGATCACCATCCGTCGCCCGCGGC 4704
Qy 806 GTGTCAATATATCATCTGTATCATCCACAAACAGACGATACGCGCTCTCTTTTATAG 865
Db 4703 GTGTCAATATATCATCTGTATCATCCACAAACAGACGATACGCGCTCTCTTTTATAG 4644
Qy 866 GTGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 925
Db 4643 GTGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 4584
Qy 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCCGC 985
Db 4583 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCCGC 4524
Qy 986 ACCGACAGACGGGCTTCACTTTCGATGTTGCTTACAGACCGGAGATATTGACATC 1045
Db 4523 ACCGACAGACGGGCTTCACTTTCGATGTTGCTTACAGACCGGAGATATTGACATC 4464
Qy 1046 ATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 4463 ATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4404
Qy 1106 ATAGCACACCTCTTTTGGACATCTTCCGGTA 1137
Db 4403 ATAGCACACCTCTTTTGGACATCTTCCGGTA 4372
```

RESULT 12

ABZ58766/C

ID ABZ58766 standard; DNA; 5584 BP.

XX AC

XX AC ABZ58766;

XX DT

XX 01-MAY-2003 (first entry)

XX DE

Donor plasmid pDONR207 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INVI-) INVITROGEN CORP.

XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.

XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence

XX Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 7; Length 5584;

Best Local Similarity 99.8%; Pred. No. 5e-149;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 GACAACTTTGTACAAAAGCTGAACGAGAAAGTAAATGATATAATATCAATATATT 85

Db 5483 GCCAACTTTGTACAAAAGCTGAACGAGAAAGTAAATGATATAATATCAATATATT 5424

Qy 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTATAAAACACATATCCAGTC 145

Db 5423 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTATAAAACACATATCCAGTC 5364

Qy 146 ACTATGAATCAACTACTTAGATGGTATTAGTCACTGTAGTCGACGAGAGCTTCCAA 205

Db 5363 ACTATGAATCAACTACTTAGATGGTATTAGTCACTGTAGTCGACGAGAGCTTCCAA 5304

Qy 206 TGTTCCTTCGGGTGATGCTCCCAACTTAGTCGACGAGAGCTTCCAAATGTTCTTCTCAA 265

Db 5303 TGTTCCTTCGGGTGATGCTCCCAACTTAGTCGACGAGAGCTTCCAAATGTTCTTCTCAA 5244

Qy 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATCGCGTATTAAATCATAAAA 325

Db 5243 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATCGCGTATTAAATCATAAAA 5184

Qy 326 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAACATCTACTCT 385

Db 5183 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAACATCTACTCT 5124

Qy 386 ATTCAATATACGCTAGTGTGATAGTCTGAAATATCATCTGATCAAGAACAAATTTTCAAC 445

Db 5123 ATTCAATATACGCTAGTGTGATAGTCTGAAATATCATCTGATCAAGAACAAATTTTCAAC 5064

QY 446 TCTTATACATTTCTCTTACAAAGTCGTTGCGCTTCATCTGATTTTCAGCCCTCTATATCTTA 505
Db 5063 TCTTATACATTTCTCTTACAAAGTCGTTGCGCTTCATCTGATTTTCAGCCCTCTATATCTTA 5004
QY 506 CTAACAGTGATAAAGTTTCTGTAATTTCTACTGATCGCTCGAGCTGCGCTGTGTATA 565
Db 5003 CTAACAGTGATAAAGTTTCTGTAATTTCTACTGATCGCTCGAGCTGCGCTGTGTATA 4944
QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAAGCGGTTTGTGATTCATTT 625
Db 4943 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAAGCGGTTTGTGATTCATTT 4884
QY 626 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACGAGACCGGACACCTGGCCATA 685
Db 4883 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACGAGACCGGACACCTGGCCATA 4824
QY 686 TCGTGTGTCATCGCGCAGCTTTCATCCCGATATGACACCGGGTAAAGTTCAACGG 745
Db 4823 TCGTGTGTCATCGCGCAGCTTTCATCCCGATATGACACCGGGTAAAGTTCAACGG 4764
QY 746 GAGACTTTATCTGACAGCAGCGTGCACCTGCGCAGGGGATACCATTCGTCGCGCGGC 805
Db 4763 GAGACTTTATCTGACAGCAGCGTGCACCTGCGCAGGGGATACCATTCGTCGCGCGGC 4704
QY 806 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTATAG 865
Db 4703 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCATTTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTTCAT 925
Db 4643 GTGTAAACCTTAACTGCATTTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTTCAT 4584
QY 926 TTCAATAAACCGGCGGACCTCAGCCATCCCTTCCTGATTTTCGCTTTCAGCGTTTCGGC 985
Db 4583 TTCAATAAACCGGCGGACCTCAGCCATCCCTTCCTGATTTTCGCTTTCAGCGTTTCGGC 4524
QY 986 ACGCAGACGCGGCTTCATTTCTGATGTTGCTTACAGACCGGAGATATTGACATC 1045
Db 4523 ACGCAGACGCGGCTTCATTTCTGATGTTGCTTACAGACCGGAGATATTGACATC 4464
QY 1046 ATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAACTGTCTGTAATACGCTGCTTC 1105
Db 4463 ATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAACTGTCTGTAATACGCTGCTTC 4404
QY 1106 ATAGCAGACCTTTTGGACATCTTCGGTA 1137
Db 4403 ATAGCAGACCTTTTGGACATCTTCGGTA 4372

RESULT 13

ID AB258768 standard; DNA; 4428 BP.

XX AC AB258768;

XX AC AB258768;

DT 01-MAY-2003 (first entry)

DE Destination plasmid pDONR212 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;

KW Nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INV-) INVITROGEN CORP.

XX
PI
XX
DR
XX
PT
PT
PT
PS
XX
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CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
SQ

Brasch MA, Cheo D, Li X, Esposito D, Byrd DN;
WPI; 2003-129436/12.
Inserting a population of nucleic acids into a second target molecule for
selecting and isolating nucleic acid molecules by mixing the second
population of nucleic acid with a second target nucleic acid.
Disclosure; Fig 27B-C; 273pp; English.
The invention relates to inserting a population of nucleic acids into a
second target molecule. The method involves (a) mixing a first population
of nucleic acid comprising one or more recombination sites with a target
nucleic acid; (b) causing some or all of the nucleic acid molecules of
the first population to recombine with the first target nucleic acid
molecules to form a second population; (c) mixing the second population
of nucleic acid with a second target nucleic acid; and (d) causing some
or all of the nucleic acid molecules of the second population to
recombine with some or all of the second target nucleic acid molecules to
form a third population of nucleic acid. The method is useful for
selecting and isolating nucleic acid molecules. The present sequence
represents the destination plasmid pDONR212 nucleotide sequence
Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;
Query Match 24.6%; Score 1102.4; DB 7; Length 4428;
Best Local Similarity 99.5%; Pred. No. 4.1e-148;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAAGCTAAATATGATATAATATCAATATATT 85
Db 939 GCCAACTTTGTACAAAAAGCTGATATCGAAGCTAAATATGATATAATATCAATATATT 998
QY 86 AAATTAAGATTTTGCATATAAAAAACAGACTACATAATATCTGTAAACACAAATATCCAGTC 145
Db 999 AAATTAAGATTTTGCATATAAAAAACAGACTACATAATATCTGTAAACACAAATATCCAGTC 1058
QY 146 ACTATGAATCACTACTTAGTGGTATTAGTACCTGTAGTCGACGAGCGCTTCCAA 205
Db 1059 ACTATGAATCACTACTTAGTGGTATTAGTACCTGTAGTCGACGAGCGCTTCCAA 1118
QY 206 TGTCTCTCGGCTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 265
Db 1119 TGTCTCTCGGCTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCTCAA 1178
QY 266 ACGGAATCGTCGATCGCTACTCGCTATTGTGCTCAATGCGCTATTAAATCATATAA 325
Db 1179 ACGGAATCGTCGATCGCTACTCGCTATTGTGCTCAATGCGCTATTAAATCATATAA 1238
QY 326 AGAATAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGACAAAAATAAAACATCTACCT 385
Db 1239 AGAATAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGACAAAAATAAAACATCTACCT 1298
QY 386 ATTATATACGCTAGTGTCTATAGTCTCTGAAATATCATCTGCATCAAGAACAAATTTCAAC 445
Db 1299 ATTATATACGCTAGTGTCTATAGTCTCTGAAATATCATCTGCATCAAGAACAAATTTCAAC 1358
QY 446 TCTTATACATTTTCTCTTAAGTCGCTTTCAGCTTTCAGCTTTCAGCTTTCAGCTTTC 505
Db 1359 TCTTATACATTTTCTCTTAAGTCGCTTTCAGCTTTCAGCTTTCAGCTTTCAGCTTTC 1418
QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGATCGCTGAGCTGGCTGTGTATA 565
Db 1419 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGATCGCTGAGCTGGCTGTGTATA 1478
QY 566 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGGTTTGTGATGTCATTT 625
Db 1479 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGGTTTGTGATGTCATTT 1538
QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACCTGGCCATA 685
Db 1539 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACCTGGCCATA 1598

QY	686	TCGGTGGTCATCATGCGGCCAGCTTTTCATCCCGGATATGCACCAACCGGGTAAAGTTTCACGG	745
Db	1599	TCGGTGGTCATCATGCGGCCAGCTTTTCATCCCGGATATGCACCAACCGGGTAAAGTTTCACGG	1658
QY	746	GAGACTTTATCTGACAGCAGACGTGCACTGCGCAGAGGGGGATCACCATCCGTCGCCCGGGC	805
Db	1659	GAGACTTTATCTGACAGCAGACGTGCACTGCGCAGAGGGGGATCACCATCCGTCGCCCGGGC	1718
QY	806	GTGTCAATAATATCATCTCTGTACATCCACAAAACAGACGATAAGCGTCTCTCTTTTATATAG	865
Db	1719	GTGTCAATAATATCATCTCTGTACATCCACAAAACAGACGATAAGCGTCTCTCTTTTATATAG	1778
QY	866	GTGTAAACCTTAAACTGCATTTCACCAAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTTCAT	925
Db	1779	GTGTAAACCTTAAACTGCATTTCACCAAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTTCAT	1838
QY	926	TTCAATAAACCGGGCGACCTTCAGGCATCCCTTCTGTATTTTCGGCTTTCAGCGTTCGGC	985
Db	1839	TTCAATAAACCGGGCGACCTTCAGGCATCCCTTCTGTATTTTCGGCTTTCAGCGTTCGGC	1898
QY	986	ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTTACACAGACGGAGATATTGACATC	1045
Db	1899	ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTTACACAGACGGAGATATTGACATC	1958
QY	1046	ATATATGCCCTTGACCAACTGATAGCTCGCTGTCAACTGTCACTGTGAATAACGTCGTTTC	1105
Db	1959	ATATATGCCCTTGACCAACTGATAGCTCGCTGTCAACTGTCACTGTGAATAACGTCGTTTC	2018
QY	1106	ATAGCACACCTCTTTTTGACATACTTCGGGTA	1137
Db	2019	ATAGCACACCTCTTTTTGACATACTTCGGGTA	2050

RESULT 14

ABZ58769	ABZ58769 standard; DNA; 4527 BP.
XX	
XX	ABZ58769;
XX	
XX	01-MAY-2003 (first entry)
DT	
XX	
XX	Destination plasmid pDONR212(F) nucleotide sequence.
DE	
XX	
XX	Nucleic acid insertion; recombination; nucleic acid selection;
KW	nucleic acid isolation; ds.
KW	
XX	
XX	Synthetic.
OS	
XX	
XX	WO200295055-A2.
PN	
XX	
XX	28-NOV-2002.
FD	
XX	
XX	21-MAY-2002; 2002WO-US015947.
PF	
XX	
XX	21-MAY-2001; 2001US-0291973P.
PR	
XX	
XX	(INVI-) INVITROGEN CORP.
EA	
XX	
XX	Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
FI	
XX	
XX	WPI; 2003-129436/12.
DR	
XX	
XX	Inserting a population of nucleic acids into a second target molecule for
PT	selecting and isolating nucleic acid molecules by mixing the second
PT	population of nucleic acid with a second target nucleic acid.
XX	
XX	Disclosure; Fig 28B-C; 273pp; English.
PS	
XX	
XX	The invention relates to inserting a population of nucleic acids into a
CC	second target molecule. The method involves (a) mixing a first population
CC	of nucleic acid comprising one or more recombination sites with a target
CC	nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC	

Db 930 GTGTAAACCTTAACTGATTTTACAGCTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCAT 989
QY 926 TTCATATAACCGGGGACCTGAGCCATCCCTTCCTGATTTTCGGCTTTCAGCGTTCGGC 985
Db 990 TTCAATAAAACCGGGGACCTGAGCCATCCCTTCCTGATTTTCGGCTTTCAGCGTTCGGC 1049
QY 986 AGCGAGACGACGGGCTTCATTTCTGATGCTGCTTACCGACCGGAGATATTCACATC 1045
Db 1050 AGCGAGACGACGGGCTTCATTTCTGATGCTGCTTACCGACCGGAGATATTCACATC 1109
QY 1046 ATATATGCTTTCAGCAACTGATAGCTGCTGCTCAACTGTCACTGTATATACGCTGCTTC 1105
Db 1110 ATATATGCTTTCAGCAACTGATAGCTGCTGCTCAACTGTCACTGTATATACGCTGCTTC 1169
QY 1106 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1137
Db 1170 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1201

RESULT 15

ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX AC
XX ABZ58770;
XX 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR212(R) nucleotide sequence.
XX XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX XX
XX WO200295055-A2.
XX PD
XX 28-NOV-2002.
XX PF
XX 21-MAY-2002; 2002WO-US015947.
XX PR
XX 21-MAY-2001; 2001US-0291973P.
XX XX
XX (INVI-) INVITROGEN CORP.
XX XX

PI Bransch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
XX XX

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX XX

XX Disclosure; Fig 29B-C; 273pp; English.
XX XX

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(R) nucleotide sequence
XX XX

SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.6%; Score 1102.4; DB 7; Length 4627;
Best Local Similarity 99.5%; Pred. No. 4.1e-148;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 85
Db 90 GCCAACCTTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAAATATCAATATATT 149
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATATCTGTAAAAACAAACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAAACAGACTACATAATATCTGTAAAAACAAACATATCCAGTC 209
QY 146 ACTATGANTCAACTACTTAGTATGATATAGTACTGTAGTCGACCGACAGCTTCCAAA 205
Db 210 ACTATGANTCAACTACTTAGTATGATATAGTACTGTAGTCGACCGACAGCTTCCAAA 269
QY 206 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTTCTCAA 265
Db 270 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCTTCCAAATGTTTCTCAA 329
QY 286 AGGAAATCGTATCCAGCCCTACTCGCTATTTGCTCAATGCCGTATTTAATCATATAAA 325
Db 330 ACAGAAATCGTATCCAGCCCTACTCGCTATTTGCTCAATGCCGTATTTAATCATATAAA 389
QY 326 AGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAAATAAAAAATCTACCT 385
Db 390 AGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAAATAAAAAATCTACCT 449
QY 386 ATTCATATACGCTAGTGTCTAGTCTCGAAATCATCTGCATCAAGAAACAATTTCAACAAC 445
Db 450 ATTCATATACGCTAGTGTCTAGTCTCGAAATCATCTGCATCAAGAAACAATTTCAACAAC 509
QY 446 TCTTATACCTTTCTTACAAAGTCTGCTCGCTTCAATCTGGATTTTTCAGCCCTATATCTTA 505
Db 510 TCTTATACCTTTCTTACAAAGTCTGCTCGCTTCAATCTGGATTTTTCAGCCCTATATCTTA 569
QY 506 CTAAACGCTGATAAAAGTTTCTGTAATTTCTAGTATCGACCTGCAGACTGGCTGTGTATA 565
Db 570 CTAAACGCTGATAAAAGTTTCTGTAATTTCTAGTATCGACCTGCAGACTGGCTGTGTATA 629
QY 566 AGGGAGCTGACATTTATATTTCCCGAGAAACATCAGGTTAATGGCCCTTTTGTATGTCATTT 625
Db 630 AGGGAGCTGACATTTATATTTCCCGAGAAACATCAGGTTAATGGCCCTTTTGTATGTCATTT 689
QY 626 TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACTGCGCCATA 685
Db 690 TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACTGCGCCATA 749
QY 686 TCGGTGCTCATCATGCGCCAGCTTTTCATCCCGATATGCACCACCGGTAAGTTTCACGG 745
Db 750 TCGGTGCTCATCATGCGCCAGCTTTTCATCCCGATATGCACCACCGGTAAGTTTCACGG 809
QY 746 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCGTCGCCCGGGC 805
Db 810 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCGTCGCCCGGGC 869
QY 806 GGTCAATAATATCACTCTGTACATCCAAACAGACGATACGGCTCTCTCTTTTATAG 865
Db 870 GGTCAATAATATCACTCTGTACATCCAAACAGACGATACGGCTCTCTCTTTTATAG 929
QY 866 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTAT 925
Db 930 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTAT 989
QY 926 TTCATATAACCGGGGACCTGAGCCATCCCTTCCTGATTTTCCGCTTTCAGCGTTCGGC 985
Db 990 TTCAATAAAACCGGGGACCTGAGCCATCCCTTCCTGATTTTCCGCTTTCAGCGTTCGGC 1049
QY 986 AGCGACACGACGGGCTTCAATTTCTGATGTTTGTGTTTACCGACCGGAGATTTGACATC 1045
Db 1050 AGCGACACGACGGGCTTCAATTTCTGATGTTTGTGTTTACCGACCGGAGATTTGACATC 1109
QY 1046 ATATATGCTTTCAGCAACTGATAGCTGCTGCTCAACTGTCACTGTATATACGCTGCTTC 1105
Db 1110 ATATATGCTTTCAGCAACTGATAGCTGCTGCTCAACTGTCACTGTATATACGCTGCTTC 1169
QY 1106 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1137

Db 1170 ATAGCACCTCTTTTGGACATACCTCGGTA 1201

Search completed: May 7, 2004, 18:28:34
Job time : 1064.31 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1193.76 Seconds
(without alignments)

16988-923 Million cell updates/sec

Title: US-10-055-001B-24_COPY_13000_17476

Perfect score: 4477

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5893172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4477	100.0	17476	15	US-10-385-546-7
3	4406.6	98.4	17458	15	US-10-055-001A-25
4	4262	95.2	17681	15	US-10-055-001A-26
5	4112.4	91.9	17862	15	US-10-055-001A-23
6	3234.8	72.3	18691	15	US-10-055-001A-13
7	1277.8	28.5	17458	15	US-10-055-001A-25
8	1273	28.4	17476	15	US-10-055-001A-24
9	1273	28.4	17476	15	US-10-385-546-7
10	1108.8	24.8	4470	15	US-10-151-690-21
11	1108.8	24.8	4892	16	US-10-357-268-1
12	1108.8	24.8	5584	15	US-10-151-690-61
13	1102.4	24.6	4428	15	US-10-151-690-62
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15	1102.4	24.6	4627	15	US-10-151-690-64
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c 17	1074.8	24.0	17681	15	US-10-055-001A-26
18	780	17.4	786	15	US-10-385-521-9
19	737	16.5	3002	15	US-10-353-454-57
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21	735.6	16.4	2873	15	US-10-356-088-55
22	735.6	16.4	2873	15	US-10-353-454-38
23	735	16.4	3034	15	US-10-356-088-48
24	735	16.4	3034	15	US-10-353-454-31
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c 31	597	13.3	5558	15	US-10-241-596-137
c 32	597	13.3	6464	15	US-10-151-690-20
c 33	597	13.3	7278	17	US-10-097-034A-37
c 34	597	13.3	9249	16	US-10-389-120-2
c 35	597	13.3	10463	16	US-10-389-120-1
c 36	597	13.3	12789	13	US-10-666-778-9
c 37	593.8	13.3	11180	9	US-09-887-576-581
c 38	478.8	10.7	528	15	US-10-162-214-4
c 39	406.8	9.1	4470	15	US-10-151-690-21
c 40	406.8	9.1	4892	16	US-10-357-268-1
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c 44	400.4	8.9	4627	15	US-10-151-690-64
c 45	323.4	7.2	2877	13	US-09-861-925-11

ALIGNMENTS

RESULT 1

US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match	100.0%	Score	4477	DB	15	Length	17476
Best Local Similarity	100.0%	Pred. No.	0				
Matches	4477	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
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DB	13000	TTTCATTTGGAGAGACACGCTCGAGACAGTTTGTACAAAAAGCTGACGAGAAACGT	13059				
QY	61	AAATGATATAATCAATATATTAATTTAGATTTTGCATAAAAAAGAGACTACATAT	120				
DB	13060	AAATGATATAATCAATATATTAATTTAGATTTTGCATAAAAAAGAGACTACATAT	13119				
QY	121	ACTGTAACCAACATATCCAGTCACATGATCAATCTAGATGGTATTAGTAC	180				

Dd 13120 ACTGTAAACACAAATATCCAGTCACTATGAAATCAACATCTTAGATGGTATTAGTGACC 13179
Qy 181 TGTAGTCAGACGAGCCTTCCAAATGTTCTTTCGGGTGATGTCGCCAATTAGTGCAGCG 240
Dd 13180 TGTAGTCAGACGAGCCTTCCAAATGTTCTTTCGGGTGATGTCGCCAATTAGTGCAGCG 13239
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Dd 13240 ACAGCCTTCCAAATGTTCTTTCAAACGGAATCGTGTATCCAGCCTACTCGCTATTGTC 13299
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Qy 421 TCTGCATCAAGAACAAATTTCAAACTCTTATATCTTCTTCAAGTGGTTCGAGTCA 480
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Qy 601 GTTAATGGCTTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGGCATTTCTCCCGCAT 660
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16360 TCACACAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCA 16419
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RESULT 2

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US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match      100.0%; Score 4477; DB 15; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCATTGGAGAGGACACGCTGAGACAAAGTTTGTACAAAAGCTGAACGAAACGTT 60
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QY	1861	AATATCTATACCAATTAATAATAATTTTAGCTTTAAAAAGTTTAAATAATTTTTTGTTAGAAT	1920
Db	14860	AATATCTATACCAATTAATAATAATTTTAGCTTTAAAAAGTTTAAATAATTTTTTGTTAGAAT	14919
QY	1921	TCCAATCTGGTGTGAATTTATCATAAACAATAATTTAAATAAACAGCTAAAGTAACAAA	1980
Db	14920	TCCAATCTGGTGTGAATTTATCATAAACAATAATTTAAATAAACAGCTAAAGTAACAAA	14979
QY	1981	TAATATCAAACATAATAGAAACAGTAATCTAAATGTAACAAAATATAATCTAAATCTAAAT	2040
Db	14980	TAATATCAAACATAATAGAAACAGTAATCTAAATGTAACAAAATATAATCTAAATCTAAAT	15039
QY	2041	AACAAAGCGAAGATCTATCATTTTATATPAGTATTTTTCATCAATCAACATTTCTTTAAT	2100
Db	15040	AACAAAGCGAAGATCTATCATTTTATATPAGTATTTTTCATCAATCAACATTTCTTTAAT	15099
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QY	2161	TTTAGTCCGAATGAATPAAPAAACAGGTAACATAGATCATGTGTCATGTGTTTATCATTTGAT	2220
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QY	2221	CTTACATATTTGGATTGATTACAGTTGGAGCTGGGTTCGAATCCATTAAGCTTGGATCCT	2280
Db	15220	CTTACATATTTGGATTGATTACAGTTGGAGCTGGGTTCGAATCCATTAAGCTTGGATCCT	15279
QY	2281	CTAGACCACCTTTGTCAAGAAAGCTGAACGAGAAACGTAATAATGATAAATAATCAATAT	2340
Db	15280	CTAGACCACCTTTGTCAAGAAAGCTGAACGAGAAACGTAATAATGATAAATAATCAATAT	15339
QY	2341	ATTAAATTAGATTTTGCATATAAANAACAGACTACATAATCTCTGTAACACATATCCA	2400
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QY	2461	ATCACCCGAGCACTTTGGCCGGAATAAATACTGTGACGGAAGATCACTTCGCAGAAATA	2520
Db	15460	ATCACCCGAGCACTTTGGCCGGAATAAATACTGTGACGGAAGATCACTTCGCAGAAATA	15519
QY	2521	AATAAATCTGGTGTCCTTGTTGATACGGGAAGCCCTGGGCCCACTTTTGGCGAAATG	2580
Db	15520	AATAAATCTGGTGTCCTTGTTGATACGGGAAGCCCTGGGCCCACTTTTGGCGAAATG	15579
QY	2581	AGACGTTGATCGGAATTCACACTCTTATACCTTTCTCTTACAAGTCGTTCCGCTTCATC	2640
Db	15580	AGACGTTGATCGGAATTCACACTCTTATACCTTTCTCTTACAAGTCGTTCCGCTTCATC	15639
QY	2641	TGATATTTACGCTCTATACTTACTAAACGCTGATAAGCTTCTGTAATTTCTACTGTATC	2700
Db	15640	TGATATTTACGCTCTATACTTACTAAACGCTGATAAGCTTCTGTAATTTCTACTGTATC	15699
QY	2701	GACCTGCAGACTGGCTGTGTATAAGGAGCCCTGACATTTATATTTCCCAGAACATCAGGT	2760
Db	15700	GACCTGCAGACTGGCTGTGTATAAGGAGCCCTGACATTTATATTTCCCAGAACATCAGGT	15759
QY	2761	TAATGGCGTTTTTGATGTCTATTTTCGCGGTGGCTGAGATCAGCACTTCTCCCGATAA	2820
Db	15760	TAATGGCGTTTTTGATGTCTATTTTCGCGGTGGCTGAGATCAGCACTTCTCCCGATAA	15819
QY	2821	CGGAGACCGGCACACTGGCCATATCGTGGTCAATCATGCGCAGCTTTTATCCCGATAT	2880
Db	15820	CGGAGACCGGCACACTGGCCATATCGTGGTCAATCATGCGCAGCTTTTATCCCGATAT	15879

Qy	2881	GCACCA	CCGGTAAAGTTTCACCGGAGAC	CTTTATCTGACAGCAGACGTGCACTGGCCAGGG	2940
Db	15880	GCA	CCACCGGGTAAAGTTTCACCGGAGAC	CTTTATCTGACAGCAGACGTGCACTGGCCAGGG	15939
Qy	2941	GGAT	CACCACTCCGTCCGTCGGCGCGTGTCAAT	TAATATCACTCTGTACATCCCAAAACAGAC	3000
Db	15940	GGAT	CACCACTCCGTCCGTCGGCGCGTGTCAAT	TAATATCACTCTGTACATCCCAAAACAGAC	15999
Qy	3001	GATAA	CGGCTCTCTCTTTTATATAGGTGTAAAC	CTTTAAACCTGCANITTCACAGTCCCTGTTC	3060
Db	16000	GATAA	CGGCTCTCTCTTTTATATAGGTGTAAAC	CTTTAAACCTGCANITTCACAGTCCCTGTTC	16059
Qy	3061	TGCT	CAGCAAAAGAGCGGTTCATTTCAAT	TAACCCGGGACCTCAGGCCATCCCTTCCTGA	3120
Db	16060	TGCT	CAGCAAAAGAGCGGTTCATTTCAAT	TAACCCGGGACCTCAGGCCATCCCTTCCTGA	16119
Qy	3121	TTTT	CCGTTTCCAGGGTTCGCGACGACAGACG	ACGGGTTCAATCTGCATGGTGTGTCTT	3180
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Qy	3181	ACCAG	ACCGGAGATATGACATCATATATATG	CCCTCAGCAACTGATAGCTGCGTGTCAA	3240
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Qy	3241	CTGTC	ACTGTAATACGCTCTTCATAGCACAC	CTCTTTTGGACATCTCTGTCTTCTGAT	3300
Db	16240	CTGTC	ACTGTAATACGCTCTTCATAGCACAC	CTCTTTTGGACATCTCTGTCTTCTGAT	16299
Qy	3301	GCAGAT	GATTTTCAGACATACACACTAGCGT	TATATGATAGGTAGATGTTTTTATTTTG	3360
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Qy	3661	ATTT	ACGTTTCTGTCAGCTTTTTTGTAC	AAACCTGTCTAGAGTCCCTGTTTAATGAG	3720
Db	16660	ATTT	ACGTTTCTGTCAGCTTTTTTGTAC	AAACCTGTCTAGAGTCCCTGTTTAATGAG	16719
Qy	3721	ATAT	GCGAGCGCTATGATGCAATATTTG	CTTTCAATTCGTTGTGCACGTTGTAA	3780
Db	16720	ATAT	GCGAGCGCTATGATGCAATATTTG	CTTTCAATTCGTTGTGCACGTTGTAA	16779
Qy	3781	AAAA	CTGAGCATGTAGCTCAGATCCCTT	ACCGCGGTTTCGGTTCATTTCTAATGAATA	3840
Db	16780	AAAA	CTGAGCATGTAGCTCAGATCCCTT	ACCGCGGTTTCGGTTCATTTCTAATGAATA	16839
Qy	3841	TATCA	CCGTTACTATCGTATTTTATGAATA	TAATATTCCTCGGTTCAATTTACTGATTTGA	3900
Db	16840	TATCA	CCGTTACTATCGTATTTTATGAATA	TAATATTCCTCGGTTCAATTTACTGATTTGA	16899
Qy	3901	CCCT	CTACTTATATGTAACAATTTAAAT	TGAAACAATATATTTGCTGCTGAATAGTTTA	3960
Db	16900	CCCT	CTACTTATATGTAACAATTTAAAT	TGAAACAATATATTTGCTGCTGAATAGTTTA	16959
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QY 4081 TCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGACACACGAGCGGCACTAATAA 4140
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QY 4381 GCGAATTTTCGGACCAACATGTCGAGGCTCAGGAGCTCAGGAGCCTGCAAGCTAGCTTA 4440
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Db 17440 CTAGTGATGATATTTCTATAGTGTCACTTAAATCTGC 17476

RESULT 3
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 98.4%; Score 4406.6; DB 15; Length 17458;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;

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QY 61 AAAATGATATAAATATCAATATATATAATTTAGATTTTGCATAAAAAACAGACTACATAAT 120
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QY 121 ACTGTAAACACACATATCCAGTCACTATGAATCACTACTTAGTGGTATTAGTGACC 180
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QY 241 ACAGCTCTTCCAAATGTTCTTCTCAAAACGGAATCGTGTATCCAGCTACTCGCTATTGTC 300
Db 13240 ACAGCTCTTCCAAATGTTCTTCTCAAAACGGAATCGTGTATCCAGCTACTCGCTATTGTC 13299
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QY 1261 TCGCTCGGCTGATGCTGCCAACTTACTGCTACAGGTCACTAATACCATCTAAGTAGTT 1320
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RESULT 4

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US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26
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Query Match 95.2%; Score 4262; DB 15; Length 17681;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 205; Gaps 1;

QY 1 TTTCAATTTGGAGAGACAGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT 60
Db 13000 TTTCAATTTGGAGAGACAGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT 13059
QY 61 AAAATGATAATAATCAATATATTTAAATAGATTTTGCATAAAAAGACTACATAAT 120
Db 13060 AAAATGATAATAATCAATATATTTAAATAGATTTTGCATAAAAAGACTACATAAT 13119
QY 121 ACTGTAACACACAACTATCCAGTCACTATGAATCACTTACTAGTGTGATTTAGTGACC 180
Db 13120 ACTGTAACACACAACTATCCAGTCACTATGAATCACTTACTAGTGTGATTTAGTGACC 13179
QY 181 TGTAGTCGACCCAGACAGCTTCCAAATGTTCTTCCGGTGATGCTGCAACTTAGTCGACCG 240
Db 13180 TGTAGTCGACCCAGACAGCTTCCAAATGTTCTTCCGGTGATGCTGCAACTTAGTCGACCG 13239
QY 241 ACAGCCTTCCAAATGTTCTTCTCAAACCGGAATCGTGTATCCAGCCTACTCGCTATTGTC 300
Db 13240 ACAGCCTTCCAAATGTTCTTCTCAAACCGGAATCGTGTATCCAGCCTACTCGCTATTGTC 13299
QY 301 CTCATGCGCGTATTAATCATATAAAGAAATGAAGAAAGAGGTGCGGCTCTTTTGTG 360
Db 13300 CTCATGCGCGTATTAATCATATAAAGAAATGAAGAAAGAGGTGCGGCTCTTTTGTG 13359
QY 361 TGTGACAAATAAAAACATCTACCTATTTCATATACGCTAGTGTCTAGTCCTGAAATCA 420
Db 13360 TGTGACAAATAAAAACATCTACCTATTTCATATACGCTAGTGTCTAGTCCTGAAATCA 13419
QY 421 TGTGATCAAGAACAAATTTCAACCTTTATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 480
Db 13420 TGTGATCAAGAACAAATTTCAACCTTTATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 13479
QY 481 TCTGGATTTTTCAGCCTCTATATCTTAAACGTTGATAAGTTTCTGTAATTTCTACTGTA 540
Db 13480 TCTGGATTTTTCAGCCTCTATATCTTAAACGTTGATAAGTTTCTGTAATTTCTACTGTA 13539
QY 541 TCGACCTGACAGCTGGCTGTATAGGAGGAGCTGACATTTATTTCCCGAGAACATCAG 600
Db 13540 TCGACCTGACAGCTGGCTGTATAGGAGGAGCTGACATTTATTTCCCGAGAACATCAG 13599
QY 601 GTTAATGGGTTTTTGATGTCAATTTTCGGGTGGCTGAGATCAGCACTTCTTCCCGAT 660
Db 13600 GTTAATGGGTTTTTGATGTCAATTTTCGGGTGGCTGAGATCAGCACTTCTTCCCGAT 13659
QY 661 AACGAGAGCGGCACACTGCGCATATCGGTGGTGTATCGCCAGCTTTCATCCCGAT 720
Db 13660 AACGAGAGCGGCACACTGCGCATATCGGTGGTGTATCGCCAGCTTTCATCCCGAT 13719
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QY	721	ATGCACCA	CCGGGTAAAGTTCA	CGGAGACTTTATCTGACAGCAGACGTGCAC	TGGCCAG	780
DB	13720	ATGCACCA	CCGGGTAAAGTTCA	CGGAGACTTTATCTGACAGCAGACGTGCAC	TGGCCAG	13779
QY	781	GGGGATCAC	CCNCCGTCG	CCCGGGGGGTGC	CATAATATACATCTCTGTACATCCACAAACAG	840
DB	13780	GGGGATCAC	CCATCCGTCG	CCCGGGGGGTGC	CAATAATATACATCTCTGTACATCCACAAACAG	13839
QY	841	ACGATAAC	GGCTCTCTCTCTTTTAT	PAGTGTAAACCTTAAACTGCATTTT	CACAGTCCCTGT	900
DB	13840	ACGATAAC	GGCTCTCTCTCTTTTAT	PAGTGTAAACCTTAAACTGCATTTT	CACAGTCCCTGT	13899
QY	901	TCTCGT	CAGCAAAAGACCGTTCATTT	CAATAAAACGGGGCACCCTCAGC	GCATCCCTTCCT	960
DB	13900	TCTCGT	CAGCAAAAGACCGTTCATTT	CAATAAAACGGGGCACCCTCAGC	GCATCCCTTCCT	13959
QY	961	GATTTTCCG	CTTTCACGCGTTCGGC	ACGACGACGACGGGCTTCATCTTCG	CATGTTGTGC	1020
DB	13960	GATTTTCCG	CTTTCACGCGTTCGGC	ACGACGACGACGGGCTTCATCTTCG	CATGTTGTGC	14019
QY	1021	TTACCGA	CCGGAGATTTGCA	NCATATATATGCTTTGAGCACTCATAGTGT	CGCTGTCT	1080
DB	14020	TTACCGA	CCGGAGATTTGAGCATCATATATGCTTTGAGCACTCATAGTGT	CGCTGTCT		14079
QY	1081	AACGTCACT	GTAAATACGCTGCTTAT	CATACACACCTCTTTTGTACATACTTCGGGTAGTG		1140
DB	14080	AACGTCACT	GTAAATACGCTGCTTAT	CATACACACCTCTTTTGTACATACTTCGGGTAGTG		14139
QY	1141	CGGATCAA	CGTCTCATTTTCGGCAAAAGTTG	GCCACGAGGCTTCCGGGTATCAACAGGGAC		1200
DB	14140	CGGATCAA	CGTCTCATTTTCGGCAAAAGTTG	GCCACGAGGCTTCCGGGTATCAACAGGGAC		14199
QY	1201	ACCAGATTTATTTATTTCTCG	GAAGTGATCTTCCTGCTCA	CAGGTATTTATTCGGCGCAAG		1260
DB	14200	ACCAGATTTATTTATTTCTCG	GAAGTGATCTTCCTGCTCA	CAGGTATTTATTCGGCGCAAG		14259
QY	1261	TGGCTCGGGTGATGCTG	CCAACTTAGTCGACTACAGGTCACT	TAATACCATCTAAGTAGTT		1320
DB	14260	TGGCTCGGGTGATGCTG	CCAACTTAGTCGACTACAGGTCACT	TAATACCATCTAAGTAGTT		14319
QY	1321	GATTCATAGT	GACTGCATATGTTGTGTTTACAGTATATATG	TAGTCTGTTTTTTATGC	AA	1380
DB	14320	GATTCATAGT	GACTGCATATGTTGTGTTTACAGTATATATG	TAGTCTGTTTTTTATGC	AA	14379
QY	1381	AACTCAATTTAAATATATATG	ATATTTATATCATTTTACGTTTCTCG	CTCAGCTTTCTTGTA		1440
DB	14380	AACTCAATTTAAATATATATG	ATATTTATATCATTTTACGTTTCTCG	CTCAGCTTTCTTGTA		14439
QY	1441	CAAGTGGTCTCAGGAAATTCGGT	TACCCAGCTTGGTAGGAAATTAATTTTCTTTT			1500
DB	14440	CAAGTGGTCTCAGGAAATTCGGT	TACCCAGCTTGGTAGGAAATTAATTTTCTTTT			14499
QY	1501	TCCTTTT	TAGTATAAAATAGTTAAGTCATGTTAAT	TAGTATGATTAATAATTAATAGTTGT		1560
DB	14500	TCCTTTT	TAGTATAAAATAGTTAAGTCATGTTAAT	TAGTATGATTAATAATTAATAGTTGT		14559
QY	1561	TATAATTTGTG	AAAAAATAAATTAATAATATATGTTT	TACATATAACACATAGTAAATGTA		1620
DB	14560	TATAATTTGTG	AAAAAATAAATTAATAATATATGTTT	TACATATAACACATAGTAAATGTA		14619
QY	1621	AAAAAATG	ACAAGTCATGTTGAAGCAGAGAGATAA	BAAGTTGAGGTAGTATATTTAT		1680
DB	14620	AAAAAATG	ACAAGTCATGTTGAAGCAGAGAGATAA	BAAGTTGAGGTAGTATATTTAT		14679
QY	1681	TTTTTAATG	CAATTTGATCGAAATGTAAGTATAT	CTAGCATTAATTTGTTTTTAATC		1740
DB	14680	TTTTTAATG	CAATTTGATCGAAATGTAAGTATAT	CTAGCATTAATTTGTTTTTAATC		14739
QY	1741	ATAATAGT	TAATCTAGCTGGTTTGATGAATAAATATCA	ATGATTAATACTATAGTAAA		1800
DB	14740	ATAATAGT	TAATCTAGCTGGTTTGATGAATAAATATCA	ATGATTAATACTATAGTAAA		14799

Qy	1801	AATAAGAAATAAATAAATTAATAATTTTTTTTATAGATTAATAGTTTATTATATAAATTA	1860
Db	14800	AATAAGAAATAAATAAATTAATAATTTTTTTTATAGATTAATAGTTTATTATATAAATTA	14859
Qy	1861	AATATCTATACCAATTAATAATTTTTTGTATTAAGTTTAAATAATTTTTTGTAGAAAT	1920
Db	14860	AATATCTATACCAATTAATAATTTTTTGTATTAAGTTTAAATAATTTTTTGTAGAAAT	14919
Qy	1921	TCCAATCTGCTGTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAAA	1980
Db	14920	TCCAATCTGCTGTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAAA	14979
Qy	1981	TATATCAAACTAATAAGAACAGTAATCTAATGTAAACAACAATAATCTAATGCTAATAT	2040
Db	14980	TATATCAAACTAATAAGAACAGTAATCTAATGTAAACAACAATAATCTAATGCTAATAT	15039
Qy	2041	AACAAAGCGCAAGATCTATCATTTTTATATAGTATTTATTTCAATCAACATTTCTTATTAAT	2100
Db	15040	AACAAAGCGCAAGATCTATCATTTTTATATAGTATTTATTTCAATCAACATTTCTTATTAAT	15099
Qy	2101	TTCTAAATTAATCTGCTAGTTTTTATTAATCTTCAATGATGACTATTAATTAATGAA	2160
Db	15100	TTCTAAATTAATCTGCTAGTTTTTATTAATCTTCAATGATGACTATTAATTAATGAA	15159
Qy	2161	TTAGTTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTGTGTTATCATTTGAT	2220
Db	15160	TTAGTTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTTGTGTTATCATTTGAT	15219
Qy	2221	CTTACATTTGGATTTGATTAACAGTTGGGAAGCTGGGTTTGAATAATCGAT	2267
Db	15220	CTTACATTTGGATTTGATTAACAGTTGGGAAGCTGGGTTTGAATAATCGAT	15279
Qy	2268	-----	2267
Db	15280	AGTTATCATCATCATATAGACACACAGAAATAAAGTAATCAGATTTACGTTTAAGCTAT	15339
Qy	2268	-----	2267
Db	15340	GTAATATTTGGCGCATTAACCAATCAATTAATAAATAATAGATCAGTTTAAAGAAAGATCAAAG	15399
Qy	2268	-----	2267
Db	15400	CTCAAAAAATAAAAAAGAGAAAGGGTCTTAACCAAGAAATAATGAAGGAGAAAAACTAGAA	15459
Qy	2268	-----AAGCTTGGATCTCTAGACCACTTTGTACAGAAAACTGCAACGAGAAA	2315
Db	15460	ATTTACCTGCACAAGCTTGGATCTCTAGACCACTTTGTACAGAAAACTGCAACGAGAAA	15519
Qy	2316	CGTAAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAACAAGACTACAT	2375
Db	15520	CGTAAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAACAAGACTACAT	15579
Qy	2376	AATACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTG	2435
Db	15580	AATACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTG	15639
Qy	2436	ACCTGTAGTCGATTAAGTTGGCGGAGATCAACCGAGCGCACTTTGCGCGGAATAAATACCTG	2495
Db	15640	ACCTGTAGTCGATTAAGTTGGCGGAGATCAACCGAGCGCACTTTGCGCGGAATAAATACCTG	15699
Qy	2496	TGACGGAAGATCACTTTGCGAGAAATAAATAATTCCTGCTGTCCTCTTCATACCGGGAAGC	2555
Db	15700	TGACGGAAGATCACTTTGCGAGAAATAAATAATTCCTGCTGTCCTCTTCATACCGGGAAGC	15759
Qy	2556	CCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGGATTTCAACAATCTTATCTTTT	2615
Db	15760	CCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGGATTTCAACAATCTTATCTTTT	15819
Qy	2616	CTCTTAACAGTCGTTGGCTTCATCTGGATTTTTCAGCTCTATATCTTACTAAACGTGATA	2675
Db	15820	CTCTTAACAGTCGTTGGCTTCATCTGGATTTTTCAGCTCTATATCTTACTAAACGTGATA	15879
Qy	2676	AAAGTTTCTGTAATTTTCTACTGTATCGACCTGACAGCTGGCTGTGATTAAGGAGCGCTGAC	2735

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2736 ATTATATATCCCGAGAACATCAGGTTAAATGGGTTTATGATGTCATTTTCGGGGGGCTG 2795
15940 ATTATATATCCCGAGAACATCAGGTTAAATGGGTTTATGATGTCATTTTCGGGGGGCTG 15999
2796 AGATCAGCACATTTCTTCCCGGATAACGGAGACCGGCACATGCGCCATATCGGGTGCATC 2855
16000 AGATCAGCACATTTCTTCCCGGATAACGGAGACCGGCACATGCGCCATATCGGGTGCATC 16059
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16060 ATCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGGAGACTTTATCT 16119
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16120 GACAGCAGCGTGCATGCGCCAGGGGATCACATCGCTGCGCCGGCGGTGTCAATAATA 16179
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16240 AACTGCATTTTCAACAGTCCCTGTTCTGCTCAGCAAAAGAGCCGTTCAATTTCAATAAACCG 16299
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16300 GGGCACTCAGCATCCCTTCTCTGATTTCCGCTTTCCAGCGTTCGGCAGCAGACGAG 16359
3156 GGCTTCATCTCGATGTTGCTTACAGACCGGAGATTTGACATCATATATGCTTGC 3215
16360 GGCTTCATCTCGATGTTGCTTACAGACCGGAGATTTGACATCATATATGCTTGC 16419
3216 AGCAACTGATAGCTGCTGCTCAACTGTCACTGTAAATACGCTGCTTCATAGCACACCTC 3275
16420 AGCAACTGATAGCTGCTGCTCAACTGTCACTGTAAATACGCTGCTTCATAGCACACCTC 16479
3276 TTTTGTACATCTCTGCTTGTGATGAGATGATTTTCAGGACTATGACACTAGCGTATA 3335
16480 TTTTGTACATCTCTGCTTGTGATGAGATGATTTTCAGGACTATGACACTAGCGTATA 16539
3336 TGAATAGGTAGATGTTTTTATTTTGTACACAAAGAGAGGCTCGCACCTCTTTTCTTA 3395
16540 TGAATAGGTAGATGTTTTTATTTTGTACACAAAGAGAGGCTCGCACCTCTTTTCTTA 16599
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16600 TTTCTTTTATGATTTAATACGGCATTGAGGACAAATAGCGAGTAGGCTGGATACGAGAT 16659
3456 TCCGTTTGAAGAACATTTGGAGGCTGTCGGTGCAGTAAAGTTGGCAGCATCACCGAA 3515
16660 TCCGTTTGAAGAACATTTGGAGGCTGTCGGTGCAGTAAAGTTGGCAGCATCACCGAA 16719
3516 GAACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACATAACCATCTAAGTAGTGTATTC 3575
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3576 ATAGTACTGATATGTTGCTTTTACAGTATATGATGCTGTTTTTATGCAAAATCT 3635
16780 ATAGTACTGATATGTTGCTTTTACAGTATATGATGCTGTTTTTATGCAAAATCT 16839
3636 AATTAAATATATGATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTTTGTACAAAC 3695
16840 AATTAAATATATGATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTTTGTACAAAC 16899
3696 TTGCTAGAGCTCCTGCTTTTATAGATATGCGAGACGCTATGATCGCATGATATTGCT 3755
16900 TTGCTAGAGCTCCTGCTTTTATAGATATGCGAGACGCTATGATCGCATGATATTGCT 16959
3756 TTCAATTTCTGTTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCCTACCGC 3815

16950 TTCAATTTCTGTTGTCAGCTTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTTTACCGC 17019
3816 CGGTTTCGGTTCACTTCAATGAATATATCACCGTTACTATCGTATTTTATGATAATA 3875
17020 CGGTTTCGGTTCACTTCAATGAATATATCACCGTTACTATCGTATTTTATGATAATA 17079
3876 TTCTCCGTTTCAATTTTACTGATTTGTAACCTTACTTATATGTACAAATTTAAAAATGAAAA 3935
17080 TTCTCCGTTTCAATTTTACTGATTTGTAACCTTACTTATATGTACAAATTTAAAAATGAAAA 17139
3936 CAATATATGTCTGCAATAGGTTTATAGGACATCTATGATAGAGCGGCACAAATACAAA 3995
17140 CAATATATGTCTGCAATAGGTTTATAGGACATCTATGATAGAGCGGCACAAATACAAA 17199
3996 CAATTTGCGTTTATTTATTTACAAATCCAAATTTTAAAAAAGGCGGACAAACCT 4055
17200 CAATTTGCGTTTATTTATTTACAAATCCAAATTTTAAAAAAGGCGGACAAACCT 17259
4055 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGGCGGCGCTAGTATCTAC 4115
17260 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGGCGGCGCTAGTATCTAC 17319
4116 GACACACGAGCGGCGAACTAATAACGTTTCACTGAAGGGAATCCGTTCCCGCGCGG 4175
17320 GACACACGAGCGGCGAACTAATAACGTTTCACTGAAGGGAATCCGTTCCCGCGCGG 17379
4176 CGCATGGGTGAGATTTCTTGAAGTTGAGTATTTGGCGCTCTACCGAAAGTTACGGG 4235
17380 CGCATGGGTGAGATTTCTTGAAGTTGAGTATTTGGCGCTCTACCGAAAGTTACGGG 17439
4236 CACCATTTCAACCGGTTCCAGCACGCGCGCGGTTAACCGACTTGTCTGCCCGCGAGATTA 17499
17440 CACCATTTCAACCGGTTCCAGCACGCGCGCGGTTAACCGACTTGTCTGCCCGCGAGATTA 17499
4296 GCAGCATTTTGTGTTGTTATGTTGGCGGCAATGAGTGCAGTCAAACTTTGACAGTGA 4355
17500 GCAGCATTTTGTGTTGTTATGTTGGCGGCAATGAGTGCAGTCAAACTTTGACAGTGA 17559
4356 CGACAAATCGTTGGCGGCTCCAGGCGCAATTTTGCACAACATGTCGAGGCTCAGCAGG 4415
17560 CGACAAATCGTTGGCGGCTCCAGGCGCAATTTTGCACAACATGTCGAGGCTCAGCAGG 17619
4416 ACCTGAGCGCATGCAAGCTAGCTTACTAGTATGATGATTTCTATAGTGTCACTTAATCT 4475
17620 ACCTGAGCGCATGCAAGCTAGCTTACTAGTATGATGATTTCTATAGTGTCACTTAATCT 17679
4476 GC 4477
17680 GC 17681

RESULT 5

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US2003004983A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match	91.9%;	Score 4112.4;	DB 15;	Length 17962;	
Best Local Similarity	93.8%;	Pred. No. 0;			
Matches 4446;	Conservative 0;	Mismatches 6;	Indels 290;	Gaps 4;	
QY	26	GACAAAGTTTGACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAATATATT	85		
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QY	86	AAATAGATTTTGCATAAAAACAGACATACATATATCTGTAAAAACACACATATCCAGTC	145		
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QY	146	ACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGAGTCGACGACAGCCCTTCCAAA	205		
Db	13241	ACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGAGTCGACGACAGCCCTTCCAAA	13300		
QY	206	TGTTCTTCGGGTGATGCTGCCAACTTAGTTCGACGACAGCCCTTCCAAATGTTCTTCTCAA	265		
Db	13301	TGTTCTTCGGGTGATGCTGCCAACTTAGTTCGACGACAGCCCTTCCAAATGTTCTTCTCAA	13360		
QY	266	ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTTCTCAATGCCGTATTAATCATRAAAA	325		
Db	13361	ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTTCTCAATGCCGTATTAATCATRAAAA	13420		
QY	326	AGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAACATCTACCT	385		
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QY	386	ATTATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTCACAAAC	445		
Db	13481	ATTATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTCACAAAC	13540		
QY	446	TCCTATACCTTTCTCTTCAAGTCGTTCCGGTTCATCTGGATTTTCAGCCTCTATACTTA	505		
Db	13541	TCCTATACCTTTCTCTTCAAGTCGTTCCGGTTCATCTGGATTTTCAGCCTCTATACTTA	13600		
QY	506	CTAAAGTCATAAAGTTCTCTGTAATTTCTACTGTATCGAACCTGCAGACTGGCTGTGTATA	565		
Db	13601	CTAAAGTCATAAAGTTCTCTGTAATTTCTACTGTATCGAACCTGCAGACTGGCTGTGTATA	13660		
QY	566	AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGGTTTTGATGTCATTT	625		
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QY	626	TCGCGGTGGTGAGATCAGCCACTCTCCCGATACAGAGACCGGACACACTGGCCATA	685		
Db	13721	TCGCGGTGGTGAGATCAGCCACTCTCTCCCGATACAGAGACCGGACACACTGGCCATA	13780		
QY	686	TCGGTGTGTCATCATGCGCCAGCTTTTCATCCCGATATGCAACCCGGGTAAAGTTCACGG	745		
Db	13781	TCGGTGTGTCATCATGCGCCAGCTTTTCATCCCGATATGCAACCCGGGTAAAGTTCACGG	13840		
QY	746	GAGACTTTATCTGACAGACAGTGCACTGGCCAGGGGGATCACCATCCGTCGCGCGGGC	805		
Db	13841	GAGACTTTATCTGACAGACAGTGCACTGGCCAGGGGGATCACCATCCGTCGCGCGGGC	13900		
QY	806	GTGTCATATATACACTCTGTACATCCAAAAACAGAGATAACCGGCTCTCTTTTATAG	865		
Db	13901	GTGTCATATATACACTCTGTACATCCAAAAACAGAGATAACCGGCTCTCTTTTATAG	13960		
QY	866	GTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAT	925		
Db	13961	GTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAT	14020		
QY	926	TTCAATAAACCGGGAGCCTCAGGCATCCCTTCTGATTTCCGCTTCCAGCGTTCCGGC	985		
Db	14021	TTCAATAAACCGGGAGCCTCAGGCATCCCTTCTGATTTTCCGCTTCCAGCGTTCCGGC	14080		
QY	986	ACGACAGACGCGGCTTCAATCTGCATGTTGTCTTACACAGACGGAGATATTGACATC	1045		
Db	14081	ACGACAGACGCGGCTTCAATCTGCATGTTGTCTTACACAGACGGAGATATTGACATC	14140		

QY	1046	ATATATGCTTGGAGCAACTGATAGTGTGCTGTCAACTGTCTCACTGTAAATACGCTGCTTC	1105		
Db	14141	ATATATGCTTGGAGCAACTGATAGTGTGCTGTCAACTGTCTCACTGTAAATACGCTGCTTC	14200		
QY	1106	ATAGCACACCTCTTTTGGACATACCTTCGGGTAGTGGCGATCAACAGTCTCAATTTTGGCAA	1165		
Db	14201	ATAGCACACCTCTTTTGGACATACCTTCGGGTAGTGGCGATCAACAGTCTCAATTTTGGCAA	14260		
QY	1166	AAGTTGGCCCGGCTTCCCGGTATCAACAGGGACACCCAGGATTTATTTATCTGCGAAG	1225		
Db	14261	AAGTTGGCCCGGCTTCCCGGTATCAACAGGGACACCCAGGATTTATTTATCTGCGAAG	14320		
QY	1226	TGATCTTCGCTGACAGGTATTTATTCGCGCAAGTGGCGGTGATGCTGCCAATCTTA	1285		
Db	14321	TGATCTTCGCTGACAGGTATTTATTCGCGCAAGTGGCGGTGATGCTGCCAATCTTA	14380		
QY	1286	GTCGACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATATGTTGT	1345		
Db	14381	GTCGACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATATGTTGT	14440		
QY	1346	GTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT	1405		
Db	14441	GTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT	14500		
QY	1406	ATATCATTTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTGG-----	1448		
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QY	1449	-----	1448		
Db	14561	TGCTTATCAATTTGTTGCAACGACAGGTCACTATCAGTCAAAAATAAAATCATTTATTCG	14620		
QY	1449	-----TCTCGAGGAATTCGGTATCCCGAGCTTGGTAAAGAAATAATATTT	1493		
Db	14621	CATCCAGCTGCGAGCTCTCGAGGAATTCGGTATCCCGAGCTTGGTAAAGAAATAATATTT	14680		
QY	1494	TCTTTTTCCTTTTAGTATATAAATAGTTAAGTGATTAATTTAGTATGATTAATAATAATA	1553		
Db	14681	TCTTTTTCCTTTTAGTATATAAATAGTTAAGTGATTAATTTAGTATGATTAATAATAATA	14740		
QY	1554	TAGTTGTTTATATTTGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACAATAGT	1613		
Db	14741	TAGTTGTTTATATTTGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACAATAGT	14800		
QY	1614	AATGTAAAAAATATGACAGTGTGTGTAACGCAAGAGATAAAAGTTGAGAGTAAGT	1673		
Db	14801	AATGTAAAAAATATGACAGTGTGTGTAACGCAAGAGATAAAAGTTGAGAGTAAGT	14860		
QY	1674	ATATTATTTTATGAAATTTGATCGAACATGTAAAGATGATATCTAGCATTAATATTTGT	1733		
Db	14861	ATATTATTTTATGAAATTTGATCGAACATGTAAAGATGATATCTAGCATTAATATTTGT	14920		
QY	1734	TTTAAATCAATAAGTAATTTCTAGCTGGTTTGTATGAATTTAAATATCAATGATTAATACTA	1793		
Db	14921	TTTAAATCAATAAGTAATTTCTAGCTGGTTTGTATGAATTTAAATATCAATGATTAATACTA	14980		
QY	1794	TAGTAAAAATAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	1853		
Db	14981	TAGTAAAAATAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	15040		
QY	1854	ATAATTTAAATATCTATACCATTTACTAAATAATTTTAGTTTAAAGTTTAAATAATTTTGT	1913		
Db	15041	ATAATTTAAATATCTATACCATTTACTAAATAATTTTAGTTTAAAGTTTAAATAATTTTGT	15100		
QY	1914	TAGAAATTCGAATCTGCTTGTAAATTTATCAATAAACAATAAATAAATAAATCAAGCTAAAG	1973		
Db	15101	TAGAAATTCGAATCTGCTTGTAAATTTATCAATAAACAATAAATAAATAAATCAAGCTAAAG	15160		
QY	1974	TAAACAAATAATATCAAACTTAATAGAACAGTAACTAAATGTAACAAAAACAATAATCTAATG	2033		
Db	15161	TAAACAAATAATATCAAACTTAATAGAACAGTAACTAAATGTAACAAAAACAATAATCTAATG	15220		
QY	2034	CTAATATAACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATTCCT	2093		

Db 15221 CTAATATAACAAAGCGCAGATCTATCATTTTATATAGTATTAATTTTCAATCAACATCTCT 15280
QY 2094 TATTAATTTCTAAATAAATCTGTAGTTTATTAATACTTCTAAATGGATGACTAATAAT 2153
Db 15281 TATTAATTTCTAAATAAATCTGTAGTTTATTAATACTTCTAAATGGATGACTAATAAT 15340
QY 2154 AAATGAAATAGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTGTTAT 2213
Db 15341 AAATGAAATAGTCGAAACATGAATAAACAAGGTAAACATGATAGATCATGTGCTGTTAT 15400
QY 2214 CATTGATCTTACATTTGGATTCATTAACATTCGGAGCTGGGTTCGAAATCGATAAGCTT 2273
Db 15401 CATTGATCTTACATTTGGATTCATTAACATTCGGAGCTGGGTTCGAAATCGATAAGCTT 15460
QY 2274 GGATCCTCTPAGA----- 2285
Db 15461 GGATCCTCTAGAGAGCTGCAGCTGGATGGCAAAATATGATTTTATTTGACTGATAGTA 15520
QY 2286 -----CCACTTTGTACAGA 2300
Db 15521 CCGTTTCGTTGCAACAAATGTGATAAGCAATGCTTTCTTAATATGCCAACTTTGTACAGA 15580
QY 2301 AAGCTGAAACGAGAAAACGTAATAATGATATAAATAATCAATATATTAATTTAGATTTTGCATA 2360
Db 15581 AAGCTGAAACGAGAAAACGTAATAATGATATAAATAATCAATATATTAATTTAGATTTTGCATA 15640
QY 2361 AAAAAAGACTACATTAATCTGTAAACACACATATCCAGTCACATGAAATCAACTACT 2420
Db 15641 AAAAAAGACTACATTAATCTGTAAACACACATATCCAGTCACATGAAATCAACTACT 15700
QY 2421 TAGATGGTATAGTCAGCTGTAGTCAGTAAGTTGGCAGCATCACCCGACGACTTTGCG 2480
Db 15701 TAGATGGTATAGTCAGCTGTAGTCAGTAAGTTGGCAGCATCACCCGACGACTTTGCG 15760
QY 2481 CCGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTGTGTCTCCCTG 2540
Db 15761 CCGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTGTGTCTCCCTG 15820
QY 2541 TTGATACCGGGAAGCCCTGGGCCAACTTTTGGGGAATAAGACGTTGATCGG----- 2593
Db 15821 TTGATACCGGGAAGCCCTGGGCCAACTTTTGGGGAATAAGACGTTGATCGGCACTACC 15880
QY 2594 -ATTTGACAACTCTTATACATTTTCTCTTACAAGTCGTTGGCTTCACTGGAATTTTCAGC 2652
Db 15881 CATTTCACAACTCTTATACATTTTCTCTTACAAGTCGTTGGCTTCACTGGAATTTTCAGC 15940
QY 2653 CTCTATACTTACTAAACGTCGATAAAGTTCTGTAAATTTCTGTATGCGACCTGCAGACT 2712
Db 15941 CTCTATACTTACTAAACGTCGATAAAGTTCTGTAAATTTCTGTATGCGACCTGCAGACT 16000
QY 2713 GCGTGTGATAAGGAGCCCTGCACATTTATATTTCCAGACATCAGGTTAATGCGGTTTT 2772
Db 16001 GCGTGTGATAAGGAGCCCTGCACATTTATATTTCCAGACATCAGGTTAATGCGGTTTT 16060
QY 2773 TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGAGACCGGCA 2832
Db 16061 TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGAGACCGGCA 16120
QY 2833 CACTGGCCATATCGGTGGTCATATGATGCGCAGCTTTTCAATCCCGATATGCAACACCGGCT 2892
Db 16121 CACTGGCCATATCGGTGGTCATATGATGCGCAGCTTTTCAATCCCGATATGCAACACCGGCT 16180
QY 2893 AAAGTTTACGGGACCTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCC 2952
Db 16181 AAAGTTTACGGGACCTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCC 16240
QY 2953 GTCCCGCGGCTGTCAATATATACATCTGTACATCCACAAACAGACGATAACGGCTCT 3012
Db 16241 GTCCCGCGGCTGTCAATATATACATCTGTACATCCACAAACAGACGATAACGGCTCT 16300
QY 3013 CTCTTTTATAGGTGTAACCTTAAACTGCAATTCACAGTCCCTGTTCTCGTCAGCAAAA 3072

Db 16301 CTCTTTTATAGGTGTAACCTTAAATGCAATTTTCCACAGTCCCTGTTCTCGTCAGCAAAA 16360
QY 3073 GAGCGGTTCAATTTCAATTAACCGGCGACCTCAGCCATCCCTTCTGATTTTCGCTTTC 3132
Db 16361 GAGCGGTTCAATTTCAATTAACCGGCGACCTCAGCCATCCCTTCTGATTTTCGCTTTC 16420
QY 3133 CAGGTTTCGGCAGCAGACGAGCGGCTTCATTTCTGCAATGTTGCTTTACAGACCGGAG 3192
Db 16421 CAGGTTTCGGCAGCAGACGAGCGGCTTCATTTCTGCAATGTTGCTTTACAGACCGGAG 16480
QY 3193 ATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTCCGTGCAACTGCTCACTGTA 3252
Db 16481 ATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTCCGTGCAACTGCTCACTGTA 16540
QY 3253 TAGCTGCTTCATAGCACACCTCTTTTGGACATCTCTGTTGACATGAGAGATGATTTT 3312
Db 16541 TAGCTGCTTCATAGCACACCTCTTTTGGACATCTCTGTTGACATGAGAGATGATTTT 16600
QY 3313 CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTATTTTGTCAACAAAAA 3372
Db 16601 CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTATTTTGTCAACAAAAA 16660
QY 3373 GAGGCTCGACCTCTTTTCTTTTATGATTTAATAACGCAATTCAGGCAATTA 3432
Db 16661 GAGGCTCGACCTCTTTTCTTTTATGATTTAATAACGCAATTCAGGCAATTA 16720
QY 3433 GCGAGTAGGCTGGATACACGATTCGCTTTCAGAGAAACATTTGGAAGCTGTCCGTCGA 3492
Db 16721 GCGAGTAGGCTGGATACACGATTCGCTTTCAGAGAAACATTTGGAAGCTGTCCGTCGA 16780
QY 3493 CTAACTTGGCAGCACTCACCCGGAAGAACATTTTGGAGGCTGTCCGTCGACTACAGTCACT 3552
Db 16781 CTAACTTGGCAGCACTCACCCGGAAGAACATTTTGGAGGCTGTCCGTCGACTACAGTCACT 16840
QY 3553 AATAACAATCAATAGTATGATTCATAGTGAATGATGATGTTGTTTACAGTATATGT 3612
Db 16841 AATAACAATCAATAGTATGATTCATAGTGAATGATGATGTTGTTTACAGTATATGT 16900
QY 3613 AGCTGTGTTTATGCAAAATCTAATTTAATAATATGATATTTATATCAATTTACGTTTC 3672
Db 16901 AGCTGTGTTTATGCAAAATCTAATTTAATAATATGATATTTATATCAATTTACGTTTC 16960
QY 3673 TCGTTTCAGCTTTTGTACAAACTTG----- 3698
Db 16961 TCGTTTCAGCTTTTGTACAAAAGTTGGCAATTAATAAAGCAATTCATCAATTTGTTG 17020
QY 3699 ----- 3698
Db 17021 CAAAGAAAGGTCATCTATCAGTCAAAAATAAATCAATTTTGGGCGCGAGATCCATGCT 17080
QY 3699 ---TCTAGAGTCTCTCTTTAATGAGATATGCGAGACGCTATGATCGATGATTTGCT 3755
Db 17081 AGCTCTAGAGTCTCTCTTTAATGAGATATGCGAGACGCTATGATCGCATGATTTGCT 17140
QY 3756 TTCAATTCCTGTTGTCACGCTTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTTACCGC 3815
Db 17141 TTCAATTCCTGTTGTCACGCTTTGTAATAAACCTGAGCATGTGTAGCTCAGATCTTACCGC 17200
QY 3816 GCGTTTCGCTTCATTTCTAATGAATATATCACCCTGTTACTATCTGATTTTATGAATAATA 3875
Db 17201 GCGTTTCGCTTCATTTCTAATGAATATATCACCCTGTTACTATCTGATTTTATGAATAATA 17260
QY 3876 TTCTCCGTTCAATTTTACTGATTTGATCCCTTACTTATATGTAACAATTTAAATGAAAA 3935
Db 17261 TTCTCCGTTCAATTTTACTGATTTGATCCCTTACTTATATGTAACAATTTAAATGAAAA 17320
QY 3936 CAATATATTTGCTGATAGTTTATGAGCAATCTATGATAGGCGCCACATTAACAAA 3995
Db 17321 CAATATATTTGCTGATAGTTTATGAGCAATCTATGATAGGCGCCACATTAACAAA 17380
QY 3996 CAATTCGCTTTTATTTATTAACAATCCAAATTTTAAATAAAGCGGCAACCGTCAACCT 4055
Db 17381 CAATTCGCTTTTATTTATTAACAATCCAAATTTTAAATAAAGCGGCAACCGTCAACCT 17440

QY 4056 AAAAGACTGATTACATAAATCTTATCAAAATTTCAAAAGCCCGGCGCTAGTATCTAC 4115
Db |||||
QY 17441 AAAAGACTGATTACATAAATCTTATCAAAATTTCAAAAGCCCGGCGCTAGTATCTAC 17500
Db |||||
QY 4116 GACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGAACTCCCGGTTCCCGCGCGG 4175
Db |||||
QY 17501 GACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGAACTCCCGGTTCCCGCGG 17560
Db |||||
QY 4176 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGTCTCTACCGAAGTTACGGG 4235
Db |||||
QY 17561 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGTCTCTACCGAAGTTACGGG 17620
Db |||||
QY 4236 CACCATTACCGGTCGACGCGCGCGGTAACCGACTTGTCTGCGCCCGGAGATTA 4295
Db |||||
QY 17621 CACCATTACCGGTCGACGCGCGGTAACCGACTTGTCTGCGCCCGGAGATTA 17680
Db |||||
QY 4296 GCAGCAATTTTTTTGGTGTATGTGGGCGCCCAAAATGAAGTCAGGTCAAACTTGACAGTGA 4355
Db |||||
QY 17681 GCAGCAATTTTTTTGGTGTATGTGGGCGCCCAAAATGAAGTCAGGTCAAACTTGACAGTGA 17740
Db |||||
QY 4356 CGACAAATCGTTGGGCGGTCGAGGCGGAATTTTGGACACATGTCGAGGCTCAGCAGG 4415
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QY 17741 CGACAAATCGTTGGGCGGTCGAGGCGGAATTTTGGACACATGTCGAGGCTCAGCAGG 17800
Db |||||
QY 4416 ACCTGAGGCGATCAAGCTAGCTTACTAGTATGATGCATATTTCTATAGTGTCACTAAATCT 4475
Db |||||
QY 17801 ACCTGAGGCGATCAAGCTAGCTTACTAGTATGATGCATATTTCTATAGTGTCACTAAATCT 17860
Db |||||
QY 4476 GC 4477
Db |||||
QY 17861 GC 17862
Db |||||

RESULT 6

US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17690)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14680)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15062)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match 72.3%; Score 3234.8; DB 15; Length 18691;
Best Local Similarity 79.5%; Pred. No. 0;
Matches 4429; Conservative 0; Mismatches 22; Indels 1121; Gaps 6;
QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAAGCTGATAAATGATATAATCAATATATT 85
Db 13121 GCCAACTTTGTACAAAAAAGCTGAACGAGAAAGCTGATAAATGATATAATCAATATATT 13180
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAAAACACACATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAAAACACACATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 205
Db 13241 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 13300
QY 206 TGTCTTCGGGTGATGCTGCCAACTTTAGTCGACGACAGCCTTCCAAATGTTCTTCTCAA 265
Db 13301 TGTCTTCGGGTGATGCTGCCAACTTTAGTCGACGACAGCCTTCCAAATGTTCTTCTCAA 13360
QY 266 ACGGAATCGTCGTATCGAGCCTTCTCGCTATTTCTCAATGCGGTATTTAAATCATAAAA 325
Db 13361 ACGGAATCGTCGTATCGAGCCTTCTCGCTATTTCTCAATGCGGTATTTAAATCATAAAA 13420
QY 326 AGAATTAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAAATAAAACATCTACCT 385

Db	13421	AGAAATAGAAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATCACTACCT	13480	Db	14501	ATATCATTTTACGTTTCTCGTTTACGCTTTCTTGTACAAAGTTGGCATTTATAAGAAAGCAT	14560
Qy	386	ATTTCATATACGCTAGTGTCTATAGTCTGTAATCACTCATCAAGAAACAAATTTTCAACAAC	445	Qy	1449	-----	1448
Db	13481	ATTTCATATACGCTAGTGTCTATAGTCTGTAATCACTCATCAAGAAACAAATTTTCAACAAC	13540	Db	14561	TGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCATCAAAATAAAAAATCAATTTATTTGC	14620
Qy	446	TCCTTATACATTTTCTCTTACAAAGTCGTTTCGGCTTCATCTGGAATTTTCAGCCTCTATACCTTA	505	Qy	1449	-----TCCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAAATAATTAATTT	1493
Db	13541	TCCTTATACATTTTCTCTTACAAAGTCGTTTCGGCTTCATCTGGAATTTTCAGCCTCTATACCTTA	13600	Db	14621	CATCCAGCTGCGAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAAGGAATTAATTAATTT	14679
Qy	506	CTAAACGTGATAAAGTTTCTGTAATTTCTGTAATTTCTGATGTAATGCGCTTAAATGATGATTA	565	Qy	1494	TCCTTTTTCCTTTTAGTATAAAAAATAGTTAAGTGTGTTAAATTTAGTATGATTAATAATAA	1553
Db	13601	CTAAACGTGATAAAGTTTCTGTAATTTCTGTAATTTCTGATGTAATGCGCTTAAATGATGATTA	13660	Db	14680	TCCTTTTTCCTTTTAGTATAAAAAATAGTTAAGTGTGTTAAATTTAGTATGATTAATAATAA	14739
Qy	566	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGTGATGATTT	625	Qy	1554	TAGTTGTTTATTAATTTGTAAGAAAAATTAATTTAATAATATATTTGTTTACATAAAACAACATAGT	1613
Db	13661	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGTGATGATTT	13720	Db	14740	TAGTTGTTTATTAATTTGTAAGAAAAATTAATTTAATAATATATTTGTTTACATAAAACAACATAGT	14799
Qy	626	TCGCGTGTGCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCCGGACACCTGGCCATA	685	Qy	1614	RATGTAAAAAATATGACAAGTGTGTAAAGACGAAGAAGATAAAAGTTTGAGAGTAAGT	1673
Db	13721	TCGCGTGTGCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCCGGACACCTGGCCATA	13780	Db	14800	AATGTAAAAAATATGACAAGTGTGTAAAGACGAAGAAGATAAAAGTTTGAGAGTAAGT	14859
Qy	686	TCGCTGTGCTATCATGCGCAGCTTTTCATCCCGATATGACACACCCGGTAAAGTTTCAACGG	745	Qy	1674	ATATTATTTTAAATGAAATTTGATCGAACATGTGAAGATGATATACCTAGCAATTAA	1726
Db	13781	TCGCTGTGCTATCATGCGCAGCTTTTCATCCCGATATGACACACCCGGTAAAGTTTCAACGG	13840	Db	14860	ATATTATTTTAAATGAAATTTGATCGAACATGTGAAGATGATATACCTAGCAATTAA	14919
Qy	746	GAGACTTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTGCGCCGGGC	805	Qy	1727	-----	1726
Db	13841	GAGACTTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTGCGCCGGGC	13900	Db	14920	CAACTTTCAACCATTAATGAAATTAAGATCACTACCGGGCGTATTTTTTGAGTTATCCAGATT	14979
Qy	806	GTGTCAATATATCATCTGTATCATCCACAAACAGAGGATAACGGCTCTCTCTTTTATAG	865	Qy	1727	-----	1726
Db	13901	GTGTCAATATATCATCTGTATCATCCACAAACAGAGGATAACGGCTCTCTCTTTTATAG	13960	Db	14980	TTTCAAGGCTAAGGAAGCTAAATCGAGAAAAAATCACTGGATATACCACCGTTGATAT	15039
Qy	866	GTGTAAACCTTTAACTGATTTTCAACAGTCCCTGTTTCTGTCAGCAAAAGAGCGGTTTAT	925	Qy	1727	-----	1726
Db	13961	GTGTAAACCTTTAACTGATTTTCAACAGTCCCTGTTTCTGTCAGCAAAAGAGCGGTTTAT	14020	Db	15040	ATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCACTAGTGTGCTCAATGACCTA	15099
Qy	926	TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCAGCGGTTTCGGC	985	Qy	1727	-----	1726
Db	14021	TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCAGCGGTTTCGGC	14080	Db	15100	TAACCAAGCCGTTACGCTGGATATTAACGGCCTTTTAAAGACCGTAAAGAAAAATAGCA	15159
Qy	986	ACCGACAGCAGCGGCTTCATCTGATGTTGCTTTACAGACCCGAGATATTTGACATC	1045	Qy	1727	-----	1726
Db	14081	ACCGACAGCAGCGGCTTCATCTGATGTTGCTTTACAGACCCGAGATATTTGACATC	14140	Db	15160	CAAGTTTATCCGGCCTTTTATTTCACTTCTTGCCGCTGATGAATGCTCATCCCGAAAT	15219
Qy	1046	ATATATGCTTTGAGCAACTGATAGTCTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC	1105	Qy	1727	-----	1726
Db	14141	ATATATGCTTTGAGCAACTGATAGTCTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC	14200	Db	15220	CGGTATGGCAATGAAGACCGGTGAGCTGGTGATAAGGGATAGTGTTCACCCCTTGTACAC	15279
Qy	1106	ATAGCACACCTCTTTTGAACATCTCGGTAGTGGCGATCAAGCTCTCAATTTTCGCCAA	1165	Qy	1727	-----	1726
Db	14201	ATAGCACACCTCTTTTGAACATCTCGGTAGTGGCGATCAAGCTCTCAATTTTCGCCAA	14260	Db	15280	CGTTTTCATGACCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTT	15339
Qy	1166	AAGTTGCGCCAGGCTTCCGGTATCAACAGGACACACAGGATTTATTTATCTGCGAAG	1225	Qy	1727	-----	1726
Db	14261	AAGTTGCGCCAGGCTTCCGGTATCAACAGGACACACAGGATTTATTTATCTGCGAAG	14320	Db	15340	CCGGCAGTTTCTACACATATTTCCGACAGATGTGGCGTGTGTACGGTGAACCACTCGCCCTA	15399
Qy	1226	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAAAGTGGTGGGTGATGCTGCGCAACTTA	1285	Qy	1727	-----	1726
Db	14321	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAAAGTGGTGGGTGATGCTGCGCAACTTA	14380	Db	15400	TTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTTCGTCTCAGCCAATCCCTGGGTGATTT	15459
Qy	1286	GTGCACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGTGATGATGTTGT	1345	Qy	1727	-----	1726
Db	14381	GTGCACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTGTGATGATGTTGT	14440	Db	15460	CACCAAGTTTGAATTTAAACGTGGCCAAATATGGACAACTTCTTCGCCCGCTTTTCCACAT	15519
Qy	1346	GTTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATTT	1405	Qy	1727	-----	1726
Db	14441	GTTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAATTAATATATTCATATTT	14500	Db	15520	GGGCAAAATATTAACGCAAGGCGCAAGAGGTGCTGATGCCGCTGGCGATTCAGGTTCACTA	15579
Qy	1406	ATATCATTTTACGTTTCTCGTTTACGCTTCTGTATCAAAAGTGG	1448	Qy	1727	-----	1726
		-----		Db	15580	TGCCGCTGTGATGGCTTCCATGTCGGCAGAAATGCTTAATGAATTAACAACAGTACTGCGA	15639

17800 TTTTGTGACAAAGTTGGCATTATATAAAAAAGCANTGCTCATCAATTTGTTGCAACGACAG 17859
3699 -----TCTAGAG 3705
17860 GTCACTATCAGTCAAAATAAAATCATTATTTGGGGCCGAGATCCATGCTAGCTCTAGAG 17919
3706 TCCGTGTTTAATGAGATATGCGAGACGCTATATGTCGATGATATTTGCTTCAATTTCTG 3765
17920 TCCGTGTTTAATGAGATATGCGAGACGCTATATGTCGATGATATTTGCTTCAATTTCTG 17979
3766 TTGTGCGCTTTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGT 3825
17980 TTGTGCGCTTTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGT 18039
3826 TCATTCTAATGAATATATACCGGTTTACTATCGTATTTTATGAATAATTTCTCGGTTTC 3885
18040 TCATTCTAATGAATATATACCGGTTTACTATCGTATTTTATGAATAATTTCTCGGTTTC 18099
3886 AATTACTGATTTGACCTACTACTTATATGACATATTTAAATGAAACCAATATATG 3945
18100 AATTACTGATTTGACCTACTACTTATATGACATATTTAAATGAAACCAATATATG 18159
3946 TGTGTAATAGTTTATAGGACATCTATGATAGAGCGCCACATAACAACTTCGGTT 4005
18160 TGTGTAATAGTTTATAGGACATCTATGATAGAGCGCCACATAACAACTTCGGTT 18219
4006 TTATTTACAAATCCAAATTTTAAAAAGCGGCGAGAACCGGTCAAACCTTAAAAAGACTGA 4065
18220 TTATTTACAAATCCAAATTTTAAAAAGCGGCGAGAACCGGTCAAACCTTAAAAAGACTGA 18279
4066 TTACATAAATCTTATCABAATTTCAAAGGCCCGGCTAGTATCTAGACACACCGA 4125
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4126 GCGCGGAATCAATAAAGCTTCACTGAAGGAACCTCCGGTTCCCGCGCGCGCATGGTG 4185
18340 GCGCGGAATCAATAAAGCTTCACTGAAGGAACCTCCGGTTCCCGCGCGCGCATGGTG 18399
4186 AGATTCCTGAGTTGAGTATGTCGCTCCGCTCAGAAAGTTAGCGGACCAATTC 4245
18400 AGATTCCTGAGTTGAGTATGTCGCTCCGCTCAGAAAGTTAGCGGACCAATTC 18459
4246 CCGCGTCCAGCAGCGCGCGGTAACCGACTTCTGCGCGGAGAAATTTATGACATTTT 4305
18460 CCGCGTCCAGCAGCGCGCGGTAACCGACTTCTGCGCGGAGAAATTTATGACATTTT 18519
4306 TTTGGTGTATGTTGGCCCCCAATGAGTGCAGGTCAAACCTTTGACGTGACGACAAATCG 4365
18520 TTTGGTGTATGTTGGCCCCCAATGAGTGCAGGTCAAACCTTTGACGTGACGACAAATCG 18579
4366 TTGGCGGGTCCAGGCGGAATTTGCGACACATGTCGAGGCTCAGCAGGACCTGCAGGC 4425
18580 TTGGCGGGTCCAGGCGGAATTTTTCGACAAATGTCGAGGCTCAGCAGGACCTGCAGGC 18639
4426 ATGCAAGCTAGCTTACTAGTGATGATATTTCTATAGTGTCACTAAATCTGC 4477
18640 ATGCAAGCTAGCTTACTAGTGATGATATTTCTATAGTGTCACTAAATCTGC 18691

RESULT 7
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 28.5%; Score 1277.8; DB 15; Length 17458;
Best Local Similarity 62.4%; Pred. No. 1e-183;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;
21 CTCGAGACGAGTTTCTACAAAAAGCTGAACGAGAAACGTAAAAATGATATAATATCAAT 80
16686 CTCGAGACGAGTTTCTACAAAAAGCTGAACGAGAAACGTAAAAATGATATAATATCAAT 16627
81 ATATTAAATTAGATTTTCATAAAAAAGCAGCTACATAATCTGTAAAAACACACATATC 140
16626 ATATTAAATTAGATTTTGCATAAAAAAGCAGCTACATAATCTGTAAAAACACACATATC 16567
141 CAGTCACTATGATCAACTTACTTAGATGGTATTTAGTACCTGTAGTCCGACGACGCTT 200
16566 CAGTCACTATGATCAACTTACTTAGATGGTATTTAGTACCTGTAGTCCGACGACGCTT 16507
201 CCAATTTCTTCGGGTGATGCTGCAAACTTAGTTCGACGACGCTTCCAAATGTTCTT 260
16506 CCAATTTCTTCGGGTGATGCTGCAAACTTAGTTCGACGACGCTTCCAAATGTTCTT 16447
261 CTCAAAACGGAATGCTGATCCAGCCTTCTCGTATTTGCTTCAATGCCGTATTAATCA 320
16446 CTCAAAACGGAATGCTGATCCAGCCTTCTCGTATTTGCTTCAATGCCGTATTAATCA 16387
321 TAAAGAAATTAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATATAAAACATC 380
16386 TAAAGAAATTAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAATATAAAACATC 16327
381 TACCTATTCAATATACGCTAGTGTCTAGTTCCTGAAAAATCATCTGCATCAAGAAATTTTC 440
16326 TACCTATTCAATATACGCTAGTGTCTAGTTCCTGAAAAATCATCTGCATCAAGAAATTTTC 16267
441 ACAACTTTTACTTTTCTTACAGTGTGCGGCTTCTCATCTGGATTTTTCAGCCTCTAT 500
16266 ATGTCAAAAAGAGGTGCTGCTATGAA---GCAGGTATTTACGTGACAGTTGACGCGACA 16210
501 ACTTACTAAAACGTGATAAAGTTTCTGTAAATTTCTATGTATCGACCTGCGACTGGCTGT 560
16209 GCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGCTCTGTTAAGCACAAACAT 16150
561 GTATAAGGGAGCTGACATTTATTTCCCGCAGAACATCAGGTTAATGGCGTTTGTGATGT 620
16149 GCAGAAATGAAGCCGCTGCTGCGTGC---GAAACGCTGGAAGAGCGGAAAAATCAGGAAG 16093
621 CATTTTCGCGGTGCTGAGATCAGCCTTCTTCCCGATATAACGAGACCGGACACATGG 680
16092 GATGGCTGAGTCCGCGTTTATTTGAATGAACGGCTCTTTTGTGACGAGAACAGGG- 16034
681 CCAATCCGTGGTCAATCATCGCCAGCTTTTCACTCCCGATATGACACACCGGTAAGTT 740
16033 -----ACTGGTGAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTATCGTC 15979
741 CACGGAGACTTTTATCTGACGAGCAGTGTGCTGCGCAGGGGATCACCATCCGTCGCC 800
15978 TGTTTGTGGATGTACAGAGTGATATTTTACACCGCCCGCGCGCGATGGTATGATGTC 15919
801 CGGCGGTGCTCAATATATCACTCTGTATCATCCAAACACAGCATACGGCTCTCTCTTT 860
15918 TGGCAGTGACGCTGCTGTGTGATTAAGTCTCCCGTGAACCTTTACCCGGTGTGATATA 15859
861 TATAGGTGTAACCTTAAACTGCAATTTCCAC-----AGTCCCTGTTTCTCGTCAGCAAAA 914
15858 TCGGGGATGAAGCTGGCGCATGATGACCCAGATATGGCCAGTGTGCGGCTCTCCGTTA 15799

QY 915 GAGCGTTCAATTAACCGGGGAGCCTCAGCCATCCCTTCTGTATTTTCGCTTC 974
Db 15798 TCGGGAGAAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAACGCCATTAACC 15739
QY 975 CAGCGTTC--GGACGCGAGACGCGGCTTCATTCTGCATGGTGTGCTTTACACGACCG 1031
Db 15738 TGAATGTTCTGGGGAATAAATGTCAGGCTCCCTATACACAG-----CCAGTCTG 15688
QY 1032 GAGATATTGACATCATATATGCTTGTAGCAACTGATAGTGTGCTGTCAACTGTCACTG 1091
Db 15687 CAGGTCGATACAGTAGAATAATACAGAACTTTATCACGTTTAGTAAGTATAGAGCTGAA 15628
QY 1092 TAAACGCTGCTTCATAGCACACCTCTTTTGACATCTCGGGTAGTG---CGATCA 1147
Db 15627 AATCCAGATGAAGCGAAGCACTTGTAAGAGAAAGTATAGAGTTGTGAATCCGATCA 15568
QY 1148 AGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACGAA 1207
Db 15567 AGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACGAA 15508
QY 1208 TTTATTTATTCGCGAAGTGATCTTCGCTCAAGGTAATTTATTCGCGCAAGTGGCTG 1267
Db 15507 TTTATTTATTCGCGAAGTGATCTTCGCTCAAGGTAATTTATTCGCGCAAGTGGCTG 15448
QY 1268 GGTGATGCTGCCAATTTAGTTCGACTACAGGTCACTAACTACCACTTAAGTAGTTGATCAT 1327
Db 15447 GGTGATGCTGCCAATTTAGTTCGACTACAGGTCACTAACTACCACTTAAGTAGTTGATCAT 15388
QY 1328 AGTGACTGGATATGTTGTTTACAGTATTAAGTAGTCTGTTTTTATGCAAAATCTAA 1387
Db 15387 AGTGACTGGATATGTTGTTTACAGTATTAAGTAGTCTGTTTTTATGCAAAATCTAA 15328
QY 1388 TTTAATATATATGATATTTATATATTTTACGTTTCTCGTTTCAGCTTCTGTGACAAAGTG 1447
Db 15327 TTTAATATATATGATATTTATATATTTTACGTTTCTCGTTTCAGCTTCTGTGACAAAGTG 15268
QY 1448 GTCTCAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATATTCTCTTTTCTCTTT 1507
Db 15267 GTCTCAGGA--TCCAGCTTAAGTAGTAAGTACG--TAATCAATCCAAATGAAGATCA 15212
QY 1508 AGTATAAATAGTAAAGTGAATTAAGTATGATTAATAATAATAGTTGTTAAAT 1567
Db 15211 ATGATAACAAATGACATGATCATATGTTTACCTGTTTATTCATGTTTCGACTAATCA 15152
QY 1568 GTGAAAAATAATTAATAATATTTGTTTACATAAACACATAGTAATGTAABAAATA 1527
Db 15151 TTTAATTAATAGTCAATCCATTTAGAAAGTTAAATAAACTACAAAGTATTAATTAGAAATTA 15092
QY 1628 TGCAAGTGTATGTAAGACGAAGAAGATAAAAGTTGAGAGTAAGTATATTTTAAAT 1687
Db 15091 ATAAGAAATGTTGATTGAATAATACTATATATAAATGATAGATCTTGGCTTTGTTATAT 15032
QY 1688 GAAATTTGATCGAAATGTAAGATGATATAGCATTAATTTGTTTAACTAATATAG 1747
Db 15031 TAGCAATTAGATATATGTTTGTATCAATTAGATTAAGTCTTCTATTTAGTTTATATTTG 14972
QY 1748 TAATTTAGCTGTTTATGATGAATTAATAATCAATGATAAATACTATAGTAAATAAGA 1807
Db 14971 TTACTTTAGCTGTTATTTAATAATTTTGTATTGATAAATAATACACAGATTTGGAATTT 14912
QY 1808 ATAATAAATAAATAATAATTTTTTATGATTAATAGTTTATTTATATAATAATAATCT 1867
Db 14911 CTAAATAAATAATTTATTAACCTTTAABACTAATAATTTAGTAATGATATGATATTTAAT 14852
QY 1868 ATACCAATTAATAATTTTAGTTTAAAGTAAATAATTTGTTAGAAAATCCAAATC 1927
Db 14851 TATATAATAACTATTAATCATAAAAAATAATTTAATTTAATTTATTTTATTTTATTTTA 14792
QY 1928 TGCTTGAATTTATCAATAAACAATAATTAATAAAGTCAAGCTTAAGTAAGCAATAATATC 1987
Db 14791 CTATAGTATTTTATCATTTGATTAATTTAATTTCAACACAGCTAGAAATTTACTATTATGATT 14732

QY 1988 AAACATAATAGAAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGTAAATAAACAAG 2047
Db 14731 AAAACAAATTAATGCTAGTATATCATCTTACATGTTTCGATCAAAATTCATTAATAATAA 14672
QY 2048 CGAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTTCTTAAA 2107
Db 14671 TATACCTTACTCTCAACCTTTTATCTCTCGTTCACACATCAGTTGTCATATTTTATTAC 14612
QY 2108 TAACTACTGTTAGTTTATTAATTAACCTTCTAAATGGAATGACTATTAATAATGAATAGTCG 2167
Db 14611 ATTACTATGTTGTTTATGTAACAAATATATTTAATAATTAATTTTTCACAAATTAACA 14552
QY 2168 AACATGAATAAACAGGTAAACATGATAGATCATGTCATGTTGTTATCATGATCTTACAT 2227
Db 14551 CTATATTAATTAATCATCTAATAATTAACATCACTTAATTAATTAATTAATTAATTAATA 14492
QY 2228 TTGATTTGATTTACAGTTTGGGAAGCTGGTTCGAAATCGATAAGCTTGGATCCTCTAGACC 2287
Db 14491 AGAAATAATTAATTTTCTCTTACAGTTTGGTACCGAAT-----TCTCTGAGACC 14446
QY 2288 ACTTTGTACAAGAAAGCTGAAACGAGAAACGTAAATGATATAAATATCAATATATTAAT 2347
Db 14445 ACTTTGTACAAGAAAGCTGAAACGAGAAACGTAAATGATATAAATATCAATATTAAT 14386
QY 2348 TAGATTTTGCATAAAAAACAGACTACATACTATCTGTGAACGAGATCACTTCGCAAGATAAATAAT 2527
Db 14385 TAGATTTTGCATAAAAAACAGACTACATACTATCTGTGAACGAGATCACTTCGCAAGATAAATAAT 14206
QY 2408 TGAATCAACTTTPAGATGTTAGTACCTGTAGTCGACTAAAGTTGGCAGCATCACCC 2467
Db 14325 TGAATCAACTTTPAGATGTTAGTACCTGTAGTCGACTAAAGTTGGCAGCATCACCC 14266
QY 2468 GACGCACTTTTGGCCGGAATAAATACTCTGTGAACGAGATCACTTCGCAAGATAAATAAT 2527
Db 14265 GACGCACTTTTGGCCGGAATAAATACTCTGTGAACGAGATCACTTCGCAAGATAAATAAT 14206
QY 2528 CTTGTGTCCTCTGTTGATACCGGGAAGCTCGGCACTTTTGGGGAATAAGACGCTT 2587
Db 14205 CTTGTGTCCTCTGTTGATACCGGGAAGCTCGGCACTTTTGGGGAATAAGACGCTT 14146
QY 2588 GATCGGATTTCAACTCTTATACCTTTCTCTTACAAGTCGTTTCGGCTTCATCTGGATTT 2647
Db 14145 GATCGG---CACTACCGAAGTATGTCAAAAGAGGTGTGCTATGAACGACGCTATTAC 14090
QY 2648 TCAGCCTCTATACTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGC 2707
Db 14089 AGTGACAGTTGACAGCAGCATCTCAGTTGCTCAAGGCATATATGATGTCAATATCTCC 14030
QY 2708 AGACTGG-----CTGTGTATAGGAGCCTGCATTTATATTTCCCAAGAACATCAG 2758
Db 14029 GGTCTGTTAAGCACAAACCATGCAAGTGAAGCCCGTCTGTCGGTGCC---GAAACGCTGG 13973
QY 2759 GTTAATGGGCTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGGAT 2818
Db 13972 AAAGCGAAAAATCAGGAAGGATGGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCT 13913
QY 2819 AACGGAGACCGGCACACTCGGCCATATCGGTGTGTCATCATGCGGCAGCTTTCATCCCGGAT 2878
Db 13912 TTTGTCTGACGAGAACAGGGA-----CTGGTGAATGCAAGTTTAAAGTTTACACCTATAA 13859
QY 2879 ATGCACACCGGGTAAAGTTTCAGGAGACTTTATCTGACAGCAGACGTCGACTGGCCAG 2938
Db 13858 AAGAGAGACGGTTATCGTCTGTTGTGGATGTACAGAGTGATTAATTTGACACGCCCGG 13799
QY 2939 GGGGATCAACCATCGTCCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAAAACAG 2998
Db 13798 GCGACGATGGTGATCCCTGCGCAGTGCACGCTGCTGTGTCAGATAAAGTCTCCCGTGA 13739
QY 2999 ACATTAACCGCTCTCTCTTTTATAGGTGAACCTTAAACTGATGCTTACCC-----AGT 3052
Db 13738 ACTTTACCGGCTGGTCATATCGGGATGAAGCTGGCATGATGACCAACCGATATGGC 13679
QY 3053 CCCTGTTCTCGTCAGCAAAAGACCGCTTTCATTTCAATAAACCGGCGGACCTCAGCCATCC 3112

Db 13678 CAGTGTGCGGCTCTCCGTTATCGGGGAAGAGTGGCTGATCTCAGCCACCGCGAAATGA 13619
Qy 3113 CTTCTGATTTTCGGCTTTCAGAGTTC- --GGCAGCAGACGACGGGCTTCATTTCTGCA 3169
Db 13618 CATMAAAGCGCATTAACCTGATGTTCTGGGAATATAAATGTCAGGCTCCCTTATACA 13559
Qy 3170 TGG- --TTGTGCTTACCAGACGGAGATATTGACATCATATATGCTTGGCACTGATA 3226
Db 13558 CAGCCAGCTGCGAGTTCGATACAGTGAAGAAATACAGAACTTTATCACGTTTAGTAAGTA 13499
Qy 3227 GCTGTGCGCTGCAACTGTCTGATTAATACGCTGCTTCATAGCACACCTCTTTTGGACATA 3286
Db 13498 TAGAGGCTGAAATCCAGATGAAGCGGACGACTTGTGAAGAAAGTATGAAGTTGTG 13439
Qy 3287 CTTCTGTTCTTGATGACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAG 3346
Db 13438 AAATTTGTTCTTGATGACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAG 13379
Qy 3347 ATGTTTATTTTGTACACAAAGAGGCTGCGACCTCTTTTCTTATTTCTTTTAT 3406
Db 13378 ATGTTTATTTTGTACACAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTAT 13319
Qy 3407 GATTTAATACGCAATGAGGACAAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGA 3466
Db 13318 GATTTAATACGCAATGAGGACAAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGA 13259
Qy 3467 AGAACATTTGGAGGCTGTCGTCGACTAAGTTGGCAGCATCACCCGAAAGACATTTGGA 3526
Db 13258 AGAACATTTGGAGGCTGTCGTCGACTAAGTTGGCAGCATCACCCGAAAGACATTTGGA 13199
Qy 3527 AGCTGTGCTGACCTACAGTCACTAATACCATCTAAGTGTGATTTGATTTGATTTGATTTG 3586
Db 13198 AGCTGTGCTGACCTACAGTCACTAATACCATCTAAGTGTGATTTGATTTGATTTGATTTG 13139
Qy 3587 ATATGTTGTTTACAGTATATAGTCTGTTTATGCAAAATCTAAATTAATATA 3646
Db 13138 ATATGTTGTTTACAGTATATAGTCTGTTTATGCAAAATCTAAATTAATATA 13079
Qy 3647 TTGATATTTATATCATTTTACGTTTCTGTTAGCTTTTGTACAAACTGTCTAGAG 3705
Db 13078 TTGATATTTATATCATTTTACGTTTCTGTTAGCTTTTGTACAAACTGTCTAGAG 13020

RESULT 8

US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Weslev, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A. for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 28.4%; Score 1273; DB 15; Length 17476;
Best Local Similarity 62.1%; Pred. No. 5.5e-183;
Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;
Qy 21 CTCGAGACAAAGTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAATCAAT 80

Db 16704 CTCTAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAAT 16645
Qy 81 ATATTAAATTTAGATTTTGCATATAAAAACAGACTACATAATACTGTAAAAACACAACATATC 140
Db 16644 ATATTAAATTTAGATTTTGCATATAAAAACAGACTACATAATACTGTAAAAACACAACATATC 16585
Qy 141 CAGTCATATGAATCAACTACTTAGATGTTTATGAGTGCCTGTGAGTCGACGAGCCTT 200
Db 16584 CAGTCATATGAATCAACTACTTAGATGTTTATGAGTGCCTGTGAGTCGACGAGCCTT 16525
Qy 201 CCAATATTTTTCGGGTGATGCTGCCAACTAGTCGACGACGACGCTTCCAAATGTTTCTT 260
Db 16524 CCAATATTTTTCGGGTGATGCTGCCAACTAGTCGACGACGACGCTTCCAAATGTTTCTT 16465
Qy 261 CTCAAACGGAATCGTCTGATCCAGCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA 320
Db 16464 CTCAAACGGAATCGTCTGATCCAGCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA 16405
Qy 321 TAAAAAGAAATPAGAAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATC 380
Db 16404 TAAAAAGAAATPAGAAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATC 16345
Qy 381 TACCTATTATATACGCTAGTGTCTGTAATCTCTGAAATCATCTGCACTCAAGAAACAAATTC 440
Db 16344 TACCTATTATATACGCTAGTGTCTGTAATCTCTGAAATCATCTGCACTCAAGAAACAAATTC 16285
Qy 441 ACAACTCTTATCTCTTCTTCAAGTCTGTCGGCTTCTATCTGGATTTTTCAGGCTCTAT 500
Db 16284 ATGTCAAAAAGAGGTGCTCTATGAA- --GCAGCGTATTACAGTGACAGTTGACAGCGACA 16228
Qy 501 ACTTACTAAAAGTGTATAAAGTTTCGTAAATTTCTACTGTATCGACCTCGAGACTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGCTGTGTAAGCACAACCAT 16168
Qy 561 GTATAAGGAGGCTGACATTTATATTCGCCAGAACATCAGGTTAATGGCTTTTGTGATGT 620
Db 16167 GCAGAAATGAAGCCCTGCTGCTGCGTGCC- --GAACGCTGGAAGCGGAAATCAGGAAG 16111
Qy 621 CATTTTTCGGGTGGTGTGAGATCAGGACCTTTCTTCCCGATTAACCGAGACCGGCACTGG 680
Db 16110 GATGCTGAGGTGCGCCGCTTTTATTGAAATGAACGGCTCTTTTGTGACGAGAACAGGG- 16052
Qy 681 CCATATCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGACCCCGGTTAAAGTT 740
Db 16051 -----ACTGGTGAATGCAAGTTTAAAGTTTACCTTATAAAGAGAGAGCCGTTATCGTC 15997
Qy 741 CACGGGAGACTTTATCTGACAGCAGACGCTGCTGCTGCGCCAGGGGGATCACCATCCGTCGCC 800
Db 15996 TGTGTTGTGATGTACAGAGTGTATTTATGACAGCCCGCGCGCGAGTGTGATCCCCC 15937
Qy 801 CGGGCGGTGTCAATAATPATCACTGTGTATATCCCAAAACAGACGATTAACGGCTCTCTCTTT 860
Db 15936 TGGCCAGTGCAGCTGTGCTGTGAGATAAAGTCTCCCGTGAACCTTTACCCGGTGGTGCA 15877
Qy 861 TATAGTGTAAACCTTTAACTGATTTTCACTCC- --AGTCCCTGTCTCTGTCGACGAAAA 914
Db 15876 TCGGGGATGAAAGCTGGCGATGTGACCAACGATATGCCAGTGTGCGGCTCTCGTTA 15817
Qy 915 GAGCCGTTCTATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGGTTTC 974
Db 15816 TCGGGGAAGAGTGGCTGTGCTCAGCCACCGCGGAAATGACATCAAAAACGCCATTAAAC 15757
Qy 975 CAGCGTTC- --GGCAGCGCAGACGACGGGCTTTCATCTGATGTTGCTGTACAGACCG 1031
Db 15756 TGATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACACAG- -----CCAGTCTG 15706
Qy 1032 GAGATATTGACATATATGCTTCCCTTCCAGCACTGATAGTGTGCTGCTCACTGTCACTG 1091
Db 15705 CAGGTCGATACAGTAGAAATTAACAGAACTTTATACAGTTTAGTAAGTATAGAGGCTGAA 15646
Qy 1092 TAATAGCTCTCTCATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTG- ---CCGATCA 1147
Db 15645 ATCCAGATGAAGCCGNAACGACTTGTGAAGAAAGATATAAGAGTTGTGAATCCGATCA 15586

1148 ACCTCTCAATTTTCGCGCAAAAGTTGGCCAGGGTTCCTCCGGTATCAACAGGAGCACACAGGA 1207
15585 ACCTCTCAATTTTCGCGCAAAAGTTGGCCAGGGTTCCTCCGGTATCAACAGGAGCACACAGGA 15526
1208 TTATTTATTTCTCGGAAAGTGAATCTTCGGTACAGGTAATTTATTCGGCGCAAGTGGGTG 1267
15525 TTATTTATTTCTCGGAAAGTGAATCTTCGGTACAGGTAATTTATTCGGCGCAAGTGGGTG 15466
1268 GGTGATGTCGCCAACTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCAT 1327
15465 GGTGATGTCGCCAACTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGTGATTCAT 15406
1328 AGTGACTGGATATGTTGTTGTATTTACAGTATTTAGTAGTCTGTTTATTCGAAATCTAA 1387
15405 AGTGACTGGATATGTTGTTGTATTTACAGTATTTAGTAGTCTGTTTATTCGAAATCTAA 15346
1388 TTATTAATATATGATTTATTTATATCATTTTACGTTCTCGTTACGTTCTTGTGTAACAAGTG 1447
15345 TTATTAATATATGATTTATTTATATCATTTTACGTTCTCGTTACGTTCTTGTGTAACAAGTG 15286
1448 GTCTCGAGGAATTCGGTACCCAGCTTGGTAAGAAA-----TAATTTATTTCTT 1497
15285 GTCTAGAGATCCAGCTTATCGATTTCGAACCCAGCTTCCCAACTGTAATCAATCCAAA 15226
1498 TTTTCCCTTTTGTATATAAATAGTAAAGTGAAGTGAATTTAGTATGATTTATTAATATAGT 1557
15225 TGTAAAGATCAATGATAACAACATGACATGATCTATCATGTTACCTGTTTATTCATGTTTC 15166
1558 TGTATTAATTTGTGAATAAATTAATTTATAAATATATTTGTACATAAACAACATAGTAATG 1617
15165 GACTAATTCATTAATTAATAGTCAATCCATTTAGAAAGTTTAATAAATACTAACAAGTATAT 15106
1618 TAAAAAATATGACAAGTGTGTGAAGACAGAAAGATAAAGTTGAGAGTAAGTATAT 1677
15105 TTAGAATTAATAGAATGTTGATTTGAATATATCTATTAATAAAGTATAGATCTTCGCG 15046
1678 TATTTTAAATGAATTTGATCGAACATGTAAGATGATATATAGCATTAATTAATTTTGTGTTTA 1737
15045 TTTGTTATATATAGCAATTAGATATGTTTGTACATATAGATTTACTGTTCTTATAGTTTG 14986
1738 ATCAATATAGTAAATCTAGCTGTTGATCAATTAATTAATTAATCAATGATAAATACTATAGT 1797
14985 ATATTTCTGTTACTTTAGCTGTGTTATTTAATATTTTGTGTTATTTGAATAAATAACAAGCAG 14926
1798 AAAAATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1857
14925 ATTGGAATTTCTAACAAAAATTTATTTAACTTTTAACTTAAATATTTAGTAAATGGTATA 14866
1858 TTAAATATCTATACCATTTACTAATATTTAGTTTAAAGTTAATAAATATTTTGTGTA 1917
14865 GATAATTTAATATATAAATAACTATTAATCATAAAAAATAATTTATTTAATTTATTTATTT 14806
1918 AATTCOAATCTGCTGTGTAATTTATCAATAAACAATAAATAAATAAATAAATAAATAAATAA 1977
14805 CTATTTTACTATAGTATTTTATCATGATTTAATTTATTTATTTATTTATTTATTTATTTAT 14746
1978 AAATAATATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAAATAAATAAATAAATAA 2037
14745 TATTTATGATTTAAACAAATATTAATGCTAGTATATCATCTTACATGTTCCGATCAAAATCA 14686
2038 TATTAACAAGGCGAAGATCTATCATTTTATATAGTATATTTTCAATCAACATTTCTTATTT 2097
14685 TTAATAAATAATATATCTTACTCTCAACTTTTATCTTCTCTCTTCTTCTTCTTCTTCTTCT 14626
2098 AATTTCTAAATAATATCTTGTAGTTTATTAACITCTTAAATGGATTGACTATTAATTAAT 2157
14625 ATTTTCTACTATGTTGTTTATGTAACAATAATATTTAATAATTTATTTTCTTCTTCTTCT 14566
2158 GAATTTAGTCGAACATGATAAACAAGGTAACATGATAGATCATGTCATGTTGTTATCATTT 2217
14565 ATTATACAACTATATTTAT 14506

2218 GATCTTTACATTTTGGATTGATTACAGTTTGGGAAGCTGGGTTCGAAATCGATATAGCTTTGGAT 2277
14505 AAAGGAAAAAAGAAATAATTTATTT-----TCCTTACCAGCTGGGTTACCGAATTT 14456
2278 CCTCTAGACCACTTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAATATCAAA 2337
14455 CCTCGAGACCACTTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAATATCAAA 14396
2338 TATATTAATTAATAGATTTTGCATATAAATAAAGACTACATATATCTGTAAACACACATAT 2397
14395 TATATTAATTAATAGATTTTGCATATAAATAAAGACTACATATATCTGTAAACACACATAT 14336
2398 CCAGTCACTATGAATCAACTACTTATAGTGTATTTAGTACCTGTAGTCCGACTAAGTTGGC 2457
14335 CCAGTCACTATGAATCAACTACTTATAGTGTATTTAGTACCTGTAGTCCGACTAAGTTGGC 14276
2458 AGCATCACCGGAGCACTTTTGGCCGAATAAATACTGTGACGGAAGATCATCTTCGAGAA 2517
14275 AGCATCACCGGAGCACTTTTGGCCGAATAAATACTGTGACGGAAGATCATCTTCGAGAA 14216
2518 ATAAATAAATCTGTGTGTCCTCTGTTGATACCGGAAGCCCTGGGCCAACTTTTGGCGAAA 2577
14215 ATAAATAAATCTGTGTGTCCTCTGTTGATACCGGAAGCCCTGGGCCAACTTTTGGCGAAA 14156
2578 ATGAGACGTTGATCGGATTTTCAAACTTTATCTTTTCTTTACAAAGTCGTTTCGGCTTC 2637
14155 ATGAGACGTTGATCGG-----CACTACCCGAAAGTATGTCAAAAAGAGGTGTGCTATGAAGC 14100
2638 ATCTGGAATTTTCACTCTATTAATACTGATTAAGTTTCTGTAAATTTCTTACTGT 2697
14099 AGCGTATTAACAGTGACAGTTTGAAGCAGCAGCTATCATGTTCTCAAGGCATATATATGAT 14040
2698 ATCGACCTCGACAGCTGG-----CTGTGATTAAGGAGCCTGACATTTATATTTCCCC 2748
14039 CAATATCTCGGTCTGTGTAAGCAACCACTGCAAGTAAGAACCCGCTGCTGCGTGC-- 13982
2749 AGAACATCAGGTTAATPGCGTTTGTGATGTCATTTTTCGGGTGGCTGAGATCAGCCACTT 2808
13981 -GAACTCGAAAGCGGAAATCAGGAAGGATGGCTGAGGTGCGCCGGTTTATTGAAAT 13923
2809 CTTCCCGGATAAGGAGACGGGACACACTGGCCATATCGGTGTCATCATCGCCGACCTTT 2868
13922 GAACGCTCTTTTGTGTCGAGAGAACAGGG-----ACTGGTGAATGCAAGTTTAAAGTTT 13869
2869 CATCCCGGATATGACACACCGGTAAGTTTCAAGGAGACTTTATCTGACAGCAGACGTG 2928
13868 ACACCTATAAAGAGAGAGACGGTTATCTGCTGTTGTGATGTACAGAGTATATTTATG 13809
2929 CACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCAATAATATCATCTGTACAT 2988
13808 ACACGCCCGGCGACGGATGGTGTATCCCGCTGGCCAGTGCAGTCTGCTGTGATATAAG 13749
2989 CCACAAACAGAGATTAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTTTAC 3048
13748 TCTCCCGTGAACCTTTACCCGGTGGTGCATATCGGGATGAAAGCTGGCGCATGATGACCA 13689
3049 C-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCAATTTCAATAAACCAGGCGAC 3102
13688 CCGATATGCCAGTGTGCGGCTCTCGTTATCGGGAAGAGTGGCTGATCTCAGCCACC 13629
3103 TCAGCCATCCCTTCTGATTTTTCGGCTTTCCAGCGTTC---GGCAGCAGACGAGCGGT 3159
13628 GCGAAATGACATCAAAAACGCCATTTAACCTGATGTTCTGGGGAATATAAATGTGAGGT 13569
3160 TCATTTCTGATG---TTGTGCTTACCAGCCGAGATATTGACATCATATATGCTTGA 3216
13568 CCGTTATACAGCCCGAGTCTGCAAGTGCAGTAGAGAAATTAAGAAATTTATCAAGT 13509
3217 GCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATAGCTGCTTCAAGCAGCTCT 3276
13508 TTAGTAAGTATAGAGGCTGAAAATCCAGATGAAGCCGAGACGACTTGTAGAGAAAGTAT 13449
3277 TTTTGACATATCTTCTGTTCTGATGCGATGATGATTTTTCAGGACTATGACACTAGCGTATAT 3336


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Db 13488 AAGAGTTGTGAAATGTTCTTTGATGCGAGATGATTTTCAGGACTATGACACTAGCGTATAT 13389
Qy 3337 GAATAGGTFAGATGTTTATTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTTAT 3396
Db 13388 GAATAGGTFAGATGTTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTTAT 13329
Qy 3397 TTTCTTTTATGATTTAATPACGGCAATAGGCAATAGCGATGAGCTGGATACGACGATT 3456
Db 13328 TTTCTTTTATGATTTAATPACGGCAATAGGCAATAGCGATGAGCTGGATACGACGATT 13269
Qy 3457 CGTTTGTAGAGAACATTTGGAGGCTCGGTGCACTAAAGTTGGCAGCATCACCCGAAG 3516
Db 13268 CGTTTGTAGAGAACATTTGGAGGCTCGGTGCACTAAAGTTGGCAGCATCACCCGAAG 13209
Qy 3517 AACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACATAACCATCAATCAAGTAGTGTGATTC 3576
Db 13208 AACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACATAACCATCAATCAAGTAGTGTGATTC 13149
Qy 3577 TAGTGACTGGATATGTTGTTTACAGTATATGATGATGATGATGATGATGATGATGATGATG 3636
Db 13148 TAGTGACTGGATATGTTGTTTACAGTATATGATGATGATGATGATGATGATGATGATGAT 13089
Qy 3637 ATTTAATATATGATATTTATATATATTTTACGTTTCTCGTTTACGTTTCTTTTGTACAACT 3696
Db 13088 ATTTAATATATGATATTTATATATATTTTACGTTTCTCGTTTACGTTTCTTTTGTACAACT 13029
Qy 3697 TGTCTAGAG 3705
Db 13028 TGTCTAGAG 13020

RESULT 9
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 28.4%; Score 1273; DB 15; Length 17476;
Best Local Similarity 62.4%; Pred. No. 5.5e-183;
Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;

Qy 21 CTCGAGACAAAGTTTGTACAAAAAGCTGGAACGAGAAACGTPAAATATGATATAAATCAAT 80
Db 16704 CTCTAGACAAGTTTGTACAAAAAGCTGACGAGAAACGTPAAATATGATATAAATCAAT 16645
Qy 81 ATATTAATATAGATTTTGCATPAAAAAAGAGTACATCAATCAATCAATCAATCAATCAATCA 140
Db 16644 ATATTAATATAGATTTTGCATPAAAAAAGAGTACATCAATCAATCAATCAATCAATCA 16585
Qy 141 CAGTCACTATGAATCACTACTTATGATGATGATGATGATGATGATGATGATGATGATGATG 200
Db 16584 CAGTCACTATGAATCACTACTTATGATGATGATGATGATGATGATGATGATGATGATGATG 16525
Qy 201 CCAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTT 260
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Db 16524 CCAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTTCTT 16465
Qy 261 CTCAAACGGGAATCGTCTGATCCAGCCCTATCTCGCTATTTGTCTCAATGCCCTTATTAATCA 320
Db 16464 CTCAAACGGGAATCGTCTGATCCAGCCCTATCTCGCTATTTGTCTCAATGCCCTTATTAATCA 16405
Qy 321 TAAAAAGAAATAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATCAATC 380
Db 16404 TAAAAAGAAATAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATCAATC 16345
Qy 381 TACCTATTCATATACGCTAGTGTCTATAGTCTCTGAAAAATCATCTGCATCAAGAAACAATTC 440
Db 16344 TACCTATTCATATACGCTAGTGTCTATAGTCTCTGAAAAATCATCTGCATCAAGAAACAATTC 16285
Qy 441 ACAATCTTATATCTTTTCTCTTCAAGTCTGTCGGCTTCATCTGGATTTTCAGCCCTCAT 500
Db 16284 ATGTCAAAAAAGAGGTGTCTATGAA--GCAGCGTATTACAGTGACAGTTGACAGCGACA 16228
Qy 501 ACTTACTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCAATATGATGATCAATATCTCCGGTCTGGTACAGCAACCAT 16168
Qy 561 GTATAAGGAGCCCTGACATTTATATCCCAAGAACATCAGGTTAATGGCGTTTGTGATGT 620
Db 16167 GCAGATGAAGCCGCTCGTCTGCGTGC--GAACGCTGGAAGCGGAAATCAGGAAG 16111
Qy 621 CATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGGATTAACGAGACCGGACACTGG 680
Db 16110 GATGGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTGTGACGAGAACAGGG- 16052
Qy 681 CCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGATATGCACACCCGGTAAAGTT 740
Db 16051 -----ACTGGTGAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGCTTATCGTC 15997
Qy 741 CACGGGAGACTTTATCTGACAGCAGCGTGCACCTGCGCCAGGGGATCACCATCCGTCGCC 800
Db 15996 TGTTTGTGGATGTACAGAGTGATATTATGACAGCCCGCGGCGAGGTGATGATCCGCC 15937
Qy 801 CGGGGTGTCATTAATATCATCTCTGTATATCCAAACAGACGATACGGCTCTCTCTTT 860
Db 15936 TGGCCAGTGCACTGCTGCTGACATAAAGTCTCCCGTGAACCTTTACCCGGTGGTGCA 15877
Qy 861 TATAGTGTAAACCTTAAACTGCAATTCACCC-----AGTCCCTGTTCTCGTCAGCAAAA 914
Db 15876 TCGGGGATGAAGCTGCGCGCATGATGACCA CGATATGCGCAGTGTCCGGTCTCCGTTA 15817
Qy 915 GAGCCGTTTCAATTAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTC 974
Db 15816 TCGGGGAAGAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAAACGCCATTAACC 15757
Qy 975 CAGCCGTTCC--GGCAGCAGACGCGGCTTCATCTCGATGTTGTGCTTACCAGACCG 1031
Db 15756 TGATGTTCTGGGGAATATAAATGTGAGGCTCCCTTATACACAG-----CCAGTCTG 15706
Qy 1032 GAGATATTGACATCATATATGCTTTCAGCACTGATAGTGTGCTGTCAACTGTCATG 1091
Db 15705 CAGGTCGATACAGTAGAATAATACAGAACTTTATCACGTTTAGTAAGTATAGAGCTGAA 15646
Qy 1092 TAAATAGCTGCTTCATAGCACACCTCTTTTGCATACACTTCGGGTAGTG---CCGATCA 1147
Db 15645 AATCCAGATGAAGCGGAACGACTTGTAAAGAAAAAGTATAAGATTGTAATCCGATCA 15586
Qy 1148 AGTCTCTATTTTCGCCAAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGACACCAAG 1207
Db 15585 AGTCTCTATTTTCGCCAAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGACACCAAG 15526
Qy 1208 TTTATTTATTCGCAAGTGTATCTTCGTCACAGGTATTTATTCGCGCAAAAGTCCGTCG 1267
Db 15525 TTTATTTATTCGCAAGTGTATCTTCGTCACAGGTATTTATTCGCGCAAAAGTCCGTCG 15466
Qy 1268 GGTGATGCTGCCAACTTAGTTCGACATACAGGTCACTAATACCATCTTAAGTAGTTGATCAT 1327
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Db 15465 GGTGATGCTGCCAACTTAGTCGACTACAGGTACATTAATACCATCTAAGTAGTTGATTCAT 15406
Qy 1328 AGTGACTGATATGTTGTTTACAGTATTAATAGTAGTCGTGTTTTTATAGGAAAATCTAA 1387
Db 15405 AGTGACTGATATGTTGTTTACAGTATTAATAGTAGTCGTGTTTTTATAGGAAAATCTAA 15346
Qy 1388 TTTAATATATGATATTTATATACATTTTACGTTTCTCGTTTCAGCTTCTTGTGACAAAGTG 1447
Db 15345 TTTAATATATGATATTTATATACATTTTACGTTTCTCGTTTCAGCTTCTTGTGACAAAGTG 15286
Qy 1448 GTCTCAGGAATTCGGTACCCAGCTTGGTAAGGAAA-----TAATATTTTCTT 1497
Db 15285 GTCTAGAGATCCAAAGCTTATCGATTTGCAATCCAGCTTCCCAACTGTAATCAATCCAAA 15226
Qy 1498 TTTTCCCTTTTAGTATTAATAATAGTAAAGTATGATGTTAATAGTAGTATTAATAATATAGT 1557
Db 15225 TGTAGATCAATGATTAACAATAGATGATCTATCATGTGTTACCTTGTGTTTATTCATGTTTC 15166
Qy 1558 TGTATATAATTGCAAAAAATAATTTATAAATAATTTGTTTACATAAAACAACATAGTAATG 1617
Db 15165 GACTAATTCATTTAATTAATAGTCAATCCATTTAGAAGTTTAATAAACTACAAGTATTAT 15106
Qy 1618 TAAAAAATATGCAAGTAGTGTAAGAGCAAGAGAATAAAAGTTGAGAGTAAGTATAT 1677
Db 15105 TTAGAAATTAATAAGAAATGTTGATTCGAAAATAATACTATATAAATAGATGATCTTCGCGC 15046
Qy 1678 TATTTTAAATGATTTGATCGACATGTAAGATGATATAGTATTAATTAATTAATTTGTTTAA 1737
Db 15045 TTTGTTATATATGATATAGATTAATGTTTGTTCATTTAGATTAATGTTTCTTATAGTTTG 14986
Qy 1738 ATCATATAGTAATTTCTAGCTGTTGATGAAATTAATATCAATGATGATAAATACTATAGT 1797
Db 14985 ATATTAATTTGTTACTTTAGCTGTTATTAATTAATTTGTTTATGATAAATTAACAAGCAG 14926
Qy 1798 AAAAAAAGAAATTAATAAATAAATAATTTTATTTTAAATGATTAATTAATTAATAA 1857
Db 14925 AATGGAATTTCTAACAAAAATTAATTAATTAATTTTAAACTAAAAATATTAGTAATGTTATA 14866
Qy 1858 TTAATAATCTATACCATTAATAATTTAGTTTAAAGTTAATAAATTTTGTGTTAGA 1917
Db 14865 GATATTTAAATATATAATAAATCTTAATCAATCAAAAAATTAATTAATTTTAAATTTATTAT 14806
Qy 1918 AATCCAAATCTGTTGTAAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTAAC 1977
Db 14805 CTATTTTACTATAGTATTTTATCATTTGATTAATTTAATTCATAAACACAGCTAGAAATAC 14746
Qy 1978 AATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAATAAATCAATCTAATGCTAA 2037
Db 14745 TATTAATGATTTAAAAACAATAATTAATGCTAGTATATCATCTTACATGTTGATCAAAATTC 14686
Qy 2038 TATAACAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATT 2097
Db 14685 TTAATAATAATATACTTACTCTCACTTTTATGTTAAACAATAATTTAATAAATTTATTTTCA 14626
Qy 2098 AATTTCTAAATAATPACTTTGATGTTTATTAATCTTCTAAATGGAATGATTAATTAAT 2157
Db 14625 ATTTTTTACATTAATGTTGTTTATGTTAAACAATAATTTAATAAATTTATTTTCA 14566
Qy 2158 GAATTAATGCAACATGAATAAACAAGTAACATGATAGATCATGTTGTTGTTATCATTT 2217
Db 14565 ATTATAACAATATTAATTAATAATCATTAATTAACATCACTTAATTTTATTAATA 14506
Qy 2218 GATCTTACATTTGGATTTGATTTACAGTTGGGAAGCTGGGTTTCAATCATGATAAGCTTGGAT 2277
Db 14505 AAAGGAAAAAAGAAATAATTAATTT-----TCCTTACCAAGCTGGGGTACCGAATTT 14456
Qy 2278 CCTCTAGACCACTTTGTACAAGAAAGCTGAAACGAGAAACGTAATAATGATATAATAATCAA 2337
Db 14455 CCTCGAGACCACTTTGTACAAGAAAGCTGAAACGAGAAAGCTGATAATAATAATCAA 14396
Qy 2338 TATATTAATTTAGATTTTGTGCTAATAAACAAGCTACATAATPACTGTGTAACACAAATAT 2397
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Qy 2458 AGCATCACCCGACGCACTTTGCGCGGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 2517
Db 14275 AGCATCACCCGACGCACTTTGCGCGGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 14216
Qy 2518 ATAAATAAATCCTGTGTGTCCTGTTGATACCGGGAAGCCCTGGGCCCACTTTTGGCGAAA 2577
Db 14215 ATAAATAAATCCTGTGTGTCCTGTTGATACCGGGAAGCCCTGGGCCCACTTTTGGCGAAA 14156
Qy 2578 ATGAGACGTTGATCCGATTTTCAAACTCTTATATCTTTCTTTTCTTACAAGTCGTTGCGCTTC 2637
Db 14155 ATGAGACGTTGATCGG-----CACTACCCGAAATGATGTCAAAAAGAGGTGTGCTATGAAGC 14100
Qy 2638 ATCTGGATTTTCAGCTCTATATCTTACTAATACGTAAGTTCGTGTAATTTCTTACTGT 2697
Db 14099 AGCGTATTACAGTGACAGTTGACAGCAGCATATCAGTTGCTCAAGGCATATATGATGT 14040
Qy 2698 ATCGACCTGCACACTGG-----CTGTGTATAGGAGCTGACATTTATTTCCCG 2748
Db 14039 CAATATCTCCGTCTGGTTAAGCACAAACATGAGAAATGAAAGCCGCTGCTCGTGCC-- 13982
Qy 2749 AGAAATCATAGGTTAATGGCGTTTTTGTATGTCATTTTCGCGTGGTGGTGTAGATCAGCCACTT 2808
Db 13981 -GACGCTGAAAACGGAATAATCAGGAAGGATGGCTGAGGTGCGCCGGTTTTATTGAAAT 13923
Qy 2809 CTTTCCCGATAAGAGAGACCGGCACACTGGCCATATCGTGTGTGTCATCATGCGCCAGCTTT 2868
Db 13922 GAACGCTCTTTTGTCTGACGAGAACAGGG-----ACTGGTGAATGTCAGTTTAAAGTTT 13869
Qy 2869 CATCCCGATATGCAACACCGGTAAAGTTACGGGAGACTTTTATCTGACAGCAGACGTG 2928
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Qy 2929 CACTGCCAGGGGGATCACCATCCGTCGCCCGGCGTGTCAATAATATCATCTGTATCAT 2988
Db 13808 ACACGCGCGGCGACGATGGTGTATCCCGCTGGCCAGTGCACGCTGCTGTCTCAGATAAAG 13749
Qy 2989 CACAAAACAGACGATACCGCTCTCTTTTATAGGTGTAAACCTTAAATGCAATTTAC 3048
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Qy 3049 C-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCCTTCATTTCAATAAACCAGGCGACC 3102
Db 13688 CCGATATGCCAGTGTGCGGCTCTCCGTTATCGGGGAAGAGTGTGCTGATCTCAGCCACC 13629
Qy 3103 TCAGCCATCCCTTCCTGATTTTCCGCTTTTCCAGCGTTC---GGCAGCGAGACGCGGCT 3159
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Qy 3217 GCAACTGATAGTGTGCTGCTCAACTGTCTACTTAATACGCTGCTTCATAGCACACCTCT 3276
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Db 13388 GAATAGTAGATGTTTTTTTATTTTGTCTACACAAAAGAGGCTCGACCTCTTTTCTTAT 13329
Qy 3397 TTTCTTTTATGATTTAATACGCAATGAGCAATAGCAGTAGGCTAGGCTGATACGAGCAT 3456
Db 13328 TTTCTTTTATGATTTAATACGCAATGAGCAATAGCAGTAGGCTAGGCTGATACGAGCAT 13269

QY 3457 CCGTTTGAGAGAACATTTGGAAGGCTGTGCGTGACCTAAGTTGGCAGCATCCCGAAG 3516
Db |||||||
QY 13268 CCGTTTGAGAGAACATTTGGAAGGCTGTGCGTGACCTAAGTTGGCAGCATCCCGAAG 13209
Db |||||||
QY 3517 AACATTTGGAAGGCTGTGCGTGACCTAAGTTGGCAGCATCCCGAAG 3576
Db |||||||
QY 13208 AACATTTGGAAGGCTGTGCGTGACCTAAGTTGGCAGCATCCCGAAG 13149
Db |||||||
QY 3577 TAGTGACTGATATGTTGTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 3636
Db |||||||
QY 13148 TAGTGACTGATATGTTGTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 13089
Db |||||||
QY 3637 ATTAAATATATGATATTTATATCAATTTTACGTTTCGTTTCAGCTTTTGTACAAACT 3696
Db |||||||
QY 13088 ATTAAATATATGATATTTATATCAATTTTACGTTTCGTTTCAGCTTTTGTACAAACT 13029
Db |||||||
QY 3697 TGCTAGAG 3705
Db |||||||
QY 13028 TGCTCGAG 13020
Db |||||||

RESULT 10

US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201
; NAME/KEY: gene
; LOCATION: (29)..(260)
; OTHER INFORMATION: attp1
; FEATURE:
; NAME/KEY: gene
; LOCATION: (656)..(961)
; OTHER INFORMATION: ccdB
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1099)..(1184)
; OTHER INFORMATION: ccdA
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1303)..(1962)
; OTHER INFORMATION: Cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2210)..(2442)
; OTHER INFORMATION: attp2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2565)..(3374)
; OTHER INFORMATION: Km^r
; FEATURE:
; NAME/KEY: gene

; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
US-10-151-690-21

Query Match 24.8%; Score 1108.8; DB 15; Length 4470;
Best Local Similarity 99.8%; Pred. No. 2.5e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAAGTTTGTACAAAAGCTGAACGAGAAAGCTGAATAATGATATAATCAATATATT 85
Db 102 GCCAACTTTTGTACAAAAGCTGAACGAGAAAGCTGAATAATGATATAATCAATATATT 161
QY 86 AATATAGATTTTGTACAAAAGCTGAACGAGAAAGCTGAATAATGATATAATCAATATATT 145
Db 162 AATATAGATTTTGTACAAAAGCTGAACGAGAAAGCTGAATAATGATATAATCAATATATT 221
QY 146 ACTATGAATCAACTACTTATAGATGGTATTAGTACCTGTAGTACCGACGAGCCCTTCCAAA 205
Db 222 ACTATGAATCAACTACTTATAGATGGTATTAGTACCTGTAGTACCGACGAGCCCTTCCAAA 281
QY 206 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACCGCAGCCTTCCAAATGTTCTTCTCAA 265
Db 282 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACCGCAGCCTTCCAAATGTTCTTCTCAA 341
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGCTATTAAATCAATAAA 325
Db 342 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGCTATTAAATCAATAAA 401
QY 326 AGAATAAGAAAAGAGTGCAGAGCCTCTTTTGTGTGACAAATPAAAAATCAATCTACCT 385
Db 402 AGAATAAGAAAAGAGTGCAGAGCCTCTTTTGTGTGACAAATPAAAAATCAATCTACCT 461
QY 386 ATTATATACGCTAGTGTCTAGTCTGAAATATCTGCAATCAATCAAGAAATTTTCAACAC 445
Db 462 ATTATATACGCTAGTGTCTAGTCTGAAATATCTGCAATCAATCAAGAAATTTTCAACAC 521
QY 446 TCTTATACCTTTTCTCTTACAAAGTCGTTCCGCTTCACTCTGATTTTTCAGGCTCTATATCTTA 505
Db 522 TCTTATACCTTTTCTCTTACAAAGTCGTTCCGCTTCACTCTGATTTTTCAGGCTCTATATCTTA 581
QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTGTAATCTGATATCGACCTGCGAGCTGGCTGTATA 565
Db 582 CTAACGCTGATAAAGTTTCTGTAATTTCTGTAATCTGATATCGACCTGCGAGCTGGCTGTATA 641
QY 566 AGGAGCCTTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGCTTTTGTGATGTCATTT 625
Db 642 AGGAGCCTTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGCTTTTGTGATGTCATTT 701
QY 626 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACCTGGCCATA 685
Db 702 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACCTGGCCATA 761
QY 686 TCGGTGTGCTATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGTTAAAGTTACGG 745
Db 762 TCGGTGTGCTATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGTTAAAGTTACGG 821
QY 746 GAGACTTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGGATCACCATCGTCCCGCGGC 805
Db 822 GAGACTTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGGATCACCATCGTCCCGCGGC 881
QY 806 GTGTCAATTAATATCACTCTGTATCATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 865
Db 882 GTGTCAATTAATATCACTCTGTATCATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 941
QY 866 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTCTAT 925
Db 942 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTCTAT 1001
QY 926 TTCAATAAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTTCGGCTTTTCCAGGTTTCGGC 985
Db 1002 TTCAATAAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTTCGGCTTTTCCAGGTTTCGGC 1061
QY 986 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTGCTTACCAACCGGAGATATTGACATC 1045

Db 1062 ACGCAGACGCGGCTTCTATTCGTCATGTTGCTTACACGACCGGAGATATTGACATC 1121
Qy 1046 ATATATGCTTGGAGCACTGATAGCTGCTGCTGCTCAACTGTCACCTGTAATACGCTGCTTC 1105
Db 1122 ATATATGCTTGGAGCACTGATAGCTGCTGCTGCTCAACTGTCACCTGTAATACGCTGCTTC 1181
Qy 1106 ATAGCACACCTCTTTTTCGACATCTTCGGGTA 1137
Db 1182 ATAGCACACCTCTTTTTCGACATCTTCGGGTA 1213

RESULT 11

US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US2003021902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; CURRENT APPLICATION NUMBER: USUR-1-20291
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4892
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (73)..(100)
; OTHER INFORMATION: T2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(563)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (959)..(1264)
; OTHER INFORMATION: ccdB gene
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1606)..(2265)
; OTHER INFORMATION: Cam(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2513)..(2744)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2868)..(3677)
; OTHER INFORMATION: Kan(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3794)..(4537)
; OTHER INFORMATION: pUC oriV / RK2 oriT
; US-10-357-268-1

Query Match 24.8%; Score 1108.8; DB 16; Length 4892;
Best Local Similarity 99.8%; Pred. No. 2.6e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 GACAAAGTTTGTACAAAAGAGCTGAACGAGAAACGTAAATGATATAATATCAATATATT 85
Db 102 GCCAACTTTGTACAAAAGAGCTGAACGAGAAACGTAAATGATATAATATCAATATATT 161
Qy 86 AAATTAGATTTTGCATAAAAGAGCTGACATATATCTGTAAACACACATATCCAGTC 145
Db 162 AAATTAGATTTTGCATAAAAGAGCTGACATATATCTGTAAACACACATATCCAGTC 221
Qy 146 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 205
Db 222 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 281
Qy 206 TGTTCCTTCGGGTGATGTCGCCAATCTAGTCGACCGACAGCCTTCCAAATGCTTCTCAA 265
Db 282 TGTTCCTTCGGGTGATGTCGCCAATCTAGTCGACCGACAGCCTTCCAAATGCTTCTCAA 341
Qy 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAATCATAAAA 325
Db 342 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAATCATAAAA 401
Qy 326 AGAAATAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAATCACTACCT 385
Db 402 AGAAATAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAATCACTACCT 461
Qy 386 ATTCAATAGCGTAGTGTGTCATAGTCCTGAAATCATCTGATCAAGAACATTTTCAAC 445
Db 462 ATTCAATAGCGTAGTGTGTCATAGTCCTGAAATCATCTGATCAAGAACATTTTCAAC 521
Qy 446 TCTTATATCTTCTCTTACAAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505
Db 522 TCTTATATCTTCTCTTACAAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 581
Qy 506 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGCTGTGTATA 565
Db 582 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGCTGTGTATA 641
Qy 566 AGGAGCCTGACATTTATATTTCCACAGAAATCAGGTTAATGGGTTTTCAGTGTCTATT 625
Db 642 AGGAGCCTGACATTTATATTTCCACAGAAATCAGGTTAATGGGTTTTCAGTGTCTATT 701
Qy 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGAGACCGGCACACTCGCCATA 685
Db 702 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGAGACCGGCACACTCGCCATA 761
Qy 686 TCGGTGTGATCATGCGCCAGCTTTTATCCCGGATATGACCCACCGGGTAAAGTTTCAGG 745
Db 762 TCGGTGTGATCATGCGCCAGCTTTTATCCCGGATATGACCCACCGGGTAAAGTTTCAGG 821
Qy 746 GAGACTTTTATCTGACACGACGCTGCACTCGCCAGGGGGATCACCATCCGTCGCGCGGC 805
Db 822 GAGACTTTTATCTGACACGACGCTGCACTCGCCAGGGGGATCACCATCCGTCGCGCGGC 881
Qy 806 GTGTCAATAATATCACTCTGTATACCAACACAGACGATAAGCGCTCTCTCTTTTATAG 865
Db 882 GTGTCAATAATATCACTCTGTATACCAACACAGACGATAAGCGCTCTCTCTTTTATAG 941
Qy 866 GTGTAAACCTTAAACTGCAATTTTACCAGTCCCTGTTCTCTGACGAAAAGAGCGGTTTCA 925
Db 942 GTGTAAACCTTAAACTGCAATTTTACCAGTCCCTGTTCTCTGACGAAAAGAGCGGTTTCA 1001
Qy 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGC 985
Db 1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGC 1061
Qy 986 ACGCAGACGACGGGCTTTCATTTGTCATGTTGTGCTTACACAGACCGAGATATTGACATC 1045
Db 1062 ACGCAGACGACGGGCTTTCATTTGTCATGTTGTGCTTACACAGACCGAGATATTGACATC 1121
Qy 1046 ATATATGCTTGGAGCACTGATAGCTGCTGCTCACTGCTCACTGTCTATACGCTGCTTC 1105
Db 1122 ATATATGCTTGGAGCACTGATAGCTGCTGCTCACTGCTCACTGTCTATACGCTGCTTC 1181

Qy	566	AGGAGCGCTGACATTTTATATCCCCGAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTT	625
Db	4943	AGGAGCGCTGACATTTTATATTTCCCCGAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTT	4884
Qy	626	TCGCGGTGGCTGAGATCAGGCACCTCTTCTCCCGATAAACGAGACCGGCACACCTGGCCATA	685
Db	4883	TCGCGGTGGCTGAGATCAGGCACCTCTTCTCCCGATAAACGAGACCGGCACACCTGGCCATA	4824
Qy	686	TCGGTGTGTATCATATGCGGCAGCTTTTCATCCCGGATATGCAACACCGGGTAAAGTTTCA	745
Db	4823	TCGGTGTGTATCATATGCGGCAGCTTTTCATCCCGGATATGCAACACCGGGTAAAGTTTCA	4764
Qy	746	GAGACTTTTATCTGACAGCAGACGCTGCACTCGCCAGAGGGGGATCACCATCCGTCGCGCCGGGC	805
Db	4763	GAGACTTTTATCTGACAGCAGACGCTGCACTCGCCAGAGGGGGATCACCATCCGTCGCGCCGGGC	4704
Qy	806	GTGTCAATAATATCACTCTGTATCATCAACAAACAGACGATAAAGCGTCTCTCTTTTATAG	865
Db	4703	GTGTCAATAATATCACTCTGTATCATCAACAAACAGACGATAAAGCGTCTCTCTTTTATAG	4644
Qy	866	GTGTAAACCTTAACTGCATTTTACAGAGTCCCTTCCAGAGTCCGCTGTCGCAAGAGCGGTT	925
Db	4643	GTGTAAACCTTAACTGCATTTTACAGAGTCCCTTCCAGAGTCCGCTGTCGCAAGAGCGGTT	4584
Qy	926	TTCAATAAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC	985
Db	4583	TTCAATAAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC	4524
Qy	986	ACGAGACGAGCGGGCTTCATCTGCACTGCTGCTGCTTACAGACCGGAGATATGACATC	1045
Db	4523	ACGAGACGAGCGGGCTTCATCTGCACTGCTGCTGCTTACAGACCGGAGATATGACATC	4464
Qy	1046	ATATATGCCCTTGAGCAACTGATAGCTGCTGCTGTCAACTGTCATGTAATACGCTGCTTC	1105
Db	4463	ATATATGCCCTTGAGCAACTGATAGCTGCTGCTGTCAACTGTCATGTAATACGCTGCTTC	4404
Qy	1106	ATAGCACACCTCTTTTGACATATCTCGGGTA	1137
Db	4403	ATAGCACACCTCTTTTGACATATCTCGGGTA	4372

RESULT 13

US-10-151-690-62

; Sequence 62, Application US/10151690

; Publication No. US2003012455A1

; GENERAL INFORMATION:

; APPLICANT: BRASCH, MICHAEL A.

; APPLICANT: CHEO, DAVID

; APPLICANT: LI, XIAO

; APPLICANT: ESPOSITO, DOMINIC

; APPLICANT: BYRD, DEVON R.N.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC

; FILE REFERENCE: 0942.5120001

; CURRENT APPLICATION NUMBER: US/10/151,690

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 10/151,690

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 60/291,973

; PRIOR FILING DATE: 2001-05-21

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 62

; LENGTH: 4428

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: plasmid pDONR212

US-10-151-690-62

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QY 939 GCGAAGCTTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAAATATCAATATATT 998
Db |||||
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 145
Db |||||
QY 999 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 1058
Db |||||
QY 146 ACTATGAATCAACTACTTAGATGATATAGTGACCTGTAGTCGACCGAGCCCTCCAAA 205
Db |||||
QY 1059 ACTATGAATCAACTACTTAGATGATATAGTGACCTGTAGTCGACCGAGCCCTCCAAA 1118
Db |||||
QY 206 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCCCTCCAAATGCTTCTCTCAA 265
Db |||||
QY 1119 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCCCTCCAAATGCTTCTCTCAA 1178
Db |||||
QY 266 ACGGAATCGTCGATATCCAGCCCTACTCGCTTATGTCCTCAATGCGGTATTAATCATAAAA 325
Db |||||
QY 1179 ACGGAATCGTCGATATCCAGCCCTACTCGCTTATGTCCTCAATGCGGTATTAATCATAAAA 1238
Db |||||
QY 326 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 385
Db |||||
QY 1239 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 1298
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QY 386 ATTATATAGCTAGTGTCTAGTCAGTTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 445
Db |||||
QY 1299 ATTATATAGCTAGTGTCTAGTCAGTTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 1358
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QY 446 TCTTATATCTTTCTTTACAGTCTGTCGCGCTTCATCTGGAATTTTCAGCCCTCTATCTTA 505
Db |||||
QY 1359 TCTTATATCTTTCTTTACAGTCTGTCGCGCTTCATCTGGAATTTTCAGCCCTCTATCTTA 1418
Db |||||
QY 506 CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 565
Db |||||
QY 1419 CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 1478
Db |||||
QY 566 AGGAGGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTTTGTATGTCATTT 625
Db |||||
QY 1479 AGGAGGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTTTGTATGTCATTT 1538
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QY 626 TCGCGTGGCTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGCACACTGGCCATA 685
Db |||||
QY 1539 TCGCGTGGCTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGCACACTGGCCATA 1598
Db |||||
QY 686 TCGGTGTGTCATCGCGCAGCTTTTCATCCCGGATGACCCAGCGGTAAAGTTCACGG 745
Db |||||
QY 1599 TCGGTGTGTCATCGCGCAGCTTTTCATCCCGGATGACCCAGCGGTAAAGTTCACGG 1658
Db |||||
QY 746 GAGACTTTTATCTGACAGCAGACGTGSCACTGGCCAGGGGGATCACATCCGTCGCGCCGGGC 805
Db |||||
QY 1659 GAGACTTTTATCTGACAGCAGACGTGSCACTGGCCAGGGGGATCACATCCGTCGCGCCGGGC 1718
Db |||||
QY 806 GTGTCAATAATATACACTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG 865
Db |||||
QY 1719 GTGTCAATAATATACACTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG 1778
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QY 866 GTGTAAACCTTAACTGATTTACCAAGTCCCTGCTCTGTCGACGAAAGAGCGGTTTCAT 925
Db |||||
QY 1779 GTGTAAACCTTAACTGATTTACCAAGTCCCTGCTCTGTCGACGAAAGAGCGGTTTCAT 1838
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QY 926 TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCCAGCGTTCCGGC 985
Db |||||
QY 1839 TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCCAGCGTTCCGGC 1898
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QY 986 ACGCAGACGAGCGGCTTCATTTCTGCATGGTTGTGCTTTACAGACCGGAGATATGACATC 1045
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QY 1899 ACGCAGACGAGCGGCTTCATTTCTGCATGGTTGTGCTTTACAGACCGGAGATATGACATC 1958
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QY 1046 ATATATGCTTTGACCACTGATGCTGTCGTGTCCTCACTGCTCACTGTAATACGCTGCTTC 1105
Db |||||
QY 1959 ATATATGCTTTGACCACTGATGCTGTCGTGTCCTCACTGCTCACTGTAATACGCTGCTTC 2018
Db |||||
QY 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137

Db 2019 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 2050

RESULT 14

US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BIRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match 24.8%; Score 1102.4; DB 15; Length 4627;

Best Local Similarity 99.5%; Pred. No. 2.4e-157;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAGCTTTGTACAAAAAGCTGAAACGAGAAACGTAATAATGATATAAATATCAATATATT 85

Db 90 GCGAAGCTTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAAATATCAATATATT 149

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 145

Db 150 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACACATATCCAGTC 209

QY 146 ACTATGAATCAACTACTTAGATGATATAGTGACCTGTAGTCGACCGAGCCCTCCAAA 205

Db 210 ACTATGAATCAACTACTTAGATGATATAGTGACCTGTAGTCGACCGAGCCCTCCAAA 269

QY 206 TGTCTTCGCGGTGATGTCGCAACTTAGTTCGACCGACAGCCCTTCCAAATGCTTCTCTCAA 265

Db 270 TGTCTTCGCGGTGATGTCGCAACTTAGTTCGACCGACAGCCCTTCCAAATGCTTCTCTCAA 329

QY 266 ACGGAATCGTCGATATCCAGCCCTACTCGCTTATGTCCTCAATGCGGTATTAATCATAAAA 325

Db 330 ACGGAATCGTCGATATCCAGCCCTACTCGCTTATGTCCTCAATGCGGTATTAATCATAAAA 389

QY 326 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAACAATCTACCT 385

Db 390 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAACAATCTACCT 449

QY 386 ATTATATAGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAACAAATTTCAAC 445

Db 450 ATTATATAGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAACAAATTTCAAC 509

QY 446 TCTTATATCTTTCTTCAAGTCGTTTCGGCTTCATCTGGATTTTCAGCTCTATATCTTA 505

Db 510 TCTTATATCTTTCTTCAAGTCGTTTCGGCTTCATCTGGATTTTCAGCTCTATATCTTA 569

QY 506 CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGCTGTGTATA 565

Db 570 CTAAACGTGATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGCTGTGTATA 629

QY 566 AGGAGGCTGACATTTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTTTGTATGTCATTT 625


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Db 630 AGGAGCCTGACATTATATCCCGAGAACATCAGGTAAATGGGCTTTTGGATGTCATT 689
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Db 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGGAGACGGCACACTGGCCATA 749
Qy 686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCGATATGCACACGGGTAAAGTTACGG 745
Db 750 TCGGTGGTCATCATGCGCCAGCTTTCATCCCGATATGCACACGGGTAAAGTTACGG 809
Qy 746 GAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTGCGCCGGGC 805
Db 810 GAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTGCGCCGGGC 869
Qy 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATTAAGCGCTCTCTTTATAG 865
Db 870 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATTAAGCGCTCTCTTTATAG 929
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Db 930 GTGTAAACCTTAAACTGCACTTTCACAGCTCCCTGTTCTCGTCAGCAAAAGACCGTTTAT 989
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Db 1050 ACGCAGACGAGCGGCTTCACTCTGATGTTGCTGTTACCGACGAGATTTGACATC 1109
Qy 1046 ATATATGCTTTGAGCAACTGATAGCTGCGGTGTCACCTGTCATGTAATACGTCGTTTC 1105
Db 1110 ATATATGCTTTGAGCAACTGATAGCTGCGGTGTCACCTGTCATGTAATACGTCGTTTC 1169
Qy 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
Db 1170 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1201

RESULT 15
US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHBO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 24.6%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 2.4e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 26 GACAAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 85
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Db 90 GCCAATTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAATATCAATATATT 149
Qy 86 AAATTAGATTTTGCATAAAAAAGCAGACTACATAATCTGTAAACACAAACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAAAAGCAGACTACATAATCTGTAAACACAAACATATCCAGTC 209
Qy 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCACCGACAGCCCTTCAAA 205
Db 210 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCACCGACAGCCCTTCAAA 269
Qy 206 TGTCTCTTCGGGTGATGTCGCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 265
Db 270 TGTCTCTTCGGGTGATGTCGCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 329
Qy 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAATATCAAAAA 325
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Qy 326 AGAAATAAGAAAGAGGTCGGAGCCTCTTTTGTGTGACAAATAAATAAACAATCTACCT 385
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Db 510 TCTTATATCTTTCTTTTCAAGTCGTTTCGGCTTCATCTGGAATTTTTCAGCCTCTATATCTTA 569
Qy 506 CTAAACGTGTATAAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGCTGTGTATATA 565
Db 570 CTAAACGTGTATAAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGCTGTGTATATA 629
Qy 566 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTATGATGTCATTT 625
Db 630 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTATGATGTCATTT 689
Qy 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATA 685
Db 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATA 749
Qy 686 TCGGTGTCTATCATGCGCCAGCTTTCATCCCGATATGCACACCGGTTAAAGTTTACGG 745
Db 750 TCGGTGTCTATCATGCGCCAGCTTTCATCCCGATATGCACACCGGTTAAAGTTTACGG 809
Qy 746 GAGACTTTATCTGACAGCAGACGTCGCACTGGCCAGGGGATCACCATCCGTGCGCCGGGC 805
Db 810 GAGACTTTATCTGACAGCAGACGTCGCACTGGCCAGGGGATCACCATCCGTGCGCCGGGC 869
Qy 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAAGCGCTCTCTTTTATAG 865
Db 870 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAAGCGCTCTCTTTTATAG 929
Qy 866 GTGTAAACCTTAAACTGCACTTTCACAGTCCCTGTTCTCGTCAGCAAAAGACGCGTTTAT 925
Db 930 GTGTAAACCTTAAACTGCACTTTCACAGTCCCTGTTCTCGTCAGCAAAAGACGCGTTTAT 989
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Db 990 TTCAATAAACCGGGGACCTCAGCCATCCCTTCCGTGATTTTCCAGCGTTTCGGC 1049
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Db 1050 ACGCAGACGAGCGGCTTCACTCTGATGTTGCTTACCGACGAGATTTGACATC 1109
Qy 1046 ATATATGCTTTGAGCAACTGATAGCTGCTGCTCAACTGTCATGTAATACGTCGTTTC 1105
Db 1110 ATATATGCTTTGAGCAACTGATAGCTGCTGCTCAACTGTCATGTAATACGTCGTTTC 1169
Qy 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
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Db 1170 ATAGCACACCTCTTTTTCACATACCTTCGGGTA 1201

Search completed: May 10, 2004, 00:05:14
Job time : 1234.76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 193.335 seconds
(without alignments)
12850.857 Million cell updates/sec

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Perfect score: 4477
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	728.8	16.3	7639	2	US-08-232-016-22
3	709.8	15.9	5399	1	US-08-084-121-1
4	709.8	15.9	5399	1	US-08-478-015-1
5	709.8	15.9	5399	3	US-08-475-975-1
6	709.8	15.9	5399	3	US-09-084-889-1
7	709.8	15.9	6555	1	US-08-351-413-2
8	709.8	15.9	6555	2	US-09-025-583-2
9	709.8	15.9	14194	4	US-09-577-424-3
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12	566.4	12.7	15397	2	US-08-673-768-1
13	325.4	7.3	420	2	US-08-379-614-2
14	325.4	7.3	420	3	US-09-225-152A-2
15	323.2	7.2	416	2	US-08-379-614-3
16	323.2	7.2	416	3	US-09-225-152A-3
17	304.4	6.8	306	2	US-08-379-614-1
18	304.4	6.8	306	3	US-09-225-152A-1
19	289.2	6.5	13188	4	US-08-961-527-70
20	191	4.3	194	1	US-07-792-466-6
21	182.8	4.1	13188	4	US-08-961-527-70
22	152.8	3.4	4909	3	US-08-556-978B-78
23	152.8	3.4	4909	3	US-08-556-978B-78
24	152.8	3.4	6043	4	US-09-630-929-4
25	152.8	3.4	6043	4	US-09-630-929-4
26	152.8	3.4	7652	1	US-07-590-988A-1
27	152.8	3.4	7652	1	US-07-590-988A-1

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29	148.4	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
30	148.4	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
31	148.4	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
32	148.4	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
33	148.4	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
34	148.4	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
35	148.4	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
36	148.4	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli
37	146.2	3.3	231	4	US-09-489-039A-4117	Sequence 4117, Ap
38	146.2	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
39	146.2	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
40	146.2	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
41	146.2	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
42	146.2	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
43	146.2	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
44	146.2	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
45	146.2	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-232-016-23
Sequence 23, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

ORGANISM: plasmid DNA designated as pps0212
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1785
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated modified bt2 (cryIab) gene, also designated as the
OTHER INFORMATION: cryIab6 gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA gene 7."
FEATURE:
NAME/KEY: misc feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
NAME/KEY: misc feature
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
OTHER INFORMATION: Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23

Query Match 16.3%; Score 728.8; DB 2; Length 7566;
Best Local Similarity 99.7%; Pred. No. 3.2e-143;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3698 GTCTAGAGTCTGCTTTAAATGAGATATCGGAGACGCTATGATCGCATGATATTGCTTT 3757
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DB 3752 CAATCTGTTGTGACGTTGAAAAAAGCTGAGATGTGTAGCTCAGATCTTACCGCG 3811
QY 3818 GTTTCGGTTCAATCTTAATGATATATCACCGTTACTATGTTATTTTATGATTAATTT 3877
DB 3812 GTTTCGGTTCAATCTTAATGATATATCACCGTTACTATGTTATTTTATGATTAATTT 3871
QY 3878 CTCGGTTCAATTTACTGTTTACCTACTACTTATATGATCAATATTAATGAAACAA 3937
DB 3872 CTCGGTTCAATTTACTGTTTACCTACTACTTATATGATCAATATTAATGAAACAA 3931
QY 3938 ATATATGCTGATAGTTTATAGCAGATCTATGATAGAGGCCACATACAAACA 3997
DB 3932 ATATATGCTGATAGTTTATAGCAGATCTATGATAGAGGCCACATACAAACA 3991
QY 3998 ATTGGTTTTTATTATTAACAATCCAAATTTTAAAAAAGCGGACGCTCAACCTAA 4057
DB 3992 ATTGGTTTTTATTATTAACAATCCAAATTTTAAAAAAGCGGACGCTCAACCTAA 4051
QY 4058 AAGACTGATTACATAAATCTTATTCAAAATTTCAAAAGGCCCGGCTAGTACTACGA 4117

DB 4052 AAGACTGATTACATAAATCTTATTCAAAATTTCAAAAGGCCCGGCTAGTACTACGA 4111
QY 4118 CACACCGAGCGCGGAACCTAATAAGTTCACTGAAGGGAACCTCCGGTTCCCGCCCGCGCG 4177
DB 4112 CACACCGAGCGCGGAACCTAATAAGTTCACTGAAGGGAACCTCCGGTTCCCGCCCGCGCG 4171
QY 4178 CATGGGTGAGATTCCTTCAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGGGCA 4237
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QY 4238 CCATTCACACCGCGTCCAGCACGCGCGCGGTAAACCGACTTGTCTCCCCGAGAAATTATGC 4297
DB 4232 CCATTCACACCGCGTCCAGCACGCGCGGTAAACCGACTTGTCTCCCCGAGAAATTATGC 4291
QY 4298 AGCATTTTTTGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAACCTTGACACTGAGC 4357
DB 4292 AGCATTTTTTGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAACCTTGACACTGAGC 4351
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DB 4352 ACAAAATCGTTGGCGGGTCCAGGGGCGAATTTTGGCACAACATGTGAGGCTCAGCAGGAC 4411
QY 4418 CTGACGAGCATGC 4429
DB 4412 CTGACGAGCATTC 4423

RESULT 2
US-08-232-016-22
Sequence 22, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
APPLICANT: CORNELIUSSEN, Marc
APPLICANT: SOETABERT, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ER 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: F39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid DNA designated as pJD884
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1869
;   OTHER INFORMATION: /note= "Coding region of a
;   OTHER INFORMATION: truncated bt2 (cryIab) gene, also designated as the bt884 gen
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1877..2110
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA gene 7."
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2480..3005
;   OTHER INFORMATION: /note= "35S promoter sequence
;   OTHER INFORMATION: derived from Cauliflower mosaic virus."
; FEATURE:
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;   LOCATION: 3006..3665
;   OTHER INFORMATION: /note= "Coding sequence of
;   OTHER INFORMATION: chloramphenicol acetyl transferase gene."
; FEATURE:
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;   LOCATION: 3666..4491
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA octopine synthase gene."
; FEATURE:
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;   LOCATION: 5684..6541
;   OTHER INFORMATION: /note= "Sequence complementary to
;   OTHER INFORMATION: Patent No. 5952547
;   OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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;   OTHER INFORMATION: /note= "TR1' and TR2' promoter
;   OTHER INFORMATION: derived from Agrobacterium T-DNA."
; US-08-232-016-22
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; Query Match 16.3%; Score 728.8; DB 2; Length 7639;
; Best Local Similarity 99.7%; Pred. No. 3.2e-143;
; Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; Qy 3698 GTCTAGAGTCCTGCTTTTAATGAGATATGCGAGAGCGCCTATGATGCGATGATATTGCTTT 3757
; Db 3776 GTCTAGAGTCCTGCTTTTAATGAGATATGCGAGAGCGCCTATGATGCGATGATATTGCTTT 3835
; Qy 3758 CAATCTGTTGTGCGACGTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3817
; Db 3836 CAATCTGTTGTGCGACGTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3895
; Qy 3818 GTTTCGGTTCAATCTGAATGATATATCAACCGTTACTATGCTATTTTATGATATATT 3877
; Db 3896 GTTTCGGTTCAATCTGAATGATATATCAACCGTTACTATGCTATTTTATGATATATT 3955
; Qy 3878 CTCGGTTCAATTTACTGATTTGACCCCTACTATATATGATATGATATTTAAATGAAACA 3937
; Db 3956 CTCGGTTCAATTTACTGATTTGACCCCTACTATATATGATATGATATTTAAATGAAACA 4015
; Qy 3938 ATATATTGCTGTAATAGTTTATAGGACATCTATGATGAGCGCCACATTAACAACA 3997
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; Qy 4058 AGACTGATTACATAAATCTTATTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA 4117
; Db 4136 AGACTGATTACATAAATCTTATTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA 4195
; Qy 4118 CACACCGAGCGCGGAACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGGCG 4177
; Db 4196 CACACCGAGCGCGGAACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGGCG 4255
; Qy 4178 CATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGCA 4237
; Db 4256 CATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGCA 4315
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; Db 4316 CCATTCAACCCGCTCCAGACGCGCGCTAAGCTTCACTGAAGGGAATCTCCGGTTCCCGCGCGGCG 4375
; Qy 4298 AGCATTTTGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACTTTGACAGTGACG 4357
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; Qy 4358 ACAAATCGTTGGCGGCTCCAGGCGGAAATTTTCGCAACAATGTCAGGCTCAGCAGGAC 4417
; Db 4436 ACAAATCGTTGGCGGCTCCAGGCGGAAATTTTCGCAACAATGTCAGGCTCAGCAGGAC 4495
; Qy 4418 CTGACGCGCATGC 4429
; Db 4496 CTGACGCGCATGC 4507
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; RESULT 3
; US-08-064-121-1
; Sequence 1, Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
FEATURE:
NAME/KEY: -
LOCATION: 1..451
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
FEATURE:
NAME/KEY: -
LOCATION: 452..1284
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
Cauliflower mosaic virus isolate CabbB-JI"
FEATURE:
NAME/KEY: -
LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycinase"
OTHER INFORMATION: phosphotransferase gene"
FEATURE:
NAME/KEY: -
LOCATION: 2101..3150
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
polyadenylation site derived from the
A. Agrobacterium T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-064-121-1
Query Match 15.9%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-139; Indels 0; Gaps 0;
Matches 711; Conservative 0; Mismatches 32;
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QY 3767 TGTGACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACGGCGGTTTCGGTT 3826
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DB 2453 ATTTACTGATGTACCTTACTATATGTAATATATTAATGAAACAAATATATTTGT 2512
QY 3947 GCTGAATAGTTTATAGGACATCTATGATAGCGGCCCAATACAAACAAATTCGGTTT 4006
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DB 2573 TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTTAAAAAGCTGAT 2632
QY 4067 TACATAATCTTATCAAAATTTAAAAAGGCCCGGCTAGTATCTACGACACACCGAG 4126
DB 2633 TACATAATCTTATCAAAATTTAAAAAGGCCCGGCTAGTATCTACGACACACCGAG 2692
QY 4127 CGGCGAATCAATACGTTCTACTGAGGAACTCCGGTTCCCGCGCGCATGGGTGA 4186
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DB 2813 CCGGTCCAGACGCGCGCGGTAAACCGACTTGTGCCCCCGGAGAAATTTATGACGCAATTTT 2872
QY 4307 TTGGTGTATGTGGGCCCCCAAAATGAAGTGAAGTCAAGTCAAACTTGACAGTGAACGCAATTCGT 4366
DB 2873 TTGGTGTATGTGGGCCCCCAAAATGAAGTGAAGTCAAGTCAAACTTGACAGTGAACGCAATTCGT 2932
QY 4367 TGGGCGGCTCCAGGCGGAATTTTGGACAAATGTCGAGGCTCAGCAGACCT 4419
DB 2933 TGGGCGGCTCCAGGCGGAATTTTGGACAAATGTCGAGGCTCAGCAGGCT 2985

RESULT 4
US-08-478-015-1
; Sequence 1, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/478,015
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
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; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY: -
; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
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; NAME/KEY: -
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; OTHER INFORMATION: /label= NPTII
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; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from the Agrobacterium T-DNA octopine synthase"
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; FEATURE:
; NAME/KEY: -
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; OTHER INFORMATION: /label= pUC18
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; US-08-478-015-1
; Query Match 15.9%; Score 709.8; DB 1; Length 5399;
; Best Local Similarity 99.7%; Pred. No. 2.7e-139;
; Matches 711; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
;
QY 3707 CTGCTTTTATGATGATCGGACGCTATGATCGCATGATTTGCTTTCAATTCGT 3766
DB 2273 CTGCTTTTATGATGATCGGACGCTATGATCGCATGATTTGCTTTCAATTCGT 2332
QY 3767 TGTGACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3826
DB 2333 TGTGACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 2392
QY 3827 CATCTTAATGAATATATACCGGTTACTATCGTATTTTATGAATATATCTCCGTTCA 3886
DB 2393 CATCTTAATGAATATATACCGGTTACTATCGTATTTTATGAATATATCTCCGTTCA 2452
QY 3887 ATTTACTGATGTACCTACTACTATATGATCAATATTAATGAATGAATATATATGT 3946
DB 2453 ATTTACTGATGTACCTACTACTATATGATCAATATTAATGAATGAATATATGT 2512
QY 3947 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAATTCGGTT 4006
DB 2513 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAATTCGGTT 2572
QY 4007 TATTATTACAAATCCAAATTTTAAAAAAGCGGACGACCGGTCAAACTTAAAGACTGAT 4066
DB 2573 TATTATTACAAATCCAAATTTTAAAAAAGCGGACGACCGGTCAAACTTAAAGACTGAT 2632
QY 4067 TACATAAATCTTATTCAAATTTTCAAAGGCCCCAGGGGCTAGTATCTACGACACCGGAG 4126
DB 2633 TACATAAATCTTATTCAAATTTTCAAAGGCCCCAGGGGCTAGTATCTACGACACCGGAG 2692
QY 4127 CGGCGAATTAATTAACGTTCTAGAGGGAATCTCGGTTTCCCGGCGCGGATGGGGTGA 4186
DB 2693 CGGCGAATTAATTAACGTTCTAGAGGGAATCTCGGTTTCCCGGCGCGGATGGGGTGA 2752
QY 4187 GATTCTTGAAGTTGAGTATTGGCGTCCGCTCTACCGAAGTTTACGGGCACCATTTCAAC 4246
DB 2753 GATTCTTGAAGTTGAGTATTGGCGTCCGCTCTACCGAAGTTTACGGGCACCATTTCAAC 2812
QY 4247 CCGGTCCAGCACGGCGCGCGGTAACCGACTTGTGCGCCGAGAAATATATCAGCAATTTT 4306
DB 2813 CCGGTCCAGCACGGCGCGCGGTAACCGACTTGTGCGCCGAGAAATATATCAGCAATTTT 2872
QY 4307 TTGGTGTATGGGCCCCCAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAATCGT 4366

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DB 2873 TTGGTGTATGTGGGCCCAATGAAGTGCAGGTCAAACTTTGACAGTGCAGCAAAATCGT 2932
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DB 2933 TGGGCGGTCAGGGCGGAATTTTGGGACAAATGTCAGGGCTCAGCAGGCGT 2985

RESULT 5
US-08-475-975-1
; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 9040332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY: -
; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosaic virus isolate CabbB-JI"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1285..2100

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LOCATION: 3161..5399
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OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-084-889-1
Query Match 15.9%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3707 CCTGCTTTTAAATGAGATATCGAGACGCTTATGATCGCATGATATTTGCTTTCAATTCGT 3766
Db 2273 CCTGCTTTTAAATGAGATATCGAGACGCTTATGATCGCATGATATTTGCTTTCAATTCGT 2332
QY 3767 TGTGACGTTTGAHAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3826
Db 2333 TGTGACGTTTGAHAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 2392
QY 3827 CATTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGATGAATATATTTCTCCGTTCA 3886
Db 2393 CATTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGATGAATATATTTCTCCGTTCA 2452
QY 3887 ATTACTGATTGTACCTACTACTTATATGTAACAATTAATAATGAHAAAACATATATTTGT 3946
Db 2453 ATTACTGATTGTACCTACTACTTATATGTAACAATTAATAATGAHAAAACATATATTTGT 2512
QY 3947 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGCCCAATTAACAACAATTTGCGTTT 4006
Db 2513 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGCCCAATTAACAACAATTTGCGTTT 2572
QY 4007 TATTATTACAAATCCAAATTTTAAAAAGGCGGAGAACCGGTCAAACTTAAAGACTGAT 4066
Db 2573 TATTATTACAAATCCAAATTTTAAAAAGGCGGAGAACCGGTCAAACTTAAAGACTGAT 2632
QY 4067 TACATAATCTTATTAATTTTCAAAAGGCCCGGCTAGTATCTACGACACCGAG 4126
Db 2633 TACATAATCTTATTAATTTTCAAAAGGCCCGGCTAGTATCTACGACACCGAG 2692
QY 4127 CGGGAATTAATACGTTTACTGAAGGGAATCTCGGTTCGCGCGCGGCGCATGGGTGA 4186
Db 2693 CGGGAATTAATACGTTTACTGAAGGGAATCTCGGTTCGCGCGCGGCGCATGGGTGA 2752
QY 4187 GATTCCTTTGAGTTGAGTATTTGGCGTCCGCTTACCGAAAGTTTACGGGACCAATCAAC 4246
Db 2753 GATTCCTTTGAGTTGAGTATTTGGCGTCCGCTTACCGAAAGTTTACGGGACCAATCAAC 2812
QY 4247 CCGGTCCAGCACGGCGCGGTTACCGACTTCTGCCCCGAGAAATTATGAGCATTTT 4306
Db 2813 CCGGTCCAGCACGGCGCGGTTACCGACTTCTGCCCCGAGAAATTATGAGCATTTT 2872
QY 4307 TTGTTGATGTGGGCCCCCAATTAAGTGCAGTCAAACTTGAACAGTACGACCAAAATCGT 4366
Db 2873 TTGTTGATGTGGGCCCCCAATTAAGTGCAGTCAAACTTGAACAGTACGACCAAAATCGT 2932
QY 4367 TGGGCGGTCACGGCGGAAATTTGGCAACAATGTCGAGGCTCAGCAGGACCT 4419
Db 2933 TGGGCGGTCACGGCGGAAATTTGGCAACAATGTCGAGGCTCAGCAGGACCT 2985

RESULT 7
US-08-351-413-2
Sequence 2, Application US/08351413
Patent No. 5750867
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSES: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
FEATURE:
NAME/KEY: -
LOCATION: 1..396 /label= pUC18
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LOCATION: complement (397..751)
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OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: complement (752..1024)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -
LOCATION: 1608..2440 /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate CabB9-J1"
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LOCATION: 2441..3256 /label= neo
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OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: -

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; LOCATION: 3257..4315
; OTHER INFORMATION: /label= 3'ocns
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA octopine synthase gene"
; FEATURE:
; NAME/KEY:
; LOCATION: 4316..6555
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; US-08-351-413-2
Query Match 15.9%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3707 CTTGCTTTTAAATGAGATATCGAGACGCTATGATCGCATGATTTTGGCTTTCAATTCTGT 3766
Db 3429 CTTGCTTTTAAATGAGATATCGAGACGCTATGATCGCATGATTTTGGCTTTCAATTCTGT 3488
QY 3767 TGTGCACTTTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGGTTTCGGTT 3826
Db 3489 TGTGCACTTTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGGTTTCGGTT 3548
QY 3827 CATTTCTAAATGAATATATCAACCGTTACTATCGTATTTTATGATTAATATTCCTCGTTCA 3886
Db 3549 CATTTCTAAATGAATATATCAACCGTTACTATCGTATTTTATGATTAATATTCCTCGTTCA 3608
QY 3887 ATTACTGATTTGACCTACTACTATATGATACAAATATTAATAATGAAAAACAATATTTGT 3946
Db 3609 ATTACTGATTTGACCTACTACTATATGATACAAATATTAATAATGAAAAACAATATTTGT 3668
QY 3947 GCTGATAGTTTATAGCGACATCTATGATAGCGCCCACTAAACAAACAAATGCGTTT 4006
Db 3669 GCTGATAGTTTATAGCGACATCTATGATAGCGCCCACTAAACAAACAAATGCGTTT 3728
QY 4007 TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTTAAAGACTGAT 4066
Db 3729 TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAAACCTTAAAGACTGAT 3788
QY 4067 TACATAAATCTTATTTCAAAATTTCAAAAGGCCCGGAGGCTGATCTACGACACACCGAG 4126
Db 3789 TACATAAATCTTATTTCAAAATTTCAAAAGGCCCGGAGGCTGATCTACGACACACCGAG 3848
QY 4127 CGGCGACTAATAACCTTCACTGAAGGACTCGGTTCCCGCGCGCGGCTGGTGA 4186
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QY 4187 GATTCTTTGAAGTTGAGTATTTGCGCTCCGCTCTACCGAAAGTTAGCGGACCAATTCAC 4246
Db 3909 GATTCTTTGAAGTTGAGTATTTGCGCTCCGCTCTACCGAAAGTTAGCGGACCAATTCAC 3968
QY 4247 CCGGTCAGCACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGATTTT 4306
Db 3969 CCGGTCAGCACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGATTTT 4028
QY 4307 TTGCTGATTTGGGCCCCCAATGAAGTGACAGTCAAACTTTGACAGTGACGACAAATCGT 4366
Db 4029 TTGCTGATTTGGGCCCCCAATGAAGTGACAGTCAAACTTTGACAGTGACGACAAATCGT 4088
QY 4367 TGGCGGGTCCAGGGCGAAATTTTGCACAAATGTTCGAGGCTCAGCAGGACCT 4419
Db 4089 TGGCGGGTCCAGGGCGAAATTTTGCACAAATGTTCGAGGCTCAGCAGGACCT 4141
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RESULT 8

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US-09-025-583-2
; Sequence 2, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
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; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,583
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pVE144 (replicable in E.coli)
; FEATURE:
; NAME/KEY:
; LOCATION: 1..396
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (397..751)
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (752..1024)
; OTHER INFORMATION: /label= barstar
; OTHER INFORMATION: /note= "coding region of the barstar gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (1025..1607)
; OTHER INFORMATION: /label= TA29
; OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
; OTHER INFORMATION: Nicotiana tabacum"
; FEATURE:
; NAME/KEY:
; LOCATION: 1508..2440
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"

FEATURE:
NAME/KEY: 2441..3256
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: 3257..4315
LOCATION: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: 4316..6555
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2

Query Match 15.9%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
3707 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
3429 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3488
3767 TGTGCAAGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3826
3489 TGTGCAAGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3548
3827 CATTCCTAATGAATATATCACCCTGACTATCGTATTTTATGATGAATATATTCCTCCGTCA 3886
3549 CATTCCTAATGAATATATCACCCTGACTATCGTATTTTATGATGAATATATTCCTCCGTCA 3608
3887 ATTTACTGATTGTACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3946
3609 ATTTACTGATTGTACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3668
3947 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAACAAATTCGGTT 4006
3669 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAACAAATTCGGTT 3728
4007 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAAACCTTAAAGACTGAT 4066
3729 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAAACCTTAAAGACTGAT 3788
4067 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGCTAGTATCTACGACACACCGAG 4126
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4127 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGCGGATGGGTGA 4186
3849 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGCGGATGGGTGA 3908
4187 GATTTCCTTGAAGTTGAGTATGCGCGTCTACCGAAGTTACGGGACCATTCAC 4246
3909 GATTTCCTTGAAGTTGAGTATGCGCGTCTACCGAAGTTACGGGACCATTCAC 3968
4247 CCGGTCCAGCAGCGCGCGGTAACCGACTTGTGCGCGGAGAAATTTATGACGATTTTT 4306
3969 CCGGTCCAGCAGCGCGCGGTAACCGACTTGTGCGCGGAGAAATTTATGACGATTTTT 4028
4307 TTGGTGTATGGGCCCGGCGGAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTC 4366
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RESULT 9

US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 15.9%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 3.7e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
3707 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
9830 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 9889
3767 TGTGCAAGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3826
9890 TGTGCAAGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 9949
3827 CATTCCTAATGAATATATCACCCTGACTATCGTATTTTATGATGAATATATTCCTCCGTCA 3886
9950 CATTCCTAATGAATATATCACCCTGACTATCGTATTTTATGATGAATATATTCCTCCGTCA 10009
3887 ATTTACTGATTGTACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3946
10010 ATTTACTGATTGTACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 10069
3947 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAACAAATTCGGTT 4006
10070 GCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCCAATTAACAAACAAATTCGGTT 10129
4007 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAAACCTTAAAGACTGAT 4066
10130 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAAACCTTAAAGACTGAT 10189
4067 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGCTAGTATCTACGACACACCGAG 4126
10190 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGCTAGTATCTACGACACACCGAG 10249
4127 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGATGGGTGA 4186
10250 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGATGGGTGA 10309
4187 GATTTCCTTGAAGTTGAGTATGCGCGTCTACCGAAGTTACGGGACCATTCAC 4246
10310 GATTTCCTTGAAGTTGAGTATGCGCGTCTACCGAAGTTACGGGACCATTCAC 10369
4247 CCGGTCCAGCAGCGCGGTAACCGACTTGTGCGCGGAGAAATTTATGACGATTTTT 4306
10370 CCGGTCCAGCAGCGCGGTAACCGACTTGTGCGCGGAGAAATTTATGACGATTTTT 10429
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RESULT 10
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; PATENT NO. 5428147
; APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1

Query Match          15.8%; Score 707; DB 6; Length 24595;
Best Local Similarity 100.0%; Pred. No. 1.7e-138;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3708 CTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGTG 3767
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QY 3768 GTGCACGCTTGTAAACACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGTTTC 3827
DB 12481 GTGCACGCTTGTAAACACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGTTTC 12422

QY 3828 ATTCTAATGAATATATCACCGGTTACTATCTGATTTTATGAATAATATCTCCGTTCAA 3887
DB 12421 ATTCTAATGAATATATCACCGGTTACTATCTGATTTTATGAATAATATCTCCGTTCAA 12362

QY 3888 TTCTACTGATTTGACCTTACTTATATGATGATGATGATGATGATGATGATGATGATGATG 3947
DB 12361 TTCTACTGATTTGACCTTACTTATATGATGATGATGATGATGATGATGATGATGATGATG 12302

QY 3948 CTGAATAGGTTTATAGCGCATCTATGATAGCGCCACATTAACAAACAAATTCGTTT 4007
DB 12301 CTGAATAGGTTTATAGCGCATCTATGATAGCGCCACATTAACAAACAAATTCGTTT 12242

QY 4008 ATTATTACAAATCCAAATTTTAAACAAAGCGGCGAGAACCGGTCAAACTTAAAGACTGAT 4067
DB 12241 ATTATTACAAATCCAAATTTTAAACAAAGCGGCGAGAACCGGTCAAACTTAAAGACTGAT 12182

QY 4068 ACATTAATCTTATCAATTTTAAACAAAGCGGCGGCTAGTATCTACGACACACCGAGC 4127
DB 12181 ACATTAATCTTATCAATTTTAAACAAAGCGGCGGCTAGTATCTACGACACACCGAGC 12122

QY 4128 GCGCAACTAATAACGTTCACTGAAGGAACTCCGTTTCCCGCGCGCGCATGGGTGAG 4187
DB 12121 GCGCAACTAATAACGTTCACTGAAGGAACTCCGTTTCCCGCGCGCGCATGGGTGAG 12062

QY 4188 ATTCCTTGAAGTTGAGTATTTGGCCGCTCCGCTCTACCGAAAGTTTACGGGCACTTCAACC 4247
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Db 12061 ATTCTTGAAGTTGATATTTGGCCGCTCCGCTCTACGAAAGTTACGGGCACTTCAACC 12002
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Db 12001 CGGTCCAGCACGGCGCGGGGTAAACCGACTTCTGCTCCCGCGAGAAATTATGACGCAATTTT 11942
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Db 11941 TGGTGTATGTTGGGCCCCCAAAATGAAGTGCAGGTGCAAACTTGAAGTGCAGCAAAATCGTT 11882
QY 4368 GGGCGGGTCCAGGCGGAAATTTTGGCACAACATGTGAGGCTCAGCAG 4414
Db 11881 GGGCGGGTCCAGGCGGAAATTTTGGCACAACATGTGAGGCTCAGCAG 11835

RESULT 11
US-08-673-768-1
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match          12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 3.8e-109;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3707 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
Db 7110 CTTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 7169
QY 3767 TGTGACGCTGTGTAACCAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGTT 3825
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Db 7170 TGTGACGTTGTAATAAAACCTGAGCATGTGTAGCTCAGATCTTACCGCGGTTTCGGTT 7229
QY 3827 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATCTTCGGTTCA 3886
Db 7230 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATCTTCGGTTCA 7289
QY 3887 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATATGAATAATATATCTT 3946
Db 7290 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATATGAATAATATATCTT 7349
QY 3947 GCTGAATAGTTTATAGCAGCATCTATGATAGAGCGCCCAATAAACAACAAATTCGGTT 4006
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QY 4127 CGCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGGTGA 4186
Db 7530 CGCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGGTGA 7589
QY 4187 GATTCCTTGAAGTTGAGTATGCGCTCGCTACGAAAGTTACGGGCAACCATTCAC 4246
Db 7590 GATTCCTTGAAGTTGAGTATGCGCTCGCTACGAAAGTTACGGGCAACCATTCAC 7649
QY 4247 CGGTCACGACGCGCGCGGTAACCG 4274
Db 7650 CGGTCACGACGCGCGCGGTAACAG 7677

RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patenlin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 3.8e-109;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3707 CTGCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTCAATCTGT 3766
Db 14394 CTGCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTCAATCTGT 14335
QY 3767 TGTGACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCTTACCGCGGTTTCGGTT 3826
Db 14334 TGTGACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCTTACCGCGGTTTCGGTT 14275
QY 3827 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATCTTCGGTTCA 3886
Db 14274 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATCTTCGGTTCA 14215
QY 3887 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATATGAATAATATATCTT 3946
Db 14214 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATATGAATAATATATCTT 14155
QY 3947 GCTGAATAGTTTATAGGAGCATCTATGATAGAGCGCCCAATAAACAACAAATTCGGTT 4006
Db 14154 GCTGAATAGTTTATAGGAGCATCTATGATAGAGCGCCCAATAAACAACAAATTCGGTT 14095
QY 4007 TATTATACAAATCCAAATTTTAAAAAGCGGAGAAACCGGTCAACCTTAAAGACTGAT 4066
Db 14094 TATTATACAAATCCAAATTTTAAAAAGCGGAGAAACCGGTCAACCTTAAAGACTGAT 14035
QY 4067 TACATAAATCTTATTCAAATTTTCAAAAGCGCCAGGGGTAGTATCTACGACACACCGAG 4126
Db 14034 TACATAAATCTTATTCAAATTTTCAAAAGCGCCAGGGGTAGTATCTACGACACACCGAG 13975
QY 4127 CGCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGGTGA 4186
Db 13974 CGCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGCGCATGGGTGA 13915
QY 4187 GATTCCTTGAAGTTGAGTATGCGCTCGCTACGAAAGTTACGGGCAACCATTCAC 4246
Db 13914 GATTCCTTGAAGTTGAGTATGCGCTCGCTACGAAAGTTACGGGCAACCATTCAC 13855
QY 4247 CGGTCACGACGCGCGGTAACCG 4274
Db 13854 CGGTCACGACGCGCGGTAACAG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: 08/379614
; PRIOR APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
;
US-08-379-614-2

Query Match          7.3%; Score 325.4; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 3.3e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 617
DB 403 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 344

QY 618 TGTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 677
DB 343 TGTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 284

QY 678 TGGCCATATCGGTGGTCATATGCGCAGCTTTCATCCCGATATGCCACCGGTAAA 737
DB 283 TGGCCATATCGGTGGTCATATGCGCAGCTTTCATCCCGATATGCCACCGGTAAA 224

QY 738 GTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
DB 223 GTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 164

QY 798 GCCCGGGCGTCAATAATATCACTCTGTATCCAAACAGACGATTAACGGCTCTCTC 857
DB 163 GCCCGGGCGTCAATAATATCACTCTGTATCCAAACAGACGATTAACGGCTCTCTC 104

QY 858 TTTTATAGGTAAACCTTAACTGCA 884
DB 103 TTTTATAGGTAAACCTTAACTGCA 77

RESULT 14
US-09-225-152A-2/c
; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMA10.001CPI
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; CURRENT APPLICATION NUMBER: US/09/225,152A
; CURRENT FILING DATE: 1998-01-04
; PRIOR APPLICATION NUMBER: 08/379614
; PRIOR FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(378)
; OTHER INFORMATION: ccdB gene of pKIL 18.
;
US-09-225-152A-2

Query Match          7.3%; Score 325.4; DB 3; Length 420;
Best Local Similarity 99.7%; Pred. No. 3.3e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 617
DB 403 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 344

QY 618 TGTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 677
DB 343 TGTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 284

QY 678 TGGCCATATCGGTGGTCATATGCGCAGCTTTCATCCCGATATGCCACCGGTAAA 737
DB 283 TGGCCATATCGGTGGTCATATGCGCAGCTTTCATCCCGATATGCCACCGGTAAA 224

QY 738 GTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
DB 223 GTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 164

QY 798 GCCCGGGCGTCAATAATATCACTCTGTATCCAAACAGACGATTAACGGCTCTCTC 857
DB 163 GCCCGGGCGTCAATAATATCACTCTGTATCCAAACAGACGATTAACGGCTCTCTC 104

QY 858 TTTTATAGGTAAACCTTAACTGCA 884
DB 103 TTTTATAGGTAAACCTTAACTGCA 77

RESULT 15
US-08-379-614-3/c
; Sequence 3, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; APPLICATION NUMBER:
; FILING DATE: 02-AUG-1993
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ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19
FEATURES:
NAME/KEY: Coding Sequence
LOCATION: 1...378
OTHER INFORMATION:
US-08-379-614-3

Query Match 7.2%; Score 323.2; DB 2; Length 416;
Best Local Similarity 99.1%; Pred. No. 9.5e-59;
Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 559 GTGTATAGGAGCGCTGACATTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGAT 618
DB 402 GTGTATACGAGCGCTGACATTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGAT 343
QY 619 GTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATACCGGAGACCGGCACACT 678
DB 342 GTCAATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATACCGGAGACCGGCACACT 283
QY 679 GGCCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCGGGTAAG 738
DB 282 GGCCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCGGGTAAG 223
QY 739 TTCACGGGAGACTTTTATCTGACGAGACGTGCACTGGCCAGGGGGATCACCATCCGTCG 798
DB 222 TTCACGGGAGACTTTTATCTGACGAGACGTGCACTGGCCAGGGGGATCACCATCCGTCG 163
QY 799 CCGGGCGGTGCAATAATATATCACTCTGTACATCCCAAAACGAGACGATTAACGGCTCTCTCT 858
DB 162 CCGGGCGGTGCAATAATATCACTCTGTACATCCCAAAACGAGACGATTAACGGCTCTCTCT 103
QY 859 TTTATAGGTGTAACCTTAACTGCATT 886
DB 102 TTTATAGGTGTAACCTTAACTGCATT 75

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
19251.609 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pun:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	496.6	11.1	713	29	AG000762 Homo sapi
3	437.2	9.8	542	14	CD109790 AGENCOURT
C 4	411.8	9.2	723	29	AG000761 Homo sapi

C	5	408.4	9.1	725	29	AG013450
C	6	404	9.0	522	14	CB997937
C	7	398.4	8.9	722	29	AG000763
C	8	357	8.0	487	14	CB395230
	9	347.4	7.8	487	14	CB395230
	10	340.2	7.6	384	12	B1174407
C	11	325.4	7.3	384	12	B1174407
C	12	301.4	6.7	337	12	BJ555980
C	13	273.2	6.1	1068	14	CF469981
C	14	271.8	6.1	1037	14	CF469119
C	15	264.4	5.9	724	29	AG000791
C	16	262.4	5.9	816	14	CF469496
C	17	257.4	5.7	557	12	BG220129
C	18	255.8	5.7	656	14	CK291800
C	19	254	5.7	569	14	CF469084
C	20	252.4	5.6	819	14	CF469247
C	21	247.4	5.5	320	29	GG206516
C	22	246	5.5	329	28	BH739300
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C	24	243.6	5.4	1035	14	CF470036
C	25	242.8	5.4	1017	14	CF470004
C	26	239.2	5.3	659	14	CK287298
C	27	235.6	5.3	859	14	CF468865
C	28	234.8	5.2	506	14	CF468964
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C	31	227.2	5.1	968	14	CF469474
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C	34	215.2	4.8	393	14	CB403984
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C	36	215.2	4.8	1020	14	CF469337
C	37	214.6	4.8	1017	14	CF468787
C	38	214.2	4.8	1042	14	CF468958
C	39	213.8	4.8	945	14	CF468807
C	40	213.2	4.8	509	14	CF468864
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C	43	203.4	4.5	1013	14	CF469353
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ALIGNMENTS

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LOCUS
DEFINITION
AG012840
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.
ACCESSION
AG012840
VERSION
AG012840.1 GI:3435047
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE
Homo sapiens genomic DNA, chromosome 21q
JOURNAL
Published Only in DataBase (1998)
REFERENCE
2 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
AUTHORS
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE
Direct Submission
JOURNAL
Submitted (20-AUG-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES
Location/Qualifiers
1..698
/organism="Homo sapiens"
/mol_type="genomic DNA"

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Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

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Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="f65H12X16"

ORIGIN

Query Match 11.6%; Score 518.4; DB 29; Length 698;
Best Local Similarity 98.9%; Pred. No. 7.5e-82;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

579 TTTATATATCCCGAAGACATCAGGTTAATGCGGTTTTTGATGTCAATTTTCGCGGTGCTGA 638
Db TTTATATATCCCGAAGACATCAGGTTAATGCGGTTTTTGATGTCAATTTTCGCGGTGCTGA 93
639 GATCAGCACTTCTTCCCGATTAACGGAGACCGGCACTGCGGCAATATCGGTGCTCATCA 698
Db GATCAGCACTTCTTCCCGATTAACGGAGACCGGCACTGCGGCAATATCGGTGCTCATCA 153
699 TGGCGCAGCTTTCATCCCGGATATGACCAACCGGGTAAAGTTTCAACGGAGACTTTATCTG 758
Db TGGCGCA-NTTTCATCCCGGATATGACCAACCGGGTAAAGTTTCAACGGAGACTTTATCTG 212
759 ACAGCAGAGTGACCTGCGGAGGGGATCAACCATCGTCCCGGGCGGTGTCATTAATAT 818
Db ACAGCAGAGTGACCTGCGGAGGGGATCAACCATCGTCCCGGGCGGTGTCATTAATAT 272
819 CACTGTGTACATCCAGACAGGATACGGCTCTCTTTTATAGGTGTAAACCTTAA 878
Db CACTGTGTACATCCAGACAGGATACGGCTCTCTTTTATAGGTGTAAACCTTAA 332
879 ACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGG 938
Db ACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGG 392
939 GGCACCTCAGCCATCCCTTCTGATTTTCGCTTTCCAGGTTTCGCGAGCAGACGCG 998
Db GGCACCTCAGCCATCCCTTCTGATTTTCGCTTTCCAGGTTTCGCGAGCAGACGCG 452
999 GCTTCAATTCGATGTTGCTTACAGACCGGATATGACATATATGACATATATGACCTTGA 1058
Db GCTTCAATTCGATGTTGCTTACAGACCGGATATGACATATATGACATATATGACCTTGA 510
1059 GCAACTGATAGCTGCTGCTCACTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
Db GCAACTGATAGC-GTCCGCTCACTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
1119 TTTTGACATCTTCGGGTA 1137
Db TTTTGACATCTTCGGGTA 588

RESULT 2
AG000762/c
LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
DEFINITION AG000762
ACCESSION AG000762.1 GI:2579570
VERSION AG000762
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 713)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 713)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp)

Tel:0427-78-9732, Fax:0427-78-9561)
Location/Qualifiers
1..713

FEATURES

source
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="64E11X4"

ORIGIN

Query Match 11.1%; Score 496.6; DB 29; Length 713;
Best Local Similarity 94.2%; Pred. No. 5.4e-78;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

583 TATTCGCCAGAACATCAGGTTAATGCGGTTTTTGATGTCAATTTTCGCGGTGCTGATC 642
Db TATATCCCGGANCATCNGTTAATGCGGTTTTTGAGGNAATTTTCGCGGTGCTGAGAAT 540
643 AGCGACTTCTTCCCGATTAACGGAGACCGGACACTGCGGCATATCGGTGCTCATCGG 702
Db AGCGACTTCTTCCCGATTAACGGAGACCGGACACTGCGGCATATCGGTGCTCATCGG 480
539 CACCAACTTTTTCGCGATTAACGGAGACCGGACACTGCGGCATATCGGTGCTCATCGG 762
Db CACCAACTTTTTCGCGATTAACGGAGACCGGACACTGCGGCATATCGGTGCTCATCGG 420
703 CCAGCTTTTCATCCCGGATATGACCAACCGGGTAAAGTTTCAACGGAGACTTTTATCTG 822
Db CCAGCTTTTCATCCCGGATATGACCAACCGGGTAAAGTTTCAACGGAGACTTTTATCTG 360
763 CAGAGTGACCTGCGGAGGGGATCAACATCGTCCCGGGCGGTGTCATTAATATCAT 882
Db CAGAGTGACCTGCGGAGGGGATCAACATCGTCCCGGGCGGTGTCATTAATATCAT 300
883 CATTTCCAGGTCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGCGA 942
Db CATTTCCAGGTCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGCGA 240
943 CTTAGGCAATCCCTTCTCGATTTTCGCTTCCAGGTTTCGCGAGCAGACGCGGCTT 1002
Db CTTAGGCAATCCCTTCTCGATTTTCGCTTCCAGGTTTCGCGAGCAGACGCGGCTT 180
1003 CATTCGATGCTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTTCGAGCAA 1062
Db CATTCGATGCTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTTCGAGCAA 122
1063 CTGATAGCTGCTGCTGCTCACTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
Db CTGATANTGCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62
1123 GACATCTTCGGGTA 1137
Db GACATCTTCGGGTA 47

RESULT 3
LOCUS CD109790
DEFINITION AGENCOURT_13988518 NIH_MGC_147 Homo sapiens CDNA clone IMAGE:30346919 5', mRNA sequence.
ACCESSION CD109790
VERSION CD109790.1 GI:30753999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Haussan
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.

Location/Qualifiers

1. 542
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30346919"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 147"
 /note="Organ: placenta; Vector: pBluescriptR; Site: 1:
 all-XhoI; Site: 2: BamH; Oligo-dr primed using primer
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 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

FEATURES

source

ORIGIN

Query Match 9.8%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 2e-67;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

QY 546 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 605
 DB 23 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 82
 QY 606 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGGCATTTCTTCCCGATACCG 665
 DB 83 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGGCATTTCTTCCCGATACCG 142
 QY 666 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGCAGCTTTCATCCCGATATGCA 725
 DB 143 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGTGAGCTTTCATCCCGATATGCA 202
 QY 726 CCAACCGGTAAAGTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 785
 DB 203 CCAACCGGTAAAGTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 262
 QY 786 TCACCATCGTCCCGGGGCTGCATATATATCTCTGATATATCTGATATCCACAGACAGCAT 845
 DB 263 TCACCATCGTCCCGGGGCTGTCAATAATATCACTCTGATATCCACAGACAGCAT 322
 QY 846 AACGGCTCTCTCTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTCG 905
 DB 323 AACGGCTCTCTCTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTCG 382
 QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTT 965
 DB 383 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTT 442
 QY 966 TCCGCTTTTCCA-CGGTTCGCGACGCGACAGC-ACGGGTTTCATTC--TGCATGCTTGCT 1021
 DB 443 TCCCTTTCCACGCTTTCGGCAGCGACAGCAACGGGCTTCATTCCTGCTGCTTGTGCT 502
 QY 1022 TACCAGACCGG-AGATATTGACATCATATATGCTTT 1056
 DB 503 TACCAGACCGGAGATATTGACATCATATATGCTTT 538

RESULT 4

AG000761/c
 LOCUS
 DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
 survey sequence.
 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Published Only in DataBase (1997)
 JOURNAL
 REFERENCE 2 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
 Location/Qualifiers
 1. 723
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="64E11X4"

ORIGIN

Query Match 9.2%; Score 411.8; DB 29; Length 723;
 Best Local Similarity 98.1%; Pred. No. 5.6e-63;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 546 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 605
 DB 450 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 391
 QY 606 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGGCATTTCTTCCCGATACCG 665
 DB 390 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGGCATTTCTTCCCGATACCG 331
 QY 666 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGCAGCTTTCATCCCGATATGCA 725
 DB 330 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGCAGCTTTCATCCCGATATGCA 271
 QY 726 CCACCGGGTAAAGTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 785
 DB 270 CCACCGGGTAAAGTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 211
 QY 786 TCACCATCGTCCCGGGGCTGCATATATATCACTCTGATATATCCACAGACAGCAT 845
 DB 210 TCACCATCGTCCCGGGGCTGTCAATAATATCACTCTGATATCCACAGACAGCAT 151
 QY 846 AACGGCTCTCTCTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTCG 905
 DB 150 AACGGCTCTCTCTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTCG 91
 QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTT 965
 DB 90 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTA 31
 QY 966 TCGG 969
 DB 30 TCAG 27

RESULT 5
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 LOCUS
 DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
 survey sequence.
 ACCESSION AG013450
 VERSION AG013450.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 725)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Published Only in DataBase (1997)
 JOURNAL
 REFERENCE 2 (bases 1 to 725)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
 Location/Qualifiers
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 /map="21q"
 /clone="64E11X4"

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Query Match 9.2%; Score 411.8; DB 29; Length 723;
 Best Local Similarity 98.1%; Pred. No. 5.6e-63;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;


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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
FEATURES
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="f32E9X13"
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Best Local Similarity 90.2%; Pred. No. 2.3e-62;
Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;
QY 580 TTATATATCCCCAGAACATCAGGTAAATGGCGTTTTCATGTCATTTTCGGGTGGCTGAG 639
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QY 640 ATCAGCCACTTCTTCCCGGATAGCGGACACCGGCACACTGGCCATATCGGTGTCATCAT 699
DB 663 ATCAGCNANTTTTCCCGGAATANGNAGCGGCACATGCGNATATCGNCTGTTTCATCAT 604
QY 700 GCGCGAGCTTTCATCCCGGATGACACCGGTAAGTTCACGGAG-ACCTTTATCTG 758
DB 603 GCGCCAGCTTTCATCCCGCAATA-GCACACGGGTAANGTTTCAGGAGAACTTTATCTG 545
QY 759 ACAGCAGACGTGCACTGGCC-AGGGGGATCACCATCGTCGCGCGCGGTGTCATAATA 817
DB 544 ACAGCAGACGTGCACTGGCCAAAGGGGATCACCATCGTNGCCGCGCGGTGTC-ATANTA 486
QY 818 TCACCTGTATACATCCAAACAGACGATAAGGCTCTCTCTTTATAGGTGTAACCTTA 877
DB 485 TCACCTGTATACATCCAAACAGACGATAAGGCTCTCTCTTTATAGGTGTAACCTTA 427
QY 878 AACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAACCG 937
DB 426 AACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAACCG 367
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DB 366 GGGACCTCAGCCATCCCTTCCTGATTTTCGGTTTCCAGGTTTCGGCAGCGAGCAGC 307
QY 998 GGCTTCATTCGATGTTGTGCTTACAGACCGGATATATGATCATATATATGCGTTG 1057
DB 306 GGCTTCATTCGATGTTGTGCTTACAGACCGGATATATGATCATATATATGCGTTG 249
QY 1058 AGCAACTGATAGCTGTGCTGCTCAACTGTCACTGTAATAGCTGCTTTCATAGCACACTC 1117
DB 248 AGCAACTGATAGCTGTGCTGCTCAACTGTCACTGTAATAGCTGCTTTCATAGCACACTC 190
QY 1118 TTTTGGACATCTTCCGGTA 1137
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Db 189 TTTTGGACATCTTCGGTA 170
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AGENCOURT_13894516 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
EST.
CB997937.1 GI:30292457
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.
Location/Qualifiers
1..522
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/db_xref="taxon:9606"
/clone="IMAGE:30348484"
/tissue_type="pre-ecampic placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH MGC 148"
note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTCTTTTCTTTTCTTTT-3', size-selected for average insert
size 2.3 kb and normalized to 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 9.0%; Score 404; DB 14; Length 522;
Best Local Similarity 96.2%; Pred. No. 1.5e-61;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 546 CTGCAGACGTGGCTGTGTATAGGAGCCCTGACATTTATATCCCGAGAACATCAGTTAA 605
DB 23 CTGCAGACGTGGCTGTGTATAGGAGCCCTGACATTTATATCCCGAGAACATCAGTTAA 82
QY 606 TGCGGTTTTTGTATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCG 665
DB 83 TGCGGTTTTTGTATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCG 142
QY 666 AGACCGGACACTGGCCATATCGGTGGTTCATATGCGCCAGCTTTCATCCCGATATGCA 725
DB 143 AGACCGGACACTGGCCATATCGGTGGTTCATATGCGCCAGCTTTCATCCCGATATGCA 202
QY 726 CACCGGGTAAAGTTACCGGAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGA 785
DB 203 CCACCGGGTAAAGTTACCGGAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGA 262
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QY 60 TAAATGATATAAATATCAATATTAATAATAGATTTTCATATAAAACAGACTCATRAA 119
 Db 487 TAAATGATATAAATATCAATATTAATAATAGATTTTCATATAAAACAGACTCATRAA 428
 QY 120 TACTGTAAACACACACATATCCAGTCACATAGATCAATCAACTACTAGATGGTATTAGTGAC 179
 Db 427 TACTGTAAACACACACATATCCAGTCACATAGATCAATCAACTACTAGATGGTATTAGTGAC 368
 QY 180 CTGTAGTCGACGACAGCCTTCGAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACC 239
 Db 367 CTGTAGTCGACGACAGCCTTCGAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACC 308
 QY 240 GACAGCCTTCGAATGTTCTTCGAACGGAATCGTGTATCCAGCTACTCCGCTATTGT 299
 Db 307 GACAGCCTTCGAATGTTCTTCGAACGGAATCGTGTATCCAGCTACTCCGCTATTGT 248
 QY 300 CCTCAATGCCGTATTAATATCAATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTT 359
 Db 247 CCTCAATGCCGTATTAATATCAATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTT 188
 QY 360 GTGTGACAAAATAAAACATCTAC-CTATTCATATAGCTAGTGTCTATGCTCTGAAAT 418
 Db 187 GTGTGACAAAATAAAACATCTACATATTCATATATCTTTAGTGTCTATGCTCCGAGTAT 128
 QY 419 CATCTGCATCAAGAACAAATTCACAACTCTTATCTTTTCTTTTACAAG 467
 Db 127 CTTCGGCATCATGACCAAGCAAGCCCTTTTATTAATGCTATCTTGGAG 79

RESULT 9
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 LOCUS OSTR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
 CB395230
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE CB395230.1 GI:30736941

ORGANISM Caenorhabditis elegans
 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 487)
 AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
 Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
 Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
 Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
 Doucette-Stamm, L., Hill, D.E. and Vidal, M.
 C. elegans ORFome version 1.1: experimental verification of the
 genome annotation and resource for proteome-scale protein
 expression

JOURNAL Nat. Genet. (2003) In press
 COMMENT Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFome
 cloning project : Contact david_hill@dfci.harvard.edu or
 marc.vidal@dfci.harvard.edu
 POLYA=No.

FEATURES
 source Location/Qualifiers
 1..487
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"

/clone lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

ORIGIN
 Query Match 7.8%; Score 347.4; DB 14; Length 487;
 Best Local Similarity 96.8%; Pred. No. 1.6e-51;
 Matches 365; Conservativity 0; Mismatches 11; Indels 1; Gaps 1;
 3291 TGTCTCTTGATGCAGATGAATTTTCAGGACTATACACTAGCTATATGAATAG-GTAGATG 3349
 Db 111 TGTTCATGATCGGAAGTACTCTCGGACTATGACACTAAAGTATATGAATATGTTAGATG 170
 QY 3350 TTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGAT 3409
 Db 171 CCTTTATTTTGTGCACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGAT 230
 QY 3410 TTAATACGGCATTGAGGACAATAGCGAGTAGCTGGATACGACGATTCGGTTTGAGAAGA 3469
 Db 231 TTAATACGGCATTGAGGACAATAGCGAGTAGCTGGATACGACGATTCGGTTTGAGAAGA 290
 QY 3470 ACATTTGGAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAGAAACATTTGGAAG 3529
 Db 291 ACATTTGGAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAGAAACATTTGGAAG 350
 QY 3530 CTGTGCGTGCATACAGGTCATATACCATCTAGTACTTGTATTCATAGTACGCTGATA 3589
 Db 351 CTGTGCGTGCATACAGGTCATATACCATCTAGTACTTGTATTCATAGTACGCTGATA 410
 QY 3590 TGTGTGTTTTTACAGTATTATGATGCTCTTTTTTATGCAAAATCTAAATTAATATATTG 3649
 Db 411 TGTGTGTTTTTACAGTATTATGATGCTCTTTTTTATGCAAAATCTAAATTAATATATTG 470
 QY 3650 ATATTATATCATTTTA 3666
 Db 471 ATATTATATCATTTTA 487

RESULT 10
 BI174407
 LOCUS
 DEFINITION
 BI174407.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
 F11F1.5, mRNA sequence.
 BI174407
 BI174407.1 GI:14640210
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE
 ORGANISM

REFERENCE 1 (bases 1 to 384)
 AUTHORS Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
 Jackson, C., Shin, I.T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
 Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
 Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.

TITLE Open-reading-frame sequence tags (OSTs) support the existence of at
 least 17,300 genes in C. elegans

JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
 MEDLINE 21135099
 PUBMED 11242119

COMMENT Contact: Reboul J, Vaglio P
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 44 Binney Street, Boston, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 2425
 Email: Jerome.Reboul@dfci.harvard.edu
 Sequence tag of Gateway entry clones. The primers used were
 designed on the predicted protein encoding ORF. C. elegans ORFome
 cloning project : Contact jerome_reboul@dfci.harvard.edu or

philippe_vaglio@dfci.harvard.edu

POLYA=No_ Location/Qualifiers

FEATURES

source

1.384

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="mixed stage"

/clone_lib="AD-wrmcDNA"

/notes="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

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Query Match          7.6%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 3.4e-50;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 101 TAAAAACAGACTACATACTGTGTAACACACACATATCCAGTCACTATGAATCAACTA 160
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Db 32 TAATACACAGACTACATACTGTGTAACACACACATATCCAGTCACTATGAATCAACTA 91

QY 161 CTTAGATGGTATTAGTCACTGTAGTCGCGCAGCGCTTCCAAATGTTCTTCGGGTGAT 220
    |||
Db 92 CTTAGATGGTATTAGTCACTGTAGTCGCGCAGCGCTTCCAAATGTTCTTCGGGTGAT 151

QY 221 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAACGGAAATCGTCGAT 280
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Db 152 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAACGGAAATCGTCGAT 211

QY 281 CCGACCTACTCGGTATTGTCCTCAATGCCGTATTAAATCATATAAGAAATAGAAAG 340
    |||
Db 212 CCAACCTACTCGGTATTGTCCTCAATGCCGTATTAAATCATATAAGAAATAGAAAG 271

QY 341 AGTGGCAGCGCTCTTTTGTGTCACAAATATAAATCACTTCTTATATATACGCTAG 400
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Db 272 AGTGGCAGCGCTCTTTTGTGTCACAAATATAAATCACTTCTTATATATACGCTAG 331

QY 401 TGTCAATAGTCGTAATCATCTGCATCAAGAACAAATTTCACTCTTATAC 453
    |||
Db 332 TGTCAATAGTCGTAATCATCTGCATCAAGAACAAATTTCACTCTTATAC 384

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RESULT 11
B1174407/c
LOCUS
DEFINITION OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
F11F1.5, mRNA sequence.

ACCESSION B1174407

VERSION B1174407.1 GI:14640210

KEYWORDS EST.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 384)

AUTHORS Rebol, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,

Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,

Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,

Brasch, M. A., Vandenhaute, J., Lamesch, P. F., Hill, D. E. and Vidal, M.

Open-reading-frame sequence tags (OSTs) support the existence of at

least 17,300 genes in C. elegans

Nat. Genet. 27 (3), 332-336 (2001)

21135099

11242119

COMMENT Contact: Rebol, J., Vaglio P

Marc Vidal Laboratory

Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.reboul@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu

POLYA=No_ Location/Qualifiers

source

1.384

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/sex="Hermaphrodite and male"

/tissue_type="whole animal"

/dev_stage="mixed stage"

/clone_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

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Query Match          7.3%; Score 325.4; DB 12; Length 384;
Best Local Similarity 98.2%; Pred. No. 1.4e-47;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3291 TGTTCCTGATGACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATGT 3350
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Db 366 TGTTCCTGATGACAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATGT 307

QY 3351 TTTTATTTTGTTCACACAAAAGAGGCTCGACCTCTTTCTTTCTTTTATGATT 3410
    |||
Db 306 TTTTATTTTGTTCACACAAAAGAGGCTCGACCTCTTTCTTTCTTTTATGATT 247

QY 3411 TAATACGGCATTTGAGGACCAATAGCGATAGGCTGGGATACGACGATTCGGTTTGAGAAGAA 3470
    |||
Db 246 TAATACGGCATTTGAGGACCAATAGCGATAGGCTGGGATACGACGATTCGGTTTGAGAAGAA 187

QY 3471 CATTGGAGGCTGTGCGTGCAGTAAAGTGGGAGCATCACCAGACACATTTGGAGGC 3530
    |||
Db 186 CATTGGAGGCTGTGCGTGCAGTAAAGTGGGAGCATCACCAGACACATTTGGAGGC 127

QY 3531 TGTGCGTGCAGTACAGTCACTTAATACCATCTAAGTAGTTGATTCATAGTGTGATAT 3590
    |||
Db 126 TGTGCGTGCAGTACAGTCACTTAATACCATCTAAGTAGTTGATTCATAGTGTGATAT 67

QY 3591 GTTGTGTTTACAGTATTATGATGCTGTTTTTTA 3625
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Db 66 GTTGTGTTTACAGTATTATGATGCTGTTTTTTA 32

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RESULT 12

BJ555980

LOCUS

DEFINITION BJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil

cDNA clone jml8n08 5', mRNA sequence.

ACCESSION BJ555980

VERSION BJ555980.1

KEYWORDS EST.

SOURCE Ipomoea nil (Japanese morning glory)

ORGANISM Ipomoea nil

REFERENCE 1 (bases 1 to 337)

AUTHORS Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,

Nitase, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.

ESTs of Japanese morning glory

Unpublished (2002)

BJ555980 337 bp mRNA linear EST 18-DEC-2002
Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jml8n08 5', mRNA sequence.

ACCESSION BJ555980

VERSION BJ555980.1

KEYWORDS EST.

SOURCE Ipomoea nil (Japanese morning glory)

ORGANISM Ipomoea nil

REFERENCE 1 (bases 1 to 337)

AUTHORS Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,

Nitase, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.

ESTs of Japanese morning glory

Unpublished (2002)

COMMENT

Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source
1..337
/organism="Ipomoea nil"
/mol_type="mRNA"
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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 2.6e-43;
Matches 313; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 546 CTCGAGCTGCTGTGTATTAAGGAGCGCTGACATTTATATTTCCCGAGACATCAGGTAA 605
DB 24 CTCGAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTTCCCGAGACATCAGGTAA 83
QY 606 TGGCGTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCACTTTTCCCGGATACCG 665
DB 84 TGGC-TTTTGTATGCCATTTTCGCGTGGCTGAGATCAGCCACTTTTCCCGGATACCG 142
QY 666 AGACCGGACACTGGCGATATCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCA 725
DB 143 AGACCGGACACTGGCGATATCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCA 202
QY 726 CCACGGGTAAAGTTACGGGAGACTTTATCTGACGACGACGTCGTCGCCAGGGGGA 785
DB 203 CCACGGGTAAAGTTACGGGAGACTTTATCTGACGACGACGTCGTCGCCAGGGGGA 262
QY 786 TCACCATCGTTCGCGCGCGCGTGTCAATTAATATCACTGTGACATCCCAACAGAGCAT 845
DB 263 TCACCATCGTTCGCGCGCGCGTGTCAATTAATATCACTGTGACATCCCAACAGAGCAT 322
QY 846 AACGCTCTCTCTTT 860
DB 323 AACGCTCTCTCTTT 337

RESULT 13

CF469981/c
LOCUS
DEFINITION
P7-B11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium
yoelii yoelii cDNA, mRNA sequence.
ACCESSION
CF469981
VERSION
CF469981.1 GI:34487353
KEYWORDS
EST.
ORGANISM
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 1068)
AUTHORS
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nusenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
Unpublished (2003)
JOURNAL
Contact: Bhanot P
Department of Pathology
New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
COMMENT
similar to NR|GI-23483806 hypothetical protein [Plasmodium yoelii
yoelii] (e-108).

FEATURES

source

Location/Qualifiers

1..1068
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev stage="axenic hepatic stages"
/lab_hosts="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exochytriotic malaria parasites does not require host
cells', (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN

Query Match 6.1%; Score 273.2; DB 14; Length 1068;
Best Local Similarity 90.0%; Pred. No. 1.7e-38;
Matches 278; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 571 GCGTGCATTTATATTTCCCGAGACATCAGGTAAATGGGTTTTCATCTCATTTTCGCG 630
DB 562 GCGTGCATTTATATTTCCCGAGACATCAGGTAAATGGGTTTTCATCTCATTTTCGCG 503
QY 631 GTGGCTGAGATCAGCCACTTTTCCCGGATACCGGAGACCGGACACTGCCCATATCGGT 690
DB 502 GTGGCTGAGATCAGCCACTTTTCCCGGATACCGGAGACCGGACACTGCCCATATCGGT 443
QY 691 GGTTCATCCTGCGGAGCTTTTCATCCCGGATATCACCCGCGGTAAAGTTACGGGAGAC 750
DB 442 GGNATCATGCGGAGCTTTTCATCCCGGATATCACCCGCGGTAAAGTTACGGGAGAC 383
QY 751 TTTATCTGACGAGAGCTGTCATGCGCAGGGGATCAGCATCCGTCGCCCGCGCTGTC 810
DB 382 TTTATCTGACGAGAGCTGTCATGCGCAGGGGATCAGCATCCGTCGCCCGCGCTGTC 323
QY 811 AATAATATCACTCTGTATATCCCAACAGACATACCGCTCTCTCTTTATAGGTGTA 870
DB 322 AANAATATCGCTCGGNNCATCCACNANANGANNANGNANGCGCTNTNTTTTTCACAGGTGNA 263
QY 871 AACCTTAA 879
DB 262 AACNTTGA 254

RESULT 14

CF469119/c
LOCUS
DEFINITION
P1CAB Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii
yoelii cDNA, mRNA sequence.
ACCESSION
CF469119
VERSION
CF469119.1 GI:34486491
KEYWORDS
EST.
ORGANISM
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 1037)
AUTHORS
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nusenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
Unpublished (2003)
JOURNAL
Contact: Bhanot P
Department of Pathology

New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
No Blast Hits ()

FEATURES source
1. .1037
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/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/notes="Vector: pCR4.OTOPO; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exochytronic malaria parasites does not require host
cells' (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN
Query Match 6.1%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 3.1e-38;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
571 GCCTGACATTATATCCCGAGACATCAGTTAATGGCGTTTGTGATGTCATTTTCGCG 630
496 GCTGACATTATATCCCGAGACATCAGTTAANGGCGTTTGTGATGTCATTTTCGCG 437
631 GTGGCTGAGATCAGCCACTTCTCCCGGATACCGGAGACCGGACACTGGCCATATCGGT 690
436 GTGGCTGAGATCAGCCACTTCTCCCGGATACCGGAGACCGGACACTGGCCATATCGGT 377
691 GGTATCATCGCCAGCTTTCATCCCGATATGACACCGGGTAAAGTTTCACGGGAGAC 750
376 GGTATCATCGCCAGCTTTCATCCCGATATGACACCGGGTAAAGTTTCACGGGAGAC 317
751 TTTATCTGACAGCAGATGTCACCTGGCCAGGGGATCACCATCGTCCCGGGCGGTGC 810
316 TTTATCTGACAGCAGATGTCACCTGGCCAGGGGATCACCATCGTCCCGGGCGGTGC 257
811 AATAATATCATCTGTATCATCCCAACAG--AGATAACGGCTCTCTTTTATAGTG 868
256 AATAAGATCATCTGTATCATCCCAACAG--AGATAACGGCTCTCTTTTATAGTG 197
869 TAAACCTTAACTGATTC 888
196 AAACCTTNNACNCCGNTC 177

RESULT 15
AG000791
LOCUS AG000791 724 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
survey sequence.
ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 724)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
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Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
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27 ACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCATTTACAGTCCCTGTCTCG 86
906 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTT 965
87 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTT 146
966 TCGCTTTTCCAGGTTTCGGCAGCAGACGAGGCTTCATTTCTGCAATGGTTGCTTACC 1025
147 TCGCTTTTCCAGGTTTCGGCAGCAGACGAGGCTTCATTTCTGCAATGGTTGCTTACC 206
1026 AGACCGGAGATATGACATCATATATATGCTTGAAGCAACTGATAGCTGCTGCTCACTG 1085
207 AGACCGGAGATATGACATC--ATATGCTTGAAGCAACTGATAGCTGCTGCTCACTG 264
1086 TCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGAACATACTTCGGGTA 1137
265 TCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGAACATACTTCGGGTA 316
Search completed: May 9, 2004, 21:55:51
Job time : 6945.71 secs

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 12095.6 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001b-13_COPY_13040_17900
Perfect score: 4861
Sequence: 1 cgggcccaataatgattt.....atcattatttggggcccgag 4861

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hug.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pin.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

SUMMARIES

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3	1193	24.5	4470	6	BD263377	BD263377 Compositi
4	1193	24.5	4939	6	BD263381	BD263381 Compositi
5	1193	24.5	5584	6	BD263402	BD263402 Compositi
6	1152.2	23.7	9019	12	AF408413	AF408413 Binary ve
7	1136	23.4	9019	12	AF408413	AF408413 Binary ve
8	1119	23.0	12677	12	AV196825	AV196825 PiggyBac
9	1111.2	22.9	12677	12	AV196825	AV196825 PiggyBac
10	1068.2	22.0	4165	6	BD263380	BD263380 Compositi
11	1032	21.2	4208	6	BD263379	BD263379 Compositi
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13	876.4	18.0	6742	12	AY048739	AY048739 CRIM plas
14	846.2	17.4	4204	6	BD263378	BD263378 Compositi
15	846.2	17.4	4470	6	BD263377	BD263377 Compositi
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ALIGNMENTS

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DEFINITION Cloning vector pHELLSGATE.
ACCESSION AJ311874
VERSION AJ311874.1 GI:15982218
KEYWORDS kanomycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; spec gene; spectinomycin resistance protein;
transposon Tn7.
SOURCE Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
REFERENCE 1
AUTHORS Wesley V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stcutjesdijk, A., Robinson, S.P.,

Gleave, A.P., Green, A.G. and Waterhouse, P.M.
 Construct design for efficient, effective and high-throughput gene
 silencing in plants
 Plant J. 27 (6), 581-590 (2001)
 21451301
 11576441
 2 (bases 1 to 18691)
 Waterhouse, P.M.
 Direct Submission
 Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
 C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
 Location/Qualifiers

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repeat_region

promoter

gene

intron

terminator

ORIGIN

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Qy      4861 G 4861
Db      17900 G 17900

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LOCUS      Cloning vector pHELLSGATE.
DEFINITION      AJ311874
ACCESSION      AJ311874
VERSION      AJ311874.1 GI:15982218
KEYWORDS      kanomycin resistance protein; neomycin phosphotransferase II; nptII
              gene; promoter; spec gene; spectinomycin resistance protein;
              transposon Tn7.
SOURCE      Cloning vector pHELLSGATE
ORGANISM      Cloning vector pHELLSGATE
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REFERENCE      1
AUTHORS      Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
              Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
              Gleave,A.P., Green,A.G. and Waterhouse,P.M.
              Construct design for efficient, effective and high-throughput gene
              silencing in plants
              Plant J. 27 (6), 581-590 (2001)
JOURNAL      21461301
MEDLINE      11576441
PUBMED
REFERENCE      2 (bases 1 to 18691)
AUTHORS      Waterhouse,P.M.
TITLE      Direct Submission
JOURNAL      Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
              C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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RESULT 3

BD263377

LOCUS

DEFINITION

BD263377

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ON

PD

PF

PI

C12N15/09

00.C12N5/00

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BD263377 4470 bp DNA linear PAT 17-JUL-2003

Compositions and methods for use in recombinational cloning of

nucleic acids.

BD263377 1. GI:33073145

JP 2002537790-A/155.

synthetic construct

artificial sequences.

1 (bases 1 to 4470)

Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.

Compositions and methods for use in recombinational cloning of

nucleic acids

Patent: JP 2002537790-A 155 12-NOV-2002;

INVITROGEN CORP

ON JP 2002537790-A/155

PD 12-NOV-2002

PF 02-MAR-2000 JP 2000602252

PI 28-MAY-1999 US 60/136744

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC

00.C12N5/00

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FEATURES

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RESULT 4
BD263381
LOCUS BD263381 4939 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263381
VERSION BD263381.1 GI:33073149
KEYWORDS JP 2002537790-A/159.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4939)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N15/10, C12N15/ PC
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FH Key Location/Qualifiers
FT source 1. .4939
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ORIGIN
Query Match 24.5%; Score 1193; DB 6; Length 4939;
Best Local Similarity 100.0%; Pred. No. 4.4e-174;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 CCTTCCAAATGTTTCTTCTCAAAACGGAATCGTATCCAGCTTACTCGCTATTGTCTCA 360
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QY 421 AAAAAATAAAAAATATACCTATTATATACGCTAGTGTATAGTCTGAAAAATCATCTG 480
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QY 481 CATCAAGAACAAATTTCAAACTCTTATACCTTTTCTTTTCAAGTCGTTCCGCTTTCATCTG 540
Db 4035 CATCAAGAACAAATTTCAAACTCTTATACCTTTTCTTTTCAAGTCGTTCCGCTTTCATCTG 4094
QY 541 GATTTTCAGCCTCTATATCTTACTTAAACGTCGATAAAGTTTCTGTAATTTCTACTGTATPCGA 600
Db 4095 GATTTTCAGCCTCTATATCTTACTTAAACGTCGATAAAGTTTCTGTAATTTCTACTGTATPCGA 4154
QY 601 CTGACACTGGCTGTGTATTAAGGAGCCCTGACATTTATATATCCCCAGAACATCAGTTA 660
Db 4155 CTGACACTGGCTGTGTATTAAGGAGCCCTGACATTTATATATCCCCAGAACATCAGTTA 4214
QY 661 ATGSCGTTTTTGTATGTCATTTTTCGCGTGCTGAGATCAGCCACTTCTTCCCGATAACG 720
Db 4215 ATGSCGTTTTTGTATGTCATTTTTCGCGTGCTGAGATCAGCCACTTCTTCCCGATAACG 4274
QY 721 GAGACCGGACACTGGCCATATCGTGGTTCATCATATGCGCCAGCTTTCATCCCGATATGC 780
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QY 781 ACCACCGGTAAAGTTTCAACGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGG 840
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QY 841 ATACCAATCCGTCGCGCGGCGTGTCAATAATATCACTCTGTATCATCCACAAACAGACGA 900
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QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGGAGCAACTGATAGCTGTGCGTGTCAACT 1140
Db 4635 CAGACCGGAGATATTGACATCATATATGCTTGGAGCAACTGATAGCTGTGCGTGTCAACT 4694
QY 1141 GTCACGTGAATACGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 1193
Db 4695 GTCACGTGAATACGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 4747

RESULT 5
BD263402/C
LOCUS BD263402 5584 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263402
VERSION BD263402.1 GI:33073170
KEYWORDS JP 2002537790-A/180.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

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REFERENCE	1 (bases 1 to 5584)
AUTHORS	Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL	Patent: JP 2002537790-A 180 12-NOV-2002;
COMMENT	INVITROGEN CORP
	OS Artificial Sequence
	PN JP 2002537790-A/180
	PD 12-NOV-2002
	PF 02-MAR-2000 JP 2000602252
	PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
	PT 12-MAY-1999 US 60/136744
	PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
	C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N15/00, C12N5/00
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	FH Key
	FT source
	FT
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Db	5564 CGGGCCCCAAATAATGATTTTATTTTGCATGATGACTGCTGTTGCTGCAACAAATTGA 5505
Qy	61 TGAGCAATGCTTTTATATGCAACTTTGTACAAAAGCTGACGAGAAACGTAAAA 120
Db	5504 TGAGCAATGCTTTTATATATGCAACTTTGTACAAAAGCTGACGAGAAACGTAAAA 5445
Qy	121 TGATATAATATCAATATATAATTAAGATTTTGCATATAAAAAACAGACTACATAACTG 180
Db	5444 TGATATAATATCAATATATAATTAAGATTTTGCATATAAAAAACAGACTACATAACTG 5385
Qy	181 TAAACACACATATCCAGTCACTAGTAATCAACTAGATTAGATTAGTACCTGTA 240
Db	5384 TAAACACACATATCCAGTCACTAGTAATCAACTAGATTAGATTAGTACCTGTA 5325
Qy	241 GTCCACCGACAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTAGTCGACCCACAG 300
Db	5324 GTCCACCGACAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTAGTCGACCCACAG 5265
Qy	301 CTTTCCAAAATGTTCTTCTCAAAACGGAAATCGTCGTAATCCAGCCTACTGCTATTGTCTCA 360
Db	5264 CTTTCCAAAATGTTCTTCTCAAAACGGAAATCGTCGTAATCCAGCCTACTGCTATTGTCTCA 5205
Qy	361 ATGCGGTATTAAATCATATAAAGAAATAAGAAAAGAGTGCAGAGCCTCTTTTGTGTG 420
Db	5204 ATGCGGTATTAAATCATATAAAGAAATAAGAAAAGAGTGCAGAGCCTCTTTTGTGTG 5145
Qy	421 ACAAAATAAAAAACATCTACCTATTTCATATACGCTAGTGTCTATAGTCTCGAAATCATCTG 480
Db	5144 ACAAAATAAAAAACATCTACCTATTTCATATACGCTAGTGTCTATAGTCTCGAAATCATCTG 5085
Qy	481 CATGAGAACAAATTTCACAACTCTTATACCTTTCTCTACAGTCGTTCCGCTTCATCTG 540
Db	5084 CATCAAGAACAAATTTCACAACTCTTATACCTTTCTCTTACAAGTCGTTCCGCTTCATCTG 5025
Qy	541 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
Db	5024 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 4965
Qy	601 CCTGCAGACTGGCTGTGTATTAAGGGAGCCTGACATTTATATTTCCCGAGAACATCAGTTA 660
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1263..1568
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1610..1736
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1762..2048
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misc_feature
complement(2073..2199)
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Best Local Similarity 68.8%; Pred. No. 7.8e-168;
Matches 1777; Conservative 0; Mismatches 678; Indels 128; Gaps 9;

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|||
Db 3587 TTAGGATCCGTCGAGATTTTCAGAGCTAAGGAAGCTAAATAGGAGAAAAAATCATCGG 3528
|||
QY 1983 ATATACCACCGTTGATATATATCCCAATGGCATCGTAAAGAACATTTTCAGGCAATTCAGTC 2042
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Db 3527 ATATACCACCGTTGATATATATCCCAATGGCATCGTAAAGAACATTTTCAGGCAATTCAGTC 3468
|||
QY 2043 AGTTGCTCAATGTACCTATAAACCAGACCGTTCAGCTGGATATTACGGCCCTTTTAAAGAC 2102
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Db 3467 AGTTGCTCAATGTACCTATAAACCAGACCGTTCAGCTGGATATTACGGCCCTTTTAAAGAC 3408
|||
QY 2103 CGTAAAGAAAAATGAAGACAAAGTTTATCCGGCTTTTATCACATTTCTCCCGCCCTGAT 2162
|||
Db 3407 CGTAAAGAAAAATGAAGACAAAGTTTATCCGGCTTTTATCACATTTCTCCCGCCCTGAT 3348
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QY 2163 GAATGCTCATCCGGAATTTCCGTATGGCAATGAAGACCGTGAGCTGGTATATGGGATAG 2222
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Db 3347 GAATGCTCATCCGGAATTTCCGTATGGCAATGAAGACCGTGAGCTGGTATATGGGATAG 3288
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QY 2223 TGTTCAACCTTTGTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAG 2282
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Db 3287 TGTTCAACCTTTGTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAG 3228
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QY 2283 TGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGCGGTGTTA 2342
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Db 3227 TGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGCGGTGTTA 3168
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QY 2343 CGGTGAAAACTCGGCTATTTCCCTAAAGGGTTTATTTGAGAAATATGTTTTTCGCTCAGC 2402
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Db 3167 CGGTGAAAACTCGGCTATTTCCCTAAAGGGTTTATTTGAGAAATATGTTTTTCGCTCAGC 3108
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QY 2463 CGCCCCGTTTTTACCAGTGGGCAATATATACCAAGGGCCAGAGGTGCTGATGCGCCT 2522
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Db 3047 CGCCCCGTTTTTACCAGTGGGCAATATATACCAAGGGCCAGAGGTGCTGATGCGCCT 2988
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QY 2523 GCGGATTCAGGTTTCATCATGCGCTCTGTGATGGCTTCATGCTCGCAGAAATGCTTAATGA 2582
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Db 2987 GCGGATTCAGGTTTCATCATGCGCTCTGTGATGGCTTCATGCTCGCAGAAATGCTTAATGA 2928
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QY 2583 ATTACACAGTACTCGGATGAGTGGCAGGGGGCGCTAATCGCGTGGATCGGCTTACT 2642
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Db 2927 ATTACACAGTACTCGGATGAGTGGCAGGGGGCGCTAATCGCGTGGATCGGCTTACT 2868
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QY 2643 AAAAGCCAGATAACAGTATGCTATTTTCGGCGCTGATTTTCGGGTATAAGAAATATATAC 2702
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Db 2867 AAAAGCCAGATAACAGTATGCTATTTTCGGCGCTGATTTTCGGGTATAAGAAATATATAC 2808
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QY 2703 TGATATGTGGGCCCATTAATAGT---AATTCAGCTGGTTTGAATGAATTAATCAATG 2759
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Db 2807 TGATATGTATACCCGAGATGTCTCAAAAAGAGGTGTCTATGAAGCAGCGTATTACAGTG 2748
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QY 2760 ATAAATACTACTAGTAAATAAATGAATAAATAAATAAATAAATAAATAAATAAATAA 2819
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Db 2747 ACAGTTGACGCGCAGCTATCAGTTGCTCAAGGCATATATGATGCTCAATATCTCCGGTC 2688
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QY 2820 TAGTTTATTTATATAAATAATCTATACCTACTATAAATAATTTTAGTTTAAAGTAAAT 2879
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Db 2687 TGGTAAGCACACCATCGAGATGAAGCCGCTCGTGGTCCGACCGTGGAAAGCGG 2628
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QY 2880 AAATAATTTTGTAGAAATTCCAATCTGCTGTGTAATTTATCAATAAACAATAATTAATA 2939
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Db 2627 AAAATCAGGAAGGATGGCTGAGGTGCGCCGGTTTATTTGAAATGAACGCGCTCTTTTGCTG 2568
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QY 2940 ACAAGCTAAAGTAAACAATAATATCAAACTAATAGAAACAGTAAATCTAATGTA----- 2992
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Query Match 23.7%; Score 1152.2; DB 12; Length 9019;

ORIGIN

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	/gene="Cmr"			1983	ATATACACACCGTTGATATATCCCAATGGCATCGTAAGAAACATTTTGAAGCATTTTCAGTC	2042
	/function="confers resistance to antibiotic chloramphenicol"			282	ATATACACACCGTTGATATATCCCAATGGCATCGTAAGAAACATTTTGAAGCATTTTCAGTC	341
	/codon_start=1			2043	AGTTGCTCAATGACCTATTAACGAGACCGTTTCAGCTGATATACGCGCTTTTAAAGAC	2102
gene	/protein_id="AAM62300.1"			342	AGTTGCTCAATGACCTATTAACGAGACCGTTTCAGCTGATATACGCGCTTTTAAAGAC	401
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				2163	GAATGCTCATCCGGAATTCGATATGGCAATGAAGAAGCGTGAGCTGGTGATATGGGATAG	2222
CDS	/gene="ccdB"	1263..1568		462	GAATGCTCATCCGGAATTTCCGATATGGCAATGAAGAAGCGTGAGCTGGTGATATGGGATAG	521
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	/note="encodes a cytotoxic protein that is a potent poison of DNA gyrase"			522	TGTTTCAACCTTGTTACACCGTTTCCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAG	581
	/product="CcdB"			2283	TGAATACACACGACGATTTCCGCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTA	2342
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				2403	CAATCCCTGGGTGAGTTTTCACAGTTTGTATTAACCGTGCCCAATATGGAACAATCTTCT	2462
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	/note="antisense orientation of Gateway conversion cassette frame A containing attR1-R2 repeats, Cmr gene and ccdB gene"			762	CGCCCCCTTTTCCACATGCGGCAATATATATACGAGCGCACAAGGTGCTGATGCCCT	821
				2523	GGCGATTGAGTTTCCATGATGCGCTGCTGATGGCTTCCATGTCGCGCAGAACTCTTAAGA	2582
gene	/gene="ccdB"	1263..1568		822	GGCGATTGAGTTTCCATGATGCGCTGCTGATGGCTTCCATGTCGCGCAGAACTCTTAAGA	881
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	/product="CcdB"			882	ATTACAAACAGTACTGCGATGAGTGGCAGCGGGCGGCGTAATCGCGTGGATCGGCTTACT	941
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	/complement(2241..2546)			1002	TGATATGTCGGGCCCATTAATAGT---AATTCTAGCTGGTTTTCATGAATTAATAATCAATG	1061
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				2999	CATAATCTAATGCTAATATATAACAAGCGCAAGATCTATCATCTTATATATAGTATTATTTTC	3058
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	/note="attR1 of Gateway conversion cassette frame A"					
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	Matches 1766;	Conservative 0;				
	Mismatches 690;	Indels 126;				
Gaps	9;					
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Db 1302 TATCGTCTGTGTTGTGATGTACAGAGTGATATTTATGACACGCCCGGCGAGCGGATGGTG 1361
QY 3059 AATCAACATCTTATTAATTTCTAAATAATACTGTAGTATTTATTAATCTCTAAATGGAT 3118
Db 1362 ATCCCCCTGGCCAGTCACGCTCTGCTGTGATGAATAGTCTCCCGTCACTTTACCCGGTG 1421
QY 3119 TGACTATTAATTAATGAATAGTGAACATGAATGAATGAATGAATGAATGAATGAATGAAT 3178
Db 1422 GTGCATATCGGGGATGAAGAGCTGGCGCATGATGACACCGATATGCGCCAGTGTGCGGGTC 1481
QY 3179 TCATT-----GTGTTATCATTTGATCTTTACATTTGATTTGATTTACAGTT 3221
Db 1482 TCGTTATCGGGGAAGAGTGGCTGATCTGACCCCGGGAATGACATCAAAACGCC 1541
QY 3222 GGGAAATTTGGGTTTC-----GAAATCGATAAGCTTGGATCTCTAGAGA-----GCTGCA 3270
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QY 3271 GCTGGATGGCAATATGATTTTATTTGACTGATGATGACCTGTTGCTGGTGAACAAATTT 3330
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Db 1662 CAAAATCTAATTAATATATGATATTTATATCATTTTACGTTCTCGTTACGTTTCTT 1721
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QY 3463 CATATCCAGTCACTATGAATCAACTACTTAGATGATGATGATGATGATGATGATGATGAT 3522
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QY 3523 T-----TGGCAGCATCACCGGAGCACTTTGGG 3550
Db 1902 TATGGGTCAACGGTTTCAAGAGAGAGAAAGACTTTTAGAGTCAACTCTGACTCTTTCT 1961
QY 3551 CCGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCCTGGTGCCTG 3610
Db 1962 TAATATGTTATGCTATTTGCTCTTTCTTCTGAACTGCAATCTTGGGATGTTT 2021
QY 3611 TTGATACCGGGAAGCCCTGGCCCAACTTTTGGGAAATGAGAGCTGTGATCGGCATACC 3670
Db 2022 TGCAGGTTCTAGCTTCTCCAAACACAGGAATTCATCGCCCGGACTGGGTTATCAACACT 2081
QY 3671 CATTTCAACTCTTATACATTTCTCTTACAGTCTGTTGGCTTCATCTCGATTTTTCAGC 3730
Db 2082 TTGTACAGAAAGCTGAACGAGAAACGTAAATGATATAAATCAATATATTAATTAATAG 2141
QY 3731 CTCTATCTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTA----- 3776
Db 2142 ATTTTGATATAAAGACAGCTACATATCTGTAATAAACAACATATCCAGTCACTATGG 2201
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Db 2202 TCGACCTGACAGCTGGCTGTGATAGGAGCCCTGACATTTATATCCCGAGAACATCAG 2261
QY 3837 GTTAATGGGTTTTTGTATGATCATTTTTCGGGTGCTGAGATCAGCACTCTTCTCCCGAT 3896
Db 2262 GTTAATGGGTTTTTGTATGATCATTTTTCGGGTGCTGAGATCAGCACTCTTCTCCCGAT 2321
QY 3897 AACGGAGCCGGCACTGGCCATATCGTGGTTCATCATGCGCAGCTTTTATCCCGAT 3956
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RESULT 8
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LOCUS PiggyBac transformation vector pb-UGIR w+, complete sequence.
DEFINITION AY196825
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
KEYWORDS
SOURCE piggyBac transformation vector pb-UGIR w+
ORGANISM piggyBac transformation vector pb-UGIR w+
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in *Drosophila* using
JOURNAL piggyBac
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC
27709, USA

FEATURES
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QY	3084	--ATAATACCTTGTAGTTTATTAACTTTCTAAATGG-----	3121				
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DB	2830	ACTTGGCAGAAACGAAATCTATCTAATATCCGTAGCGCTATAATGTGTAGTATAGCGA	2889				
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Qy 3184 -----GTGTTATCATTTGATCTTACATTTGATTTGATTTGATTTGATTTGATTTGAT 3232
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RESULT 10

BD263380

LOCUS

DEFINITION

BD263380

BD263380

VERSION

BD263380.1

KEYWORDS

JP 2002537790-A/158

SOURCE

synthetic construct

ORGANISM

artificial sequences

REFERENCE

1 (bases 1 to 4165)

AUTHORS

Hartley, J.L., Brasch, M.A., Temple, G.P. and Cheo, D.

TITLE

Compositions and methods for use in recombinational cloning of

nucleic acids

JOURNAL

Patent: JP 2002537790-A 158 12-NOV-2002;

COMMENT

INVITROGEN CORP

OS

Artificial Sequence

PN

JP 2002537790-A/158

PD

12-NOV-2002

PF

02-MAR-2000

JP 2000602252

PR

02-MAR-1999

US 60/122389

23-MAR-1999

US 60/126049

PR 28-MAY-1999

US 60/136744

BD263380 4165 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of
nucleic acids.

BD263380
BD263380.1 GI:33073148
JP 2002537790-A/158
synthetic construct
artificial sequences

REFERENCE
1 (bases 1 to 4165)
Hartley, J.L., Brasch, M.A., Temple, G.P. and Cheo, D.
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nucleic acids

Patent: JP 2002537790-A 158 12-NOV-2002;
INVITROGEN CORP
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PD
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PF
02-MAR-2000 JP 2000602252
PR
02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744

	PI	JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO	PC
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QY	781	ACCACCGGTAAGTTTACCGGGAGACTTTATCTGACAGCAGAGTGCACCTGGCCAGGGG 840									
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DEFINITION CRIM plasmid pCAH63, 4782 bp DNA circular SYN 17-OCT-2001
ACCESSION AY048740
VERSION AY048740.1 GI:16209176
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ORIGIN

Query Match 18.0%; Score 876.4; DB 12; Length 4782;
Best Local Similarity 71.6%; Pred. No. 2.4e-125;
Matches 1259; Conservative 0; Mismatches 441; Indels 58; Gaps 6;

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DB 4299 TGAGAGCTTGTATCGGCACGTAAGAGGTTCCAACTTTTCCACATAATGAATAAGATCACTA 4240
QY 1912 CCGGGCGTATTTTTCAGTTATTCGAGATTTTCAGAGGCTTAAGAGCTTAATGAGGAAA 1971
DB 4239 CCGGGCGTATTTTTCAGTTATTCGAGATTTTCAGAGGCTTAAGAGCTTAATGAGGAAA 4180
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QY 2092 TTTTAAAGACCGTAAGAAATAAGACACAGTTTTCACGCTTTTATCCGCTTTTATTCACATTCCT 2151
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QY 2152 GCGCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGTGAGCTGGTG 2211
DB 3999 GCGCGCTGATGAATGCTCATCCGAAATTCGGTATGGCAATGAAGACGGTGAGCTGGTG 3940
QY 2212 ATATGGATAGTGTTCACCGCTTTACACCGTTTTCATGAGCAGAACTGAAACGTTTTCAC 2271
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RESULT 13

AY048739/c
LOCUS 6742 bp DNA
DEFINITION CRIM plasmid pCAH56, complete sequence.
ACCESSION AY048739
VERSION AY048739.1 GI:16209172
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE

CRIM plasmid pCAH56
artificial sequences; vectors.
1 (bases 1 to 6742)
Haldemann, A. and Wanner, B.L.
Conditional-replication, integration, excision, and retrieval
plasmid-host systems for gene structure-function studies of
bacteria
J. Bacteriol. 183 (21), 6384-6393 (2001)
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11591683
2 (bases 1 to 6742)

AUTHORS	Haldemann, A. and Wanner, B.I.
TITLE	Direct Submission
JOURNAL	Submitted (29-JUL-2001) Biological Sciences, Purdue University, Lilly Hall, West Lafayette, IN 47907, USA
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Query Match	18.0%; Score 876.4; DB 12; Length 6742;
Best Local Similarity	71.6%; Pred. No. 2.3e-125;
Matches 1259; Conservative	0; Mismatches 441; Indels 58; Gaps 6;
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RESULT 14
BD263378
LOCUS
DEFINITION BD263378 4204 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263378 1 GI:33073146
VERSION BD263378.1
KEYWORDS JP 2002537790-A/156.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4204)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 156 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/156
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
00, C12N5/00
CC pDONR202
CC attP1
CC ori
CC KmR
CC attP2
CC CmR
CC inactivated codA
CC ccdB
CC Key
FH Location/Qualifiers
(127) . . (269)
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FT gene (486) . . (1059)
FT gene (1228) . . (2107)
FT gene (2140) . . (2381)
FT gene (2629) . . (3288)
FT gene (3408) . . (3492)
FT gene (3630) . . (3935).
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 98.5%; Pred. No. 1.1e-120; Indels 0;
Matches 854; Conservative 0; Mismatches 13; Gaps 0;
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Db 2518 TGAGACGTTGATCGGCACGTAAGAGTTCCAACTTTCCACCATAATGAATAAGATCACTA 2577
QY 1912 CCGGCGGATATTTTGGAGTTATCGAGATTTTCAGAGCTAAGGAAGCTTAAATGAGAAA 1971
Db 2578 CCGGCGGATATTTTGGAGTTATCGAGATTTTCAGAGCTAAGGAAGCTTAAATGAGAAA 2637
QY 1972 AAAATCACTGGATATACACACCGTTGATATATCCCAATGGCATCGTAAAGAAACATTTTGAG 2031
Db 2638 AAAATCACTGGATATACACACCGTTGATATATCCCAATGGCATCGTAAAGAAACATTTTGAG 2697
QY 2032 GCATTTCACTAGTGTGCTCAATGTACTATATACAGACCGTTTCAGCTGGATATACGGCC 2091
Db 2698 GCATTTCACTAGTGTGCTCAATGTACTATATACAGACCGTTTCAGCTGGATATACGGCC 2757
QY 2092 TTTTAAAGACCGTAAAGAAATAAAGCAAGTTTATCCGGCCTTTATTCACATCTTT 2151
Db 2758 TTTTAAAGACCGTAAAGAAATAAAGCAAGTTTATCCGGCCTTTATTCACATCTTT 2817
QY 2152 GCCCGCTGATGAATGCTCATCCGGAATTCCTGTGGCAATGGAAGACGGTGAGCTGGTG 2211
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QY 2212 ATATGGATAGTGTTCACCCCTTTGTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 2271
Db 2878 ATATGGATAGTGTTCACCCCTTTGTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 2937
QY 2272 TCGCTCTGGAGTGAATACCAACGAGTTTCGCGAGTTTCTACATATATTCGCAAGAT 2331
Db 2938 TCGCTCTGGAGTGAATACCAACGAGTTTTCGCGAGTTTCTACATATATTCGCAAGAT 2997
QY 2332 GTGGCGTGTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTCAGAAATATGTTT 2391
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QY 2392 TTGCTCTAGCCATATCCCTGGGTGAGTTTCACAGTTTGTATTAACGTCGCAATATG 2451
Db 3058 TTGCTCTAGCCATATCCCTGGGTGAGTTTCACAGTTTGTATTAACGTCGCAATATG 3117
QY 2452 GACAACTCTTCGCCCCCGCTTTTACCATTGGGCAATAATATATACGCAAGCGCAAGGTG 2511
Db 3118 GACAACTCTTCGCCCCCGCTTTTACCATTGGGCAATAATATATACGCAAGCGCAAGGTG 3177
QY 2512 CTGATCCCGCTGGCGATTACAGTTTCATCATCGCTGTGATGGCTTCATGTCGCGAGA 2571
Db 3178 CTGATCCCGCTGGCGATTACAGTTTCATCATCGCTGTGATGGCTTCATGTCGCGAGA 3237
QY 2572 ATGCTTAATGAATTAACAACAGTACTCGGATGAGTGGCGGGCGGCTAAATCGCGTGA 2631
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QY 2632 TCCGGCTTACTAAAGCCAGATAACAGTATGCGCTATTTTTCGCGCTGATTTTTCGCGTATA 2691
Db 3298 TCCGGCTTACTAAAGCCAGATAACAGTATGCGCTATTTTTCGCGCTGATTTTTCGCGTATA 3357
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QY 2692 AGAATATATCTGATATGTCGGGCCCA 2718
Db 3358 AGAATATATCTGATATGATATACCGCA 3384

RESULT 15

BD263377/c

LOCUS

DEFINITION

BD263377

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PATENT

INVENTOR

OS

PN

PD

PF

PR

PI

C12N15/09

C07K14/00

C12N1/15

C12N1/21

C12N1/10

C12N1/15

C12N1/10

C12N1/15

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QY 2692 AGAATATATCTGATATGTCGGGCCCA 2718
Db 3358 AGAATATATCTGATATGATATACCGCA 3384

BD263377

Compositions and methods for use in recombinational cloning of

nucleic acids.

BD263377

JP 2002537790-A/155.

synthetic construct

artificial sequences.

1 (bases 1 to 4470)

Compositions and methods for use in recombinational cloning of

nucleic acids

Hartley J.L., Brasch M.A., Temple G.F. and Cheo D.

Compositions and methods for use in recombinational cloning of

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Patent: JP 2002537790-A 155 12-NOV-2002;

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C07K14/00

C12N1/15

C12N1/21

C12N1/10

C12N1/15

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C12N1/21

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QY 2692 AGAATATATCTGATATGTCGGGCCCA 2718
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C12N15/09

C07K14/00

C12N

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1119.77 Seconds
(without alignments)
18441.778 Million cell updates/sec

Title: US-10-055-001b-13_copy_13040_17900

Perfect score: 4861

Sequence: 1 cggggcccaataatgattt.....atcattattggggcccgag 4861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_25Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2563.2	52.7	17476	6	ABQ82141 Acceptor
3	2528	52.0	17681	6	ABQ82143 Acceptor
4	2510.6	51.6	17458	6	ABQ82142 Acceptor
c 5	1462.6	30.1	18691	6	ABQ82130 Acceptor
6	1193	24.5	4470	3	AAC55521 Donor pla
7	1193	24.5	4470	3	ABZ58767 Destinati
8	1193	24.5	4892	8	ADA50329 Plasmid v
9	1193	24.5	4939	3	AAC55525 Donor pla
c 10	1193	24.5	5584	3	AAC55632 Donor pla
c 11	1193	24.5	5584	7	ABZ58766 Donor pla
12	1186.6	24.4	4428	7	ABZ58768 Destinati
13	1186.6	24.4	4627	7	ABZ58769 Destinati
14	1186.6	24.4	4627	7	ABZ58770 Destinati
15	1068.2	22.0	4165	3	AAC55524 Donor pla
16	1032	21.2	4208	3	AAC55523 Donor pla
17	846.2	17.4	4204	3	AAC55522 Donor pla
c 18	846.2	17.4	4428	7	ABZ58768 Destinati
c 19	846.2	17.4	4470	3	AAC55521 Donor pla
c 20	846.2	17.4	4470	7	ABZ58767 Destinati
c 21	846.2	17.4	4627	7	ABZ58769 Destinati
c 22	846.2	17.4	4627	7	ABZ58770 Destinati
c 23	846.2	17.4	4892	8	ADA50329 Plasmid v

24	846.2	17.4	5584	3	AAC555632	Donor pla
25	846.2	17.4	5584	7	ABZ58766	Donor pla
26	844.6	17.4	1846	6	AD44626	Gateway t
27	844.6	17.4	4208	3	AAC55523	Donor pla
28	844.6	17.4	5156	3	AAC55526	Donor pla
29	844.6	17.4	5848	3	AAC55481	Destinati
30	844.6	17.4	5957	3	AAC55467	Destinati
31	844.6	17.4	5957	3	AAC55464	Destinati
32	844.6	17.4	6422	3	AAC55483	Destinati
33	844.6	17.4	6464	3	AAC55454	Destinati
34	844.6	17.4	6464	7	ABZ58765	Destinati
35	844.6	17.4	6526	3	AAC55471	Destinati
36	844.6	17.4	6553	3	AAC55456	Destinati
37	844.6	17.4	6613	3	AAC55493	Destinati
38	844.6	17.4	6668	3	AAC55495	Destinati
39	844.6	17.4	6708	3	AAC55475	Destinati
40	844.6	17.4	6964	3	AAC55461	Destinati
41	841.4	17.3	4554	3	AAC55541	atR read
42	841.4	17.3	8815	3	AAC55630	Destinati
43	841.4	17.3	8923	3	AAC55504	Destinati
44	841.4	17.3	11713	3	AAC55501	Destinati
45	841.4	17.3	12288	3	AAC55629	Destinati

ALIGNMENTS

RESULT 1

ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.

XX AC ABQ82130;

XX DT 11-DEC-2002 (first entry)

XX DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.

XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;

XX KW recombination site; double stranded RNA; plant; ds.

XX OS Synthetic.

XX PN WO200259294-A1.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-AU000073.

XX PR 26-JAN-2001; 2001US-0264067P.

XX PR 29-NOV-2001; 2001US-0333743P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Wesley S, Waterhouse P, Helliwell C;

XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

XX Claim 13; Page 62-72; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.

Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

Query Match 100.0%; Score 4861; DB 6; Length 18691;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TGAGCAATGCTTTTATATGTCACCACTTTGTACAAAAAGCTGAAACGAGAAACGTAAAA	120
DB	13100	TGAGCAATGCTTTTATATGTCACCACTTTGTACAAAAAGCTGAAACGAGAAACGTAAAA	13159
QY	121	TGATATAATATCAATATATTAATTAATAGATTGCAATTAATAAACAAGACATACATACTG	180
DB	13160	TGATATAATATCAATATATTAATTAATAGATTGCAATTAATAAACAAGACATACATACTG	13219
QY	181	TAAACACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGGTATTAGTACCTGTA	240
DB	13220	TAAACACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGGTATTAGTACCTGTA	13279
QY	241	GTGACCGACAGCCTTCCAAATGTTCTTCCGGTGATGCTGCCAATTAAGTCCGACGACAG	300
DB	13280	GTGACCGACAGCCTTCCAAATGTTCTTCCGGTGATGCTGCCAATTAAGTCCGACGACAG	13339
QY	301	CCCTCCAAATGTTCTTCCAAACGGAATCGTGTGATCCAGCCTACTCGCTATTGCTCTCA	360
DB	13340	CCCTCCAAATGTTCTTCCAAACGGAATCGTGTGATCCAGCCTACTCGCTATTGCTCTCA	13399
QY	361	ATGCCGTATTAAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTTTGTGTG	420
DB	13400	ATGCCGTATTAAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTTTGTGTG	13459
QY	421	ACAAATATAAACAATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAATCATCTG	480
DB	13460	ACAAATATAAACAATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAATCATCTG	13519
QY	481	CATCAAGAACAAATTCACAACTCTATCTTTCTCTTCAAGTCTGTCGCTTCACTG	540
DB	13520	CATCAAGAACAAATTCACAACTCTATCTTTCTCTTCAAGTCTGTCGCTTCACTG	13579
QY	541	GAATTTTCAAGCCTCTACTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA	600
DB	13580	GAATTTTCAAGCCTCTACTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA	13639
QY	601	CCCTGACAGCTGGTGTATTAAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	660
DB	13640	CCCTGACAGCTGGTGTATTAAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	13699
QY	661	ATGGCGTTTTTGATGTCATTTTCGCGTGGCTCAGATCAGCCACTTCTTCCCGATAACG	720
DB	13700	ATGGCGTTTTTGATGTCATTTTCGCGTGGCTCAGATCAGCCACTTCTTCCCGATAACG	13759
QY	721	GAGACCGGACACTGGCCATATCGGTGGTTCATCGCCAGCTTTCATCCCGCATATGCG	780
DB	13760	GAGACCGGACACTGGCCATATCGGTGGTTCATCGCCAGCTTTCATCCCGCATATGCG	13819
QY	781	ACCACCGGGTAAAGTTTCA CGGAGACTTTATCTGACAGCAGCTGCACCTGCGCGGGG	840

DB	13820	ACCACCGGGTAAAGTTTCA CGGAGACTTTATCTGACAGCAGCTGCATCGCCAGGGG	13879
QY	841	ATCACCATCCGTCGCCCCGGGGGTGTCAATAATATCACCTCTGTACATCCACAAACAGAGA	900
DB	13880	ATCACCATCCGTCGCCCCGGGGGTGTCAATAATATCACCTCTGTACATCCACAAACAGAGA	13939
QY	901	TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCATTTTCAACAGTCCCTGTTCTC	960
DB	13940	TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCATTTTCAACAGTCCCTGTTCTC	13999
QY	961	GTACAGCAAAAGAGCGCTTCAATTTCAATAAAGCGGCGACCTCAGCATCCCTTCTCTGATT	1020
DB	14000	GTACAGCAAAAGAGCGCTTCAATTTCAATAAAGCGGCGACCTCAGCATCCCTTCTCTGATT	14059
QY	1021	TTCCGCTTTCCAGCGTTCGGCACGACGACGCGGCTTCATTTCTGCATGGTTGTGCTTAC	1080
DB	14060	TTCCGCTTTCCAGCGTTCGGCACGACGACGCGGCTTCATTTCTGCATGGTTGTGCTTAC	14119
QY	1081	CAGACCGGAGATATTGACATCATATATGCTTTGAGCACTGATAGTCTGCTGCTGCAACT	1140
DB	14120	CAGACCGGAGATATTGACATCATATATGCTTTGAGCACTGATAGTCTGCTGCTGCAACT	14179
QY	1141	GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGAACATCTTCGGGTAGTGCCGA	1200
DB	14180	GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGAACATCTTCGGGTAGTGCCGA	14239
QY	1201	TCACGCTCTCAATTTTCGCGCAAAAGTTGGCCGACGCGGCTTCCCGGTATCAACAGGACACA	1260
DB	14240	TCACGCTCTCAATTTTCGCGCAAAAGTTGGCCGACGCGGCTTCCCGGTATCAACAGGACACA	14299
QY	1261	GGATTTATTTATTTTCGCGAAGTGATCTTCGGTCAAGGTATTTATTCGGCGCAAGTGGG	1320
DB	14300	GGATTTATTTATTTTCGCGAAGTGATCTTCGGTCAAGGTATTTATTCGGCGCAAGTGGG	14359
QY	1321	TGGGTGATGCTGCCAATCTAGTGCACCTACAGTCACTTAATACCATCTAAGTAGTGTGATT	1380
DB	14360	TGGGTGATGCTGCCAATCTAGTGCACCTACAGTCACTTAATACCATCTAAGTAGTGTGATT	14419
QY	1381	CATAGTGAAGTGGATATGTTGTTTTACAGTATTTATGATGCTGTTTTTATGCAAAATC	1440
DB	14420	CATAGTGAAGTGGATATGTTGTTTTACAGTATTTATGATGCTGTTTTTATGCAAAATC	14479
QY	1441	TAAATTAATAATATGATATTTATATCAATTTACGCTTTCTTCGTTCAAGCTTCTTTGACAAA	1500
DB	14480	TAAATTAATAATATGATATTTATATCAATTTACGCTTTCTTCGTTCAAGCTTCTTTGACAAA	14559
QY	1501	GTGCGCATTAAGAAGACATGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGT	1560
DB	14540	GTGCGCATTAAGAAGACATGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGT	14599
QY	1561	CAAAATAAATCATTTTGGCCATCCAGCTCCGCTCCGAGGAATTCGGTACCCCAAT	1620
DB	14600	CAAAATAAATCATTTTGGCCATCCAGCTCCGCTCCGAGGAATTCGGTACCCCAAT	14659
QY	1621	TGTTAAGAAATAATATTTCTTTTCTTTTATAGTATAAAATAGTTAAGTAGTGTAA	1680
DB	14660	TGTTAAGAAATAATATTTCTTTTCTTTTATAGTATAAAATAGTTAAGTAGTGTAA	14719
QY	1681	TTAGTATGATTAATAATAATATAGTTGTTTAAATTTGTGAAAAATAATTTTATAATATATT	1740
DB	14720	TTAGTATGATTAATAATAATATAGTTGTTTAAATTTGTGAAAAATAATTTTATAATATATT	14779
QY	1741	GTTTTACATAAAACATAGTAAATGTAAAAAATAATGACAAGTGTGTGTAAGACGAAGAA	1800
DB	14780	GTTTTACATAAAACATAGTAAATGTAAAAAATAATGACAAGTGTGTGTAAGACGAAGAA	14839
QY	1801	GATAAAGTTGAGAGTAAAGTATATTTATTTTAAATGAAATTTTGAATCGAATGTAAGATGAT	1860
DB	14840	GATAAAGTTGAGAGTAAAGTATATTTATTTTAAATGAAATTTTGAATCGAATGTAAGATGAT	14899
QY	1861	ATACCGCGGTAAAGGTTTCCAACTTTCCCATTAATGAATAAGATCACTACCGGCGGTA	1920

Db 14900 ATACGGCCGTTAAGAGTTTCCAACTTTACCAATAATGAATAGATCACTACCGGGCGTA 14959
QY 1921 TTTTGTGAGTTATCGAGATTTTCAGAGCTAAGGAGCTAAATGAGGAAAAAATCACT 1980
Db 14960 TTTTGTGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATGAGGAAAAAATCACT 15019
QY 1981 GGATATACACCGTTTGATATATCCCAATGGCATCGTAAAGAACATTTTCAGGAGCATTTTCAG 2040
Db 15020 GGATATACACCGTTTGATATATCCCAATGGCATCGTAAAGAACATTTTCAGGAGCATTTTCAG 15079
QY 2041 TCAGTTGCTCAATGTACCTATAACACAGACCGTTTCAGCTGGATATACGCGCTTTTAAAG 2100
Db 15080 TCAGTTGCTCAATGTACCTATAACACAGACCGTTTCAGCTGGATATACGCGCTTTTAAAG 15139
QY 2101 ACCGTAAGAAAAATAGCACAAGTTTATCGGCCCTTTTATTCACATTTCTGCCCGCGCTG 2160
Db 15140 ACCGTAAGAAAAATAGCACAAGTTTATCGGCCCTTTTATTCACATTTCTGCCCGCGCTG 15199
QY 2161 ATGAATGCTCATCGGGAATTCGGTATGGCAATGAAAGACGGTGAGCTGGTATATGGGAT 2220
Db 15200 ATGAATGCTCATCGGGAATTCGGTATGGCAATGAAAGACGGTGAGCTGGTATATGGGAT 15259
QY 2221 AGTTTCAACCTTGTATACCGTTTTCATGAGCAAACTGAAACGGTTTCATCGCTCGG 2280
Db 15260 AGTTTCAACCTTGTATACCGTTTTCATGAGCAAACTGAAACGGTTTCATCGCTCGG 15319
QY 2281 AGTGAATACACGACGATTTTCGGGAGTTTTCACATATATTCGCAAGATGTGGCGTGT 2340
Db 15320 AGTGAATACACGACGATTTTCGGGAGTTTTCACATATATTCGCAAGATGTGGCGTGT 15379
QY 2341 TAGCGTGAACCCCTGCGCTATTTCCCTAAAGGGTTTATTGAGAAATGTTTTTCGCTCA 2400
Db 15380 TAGCGTGAACCCCTGCGCTATTTCCCTAAAGGGTTTATTGAGAAATGTTTTTCGCTCA 15439
QY 2401 GCCAATCCCTGGTGTAGTTTACAGCTTTTGAATTAAGCGTGGCCAAATGAGCAACTTC 2460
Db 15440 GCCAATCCCTGGTGTAGTTTACAGCTTTTGAATTAAGCGTGGCCAAATGAGCAACTTC 15499
QY 2461 TTCCGCCCGCTTTTACCAATGGCAATATATACGCAAGGGGACAAAGGTGCTGATCGCG 2520
Db 15500 TTCCGCCCGCTTTTACCAATGGCAATATATACGCAAGGGGACAAAGGTGCTGATCGCG 15559
QY 2521 CTGGCGAATCAGGTTTCATCGCGCTGTGTGATGGCTTCCATGTCCGCAAGATGCTTAAT 2580
Db 15560 CTGGCGAATCAGGTTTCATCGCGCTGTGTGATGGCTTCCATGTCCGCAAGATGCTTAAT 15619
QY 2581 GAATTAACACGTAAGTGTGATGGTGGCGAGGGGGCGCTAATCGCGTGGATCCGCTTA 2640
Db 15620 GAATTAACACGTAAGTGTGATGGTGGCGAGGGGGCGCTAATCGCGTGGATCCGCTTA 15679
QY 2641 CTAAAGCCAGATAACAGATATGCTATTTTCGCGCTGATTTTTTCGCGTATAAGAAATATAT 2700
Db 15680 CTAAAGCCAGATAACAGATATGCTATTTTCGCGCTGATTTTTTCGCGTATAAGAAATATAT 15739
QY 2701 ACTGATATGTCGGGCCCTAATAGTAATTTCTAGCTGTTTGTAGTAATTAATCAATGA 2760
Db 15740 ACTGATATGTCGGGCCCTAATAGTAATTTCTAGCTGTTTGTAGTAATTAATCAATGA 15799
QY 2761 TAAATACTATAGTAAATTAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2820
Db 15800 TAAATACTATAGTAAATTAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15859
QY 2821 AGTTTATTAATAAATAATCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAA 2880
Db 15860 AGTTTATTAATAAATAATCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAA 15919
QY 2881 AATATTTGTAGAAATTCGAATCTGTTGTAATTTTATCAATAAACAATAAATAAATAAATAA 2940
Db 15920 AATATTTGTAGAAATTCGAATCTGTTGTAATTTTATCAATAAACAATAAATAAATAAATAA 15979
QY 2941 CAAGCTAAAGTAACAATAATATCAAACTAATAGAACAGTAATCTAATGTAACAAACA 3000
Db 15980 CAAGCTAAAGTAACAATAATATCAAACTAATAGAACAGTAATCTAATGTAACAAACA 16039

QY 3001 TAACTAATGCTAATATATAAAGCGCAAGATCTATCATTTTATATAGTATATTTTCAA 3060
Db 16040 TAACTAATGCTAATATATAAAGCGCAAGATCTATCATTTTATATAGTATATTTTCAA 16099
QY 3061 TCAACATTTCTTATTAATTTCTAAATAATACTTGTAGTTTATTAATCTTCTAAATCGATTG 3120
Db 16100 TCAACATTTCTTATTAATTTCTAAATAATACTTGTAGTTTATTAATCTTCTAAATCGATTG 16159
QY 3121 ACTATTAATTAATGAATTTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTC 3180
Db 16160 ACTATTAATTAATGAATTTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTC 16219
QY 3181 ATTTGTGTTATCATTTGATCTTACATTTTGATTTGATTTACAGTTGGGAAATTTGGTTTCAAAT 3240
Db 16220 ATTTGTGTTATCATTTGATCTTACATTTTGATTTGATTTACAGTTGGGAAATTTGGTTTCAAAT 16279
QY 3241 CGATAAGCTTGGATCCTCTAGAGAGCTGAGCTGGATGSCAAATAATGATTTTATTTTGA 3300
Db 16280 CGATAAGCTTGGATCCTCTAGAGAGCTGAGCTGGATGSCAAATAATGATTTTATTTTGA 16339
QY 3301 CTGATAGTGAACCTGTTGTTGCAACAAATTTGATTAAGCAATGCTTTCTTATTAATGCAACT 3360
Db 16340 CTGATAGTGAACCTGTTGTTGCAACAAATTTGATTAAGCAATGCTTTCTTATTAATGCAACT 16399
QY 3361 TTGTACAAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATTAATTTAG 3420
Db 16400 TTGTACAAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATTAATTTAG 16459
QY 3421 ATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAACATATCCAGTCACTATGA 3480
Db 16460 ATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAACATATCCAGTCACTATGA 16519
QY 3481 ATCAACTACTAGATGTTATTTAGTGAACCTGTAGTGCAGCTAGTGGAGACATCAACCCGAC 3540
Db 16520 ATCAACTACTAGATGTTATTTAGTGAACCTGTAGTGCAGCTAGTGGAGACATCAACCCGAC 16579
QY 3541 GCACCTTTCGCGCGAATAAATACTCTGTCGGAAGATCACTTCGCGAATAAATAAATACTCT 3600
Db 16580 GCACCTTTCGCGCGAATAAATACTCTGTCGGAAGATCACTTCGCGAATAAATAAATACTCT 16639
QY 3601 GGTGTCCTGTTGTATACCGGGAAGCCCTGGGCAACCTTTTGGCGAAATAGAGACGTTGAT 3660
Db 16640 GGTGTCCTGTTGTATACCGGGAAGCCCTGGGCAACCTTTTGGCGAAATAGAGACGTTGAT 16699
QY 3661 CGGCACTACCAATTTCAACACTTTTATCTTTTACAGTGCCTTGGCTTCTCATCTG 3720
Db 16700 CGGCACTACCAATTTCAACACTTTTATCTTTTACAGTGCCTTGGCTTCTCATCTG 16759
QY 3721 GATTTTCAGCCTCTATCTTACTTAAACGTTGATAAAGTTTCTGTAAATTTCTACTGTATCGA 3780
Db 16760 GATTTTCAGCCTCTATCTTACTTAAACGTTGATAAAGTTTCTGTAAATTTCTACTGTATCGA 16819
QY 3781 CCTGCAGACTGGCTGTGTATAGGAGGCTGCATTTATATTTCCCGAGAACATCAGTTTA 3840
Db 16820 CCTGCAGACTGGCTGTGTATAGGAGGCTGCATTTATATTTCCCGAGAACATCAGTTTA 16879
QY 3841 ATGGCGTTTTTTCATGCTCAATTTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACG 3900
Db 16880 ATGGCGTTTTTTCATGCTCAATTTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACG 16939
QY 3901 GAGACCGGCACACTGGCCATATCGGTGTTCTATCGCGCAGCTTTTCTATCCCGGATATGC 3960
Db 16940 GAGACCGGCACACTGGCCATATCGGTGTTCTATCGCGCAGCTTTTCTATCCCGGATATGC 16999
QY 3961 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACGACGACGTCGCTGCCAGGGGG 4020
Db 17000 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACGACGACGTCGCTGCCAGGGGG 17059
QY 4021 ATCAGCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 4080
Db 17060 ATCAGCATCCGTCGCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 17119

Qy	4081	TAACGGCTCTCTCTTTATATAGTGTHAACTTTAAACCTGCACTTTACAGTAGTCCCTGTGTTCTC	4140
Db	17120	TAACGGCTCTCTCTTTATATAGGTGTAAACCTTTAAACCTGCACTTTACAGTAGTCCCTGTGTTCTC	17179
Qy	4141	GTCAAGAAAAGAGCGCGTTTCATTTCAATAAACCGGGCGACCTCAGAGCCATCCCTTCCCTGATT	4200
Db	17180	GTCAAGAAAAGAGCGCGTTTCATTTCAATAAACCGGGGGAGCCTCAGGCATCCCTTCTCTGATT	17239
Qy	4201	TTCCGCTTTTCCAGCGTTTCGGCACGCGAGACGCGGGCTTCATTCTGCACTGGTGTGCTTTAC	4260
Db	17240	TTCCGCTTTTCCAGCGTTTCGGCACGCGAGACGCGGGCTTCATTCTGCGATGTTGCTTTAC	17299
Qy	4261	CAGACCGGAGATATTGACATCATATATAGCTTTGAGCAACTGATAGCTGTCGCTGTCAACT	4320
Db	17300	CAGACCGGAGATATTGACATCATATATAGCTTTGAGCAACTGATAGCTGTCGCTGTCAACT	17359
Qy	4321	GTCACTGTAAATACGCTGCTTCATAGCACACCTTCCTTTTGGACATACCTCTGTTCTTTGATGC	4380
Db	17360	GTCACTGTAAATACGCTGCTTCATAGCACACCTTCCTTTTGGACATACCTCTGTTCTTTGATGC	17419
Qy	4381	AGATGATTTTCAGGACTATGACACTAGCTATATGAATAGGTAGATGTTTTTATTTTGTCT	4440
Db	17420	AGATGATTTTCAGGACTATGACACTAGCTATATGAATAGGTAGATGTTTTTATTTTGTCT	17479
Qy	4441	ACACAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTTTATGATTTAATACGGCAATT	4500
Db	17480	ACACAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTTTATGATTTAATACGGCAATT	17539
Qy	4501	GAGGACAATAGCGAGTAGGCTGGATACGACGATTCGGTTTGAGAAGAACATTTGGAAGGC	4560
Db	17540	GAGGACAATAGCGAGTAGGCTGGATACGACGATTCGGTTTGAGAAGAACATTTGGAAGGC	17599
Qy	4561	TGTCGGTTCGACTAAGTTGGGAGCATCACCGGAAGAACATTTGGAAAGGCTGTGGTFCGACT	4620
Db	17600	TGTCGGTTCGACTAAGTTGGGAGCATCACCGGAAGAACATTTGGAAAGGCTGTGGTFCGACT	17659
Qy	4621	ACAGGTCACCTAATPACCATCTAAGTAGTTCATATAGTAGTACGACGGATATGTTGTGTTTTAC	4680
Db	17660	ACAGGTCACCTAATPACCATCTAAGTAGTTCATATAGTAGTACGACGGATATGTTGTGTTTTAC	17719
Qy	4681	AGTATTATGTAGTCTGTGTTTTTATGCAAAATCTAAATTAATATATTTGATATATCAT	4740
Db	17720	AGTATTATGTAGTCTGTGTTTTTATGCAAAATCTAAATTAATATATTTGATATATCAT	17779
Qy	4741	TTTTAGTTTCTCGTTTTCAGCTTTTTTGTGACAAAGTTGGCATTTAAAAAGCATTTGCTCAT	4800
Db	17780	TTTTAGTTTCTCGTTTTCAGCTTTTTTGTGACAAAGTTGGCATTTAAAAAGCATTTGCTCAT	17839
Qy	4801	CAATTTGTTGCAACGAACAGGTCACATCATCAGTCAAAATAAAATCATTTATTTGGGGCCCGA	4860
Db	17840	CAATTTGTTGCAACGAACAGGTCACATCATCAGTCAAAATAAAATCATTTATTTGGGGCCCGA	17899
Qy	4861	G 4861	
Db	17900	G 17900	

RESULT 2

AB082141

ABQ82141
ID ABQ82141 standard; DNA; 17476 BP.

XX
XX
XX

AC ABQ8

XX
XX

DT 11-DEC-2002 (first entry)

XX

DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX

[illegible]KW
recd

XX

OS
Synthesis

XX

PN WO200259294-A1.

XX	01-AUG-2002.
PD	
XX	
XX	24-JAN-2002; 2002WO-AUO00073.
FF	
XX	
XX	26-JAN-2001; 2001US-0264067P.
PR	
FR	29-NOV-2001; 2001US-0333743P.
XX	
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	
XX	
PI	Wesley S, Waterhouse P, Helliwell C;
XX	
DR	WPT; 2002-682669/73.
XX	
PT	New vectors comprising operably linked DNA fragments having an origin of
PT	replication, a selectable marker and a chimeric DNA construct, useful for
PT	silencing target nucleic acids and for producing large amounts of double-
PT	stranded RNA.
XX	
PS	Claim 15; Page 74-83; 10app; English.
XX	
CC	The present invention describes a vector (I) comprising operably linked
CC	DNA fragments having: (a) origin of replication allowing replication in a
CC	recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC	selectable marker region capable of being expressed in the recipient cell
CC	; and (c) a chimeric DNA construct comprising: (i) promoter or promoter cell
CC	region capable of being recognized by RNA polymerases of a eukaryotic
CC	cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC	fourth recombination sites; (iii) 3' transcription terminating and
CC	polyadenylation region functional in the eukaryotic cell. The first and
CC	fourth recombination sites, or the second and third recombination sites
CC	are capable of reacting with a same recombination site, and preferably
CC	are identical. The first and second recombination sites, or the third and
CC	fourth recombination sites, do not recombine with each other or with a
CC	same recombination site. The vector is useful for producing large amounts
CC	of double-stranded RNA which can be used for silencing target nucleic
CC	acid sequences. The vectors can also be used to convert a DNA fragment
CC	into an inverted repeat structure. Plants transformed with a vector from
CC	the present invention can be used in a conventional breeding scheme to
CC	produce more plants with the same characteristics or to introduce a
CC	chimeric gene for reduction of the phenotypic expression of nucleic
CC	acids. The present sequence represents an acceptor vector nucleotide
CC	sequence from the present invention
XX	
SQ	Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
	Query Match 52.7%; Score 2563.2; DB 6; Length 17476;
	Best Local Similarity 77.7%; Pred. No 0;
	Matches 3651; Conservative 0; Mismatches 23; Indels 1024; Gaps 5;
Qy	82 GCCAACCTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 141
Db	13025 GACAAGTTTTGTACAAAAAGCTCAACGAGAAACGTAATAATGATATAAATATCAATATATT 13084
Qy	142 AAATTAGATTTTGCATATAAAAACAGACTCATTAATCTCTAAACACACATATCCAGTC 201
Db	13085 AAATTAGATTTTGCATATAAAAACAGACTCATTAATCTCTAAACACACATATCCAGTC 13144
Qy	202 ACTATGAATCAACTACTTAGATGGTATTAGTCACCTTGATCGACCGCAGCGCTTCCAAA 261
Db	13145 ACTATGAATCAACTACTTAGATGGTATTAGTCACCTTGATCGACCGCAGCGCTTCCAAA 13204
Qy	262 TGTTCTTCGGGTGATCGTCGCAACTTAGTCGACCGCACGCCCTTCCAATGTTCTCTCAA 321
Db	13205 TGTTCTTCGGGTGATCGTCGCAACTTAGTCGACCGCACGCCCTTCCAATGTTCTCTCAA 13264
Qy	322 ACCGAATCGTCGPATCCAGCTACTCGCTATTGTCTCTCAATGCCGTATTAAATCATATAA 381
Db	13265 ACCGAATCGTCGPATCCAGCTACTCGCTATTGTCTCTCAATGCCGTATTAAATCATATAA 13324
Qy	382 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGACAAAAATAAAAAATCATCTACT 441
Db	13325 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGACAAAAATAAAAAATCATCTACT 13384

RESULT 3
ID ABQ82143
XX ABQ82143 standard; DNA; 17681 BP.
XX AC ABQ82143;
XX XX
XX DT 11-DEC-2002 (first entry)
XX DE Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX KW recombination site; double stranded RNA; plant; ds.
XX OS Synthetic.
XX XX
XX PN WO200259294-A1.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-AUC000073.
XX PR 26-JAN-2001; 2001US-0264067P.
XX PR 29-NOV-2001; 2001US-0333743P.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX XX
XX PI Wesley S, Waterhouse P, Helliwell C;
XX DR WPI; 2002-682669/73.
XX PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX PS Claim 17; Page 93-102; 104pp; English.
XX CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
XX sequence from the present invention
SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;
Query Match 52.0%; Score 2528; DB 6; Length 17681;
Best Local Similarity 76.5%; Pred. No. 0;
Matches 3682; Conservative 0; Mismatches 85; Indels 1043; Gaps 6;
QY 82 GCCAACTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 141
Dd 13025 GACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 13084
QY 142 AAATTAGATTTTGCATAAAAACAGACTACATATATCTGTAAAAACACACATATCCAGTC 201

Db 13085 AAATTAGATTTTGCATAAAAACAGACTACATATATCTGTAAAAACACACATATCCAGTC 13144
QY 202 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 261
Db 13145 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAA 13204
QY 262 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 321
Db 13205 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 13264
QY 322 ACGGAATCGTCTGATATCCAGCCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 381
Db 13265 ACGGAATCGTCTGATATCCAGCCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 13324
QY 382 AGAAATAGAAAAGAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAAACATCTACCT 441
Db 13325 AGAAATAGAAAAGAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAAACATCTACCT 13384
QY 442 ATTCATATACGCTAGTGTCTAGTCTGAAATCATCTGCAATCAAGAACAAATTTTCAACAC 501
Db 13385 ATTCATATACGCTAGTGTCTAGTCTGAAATCATCTGCAATCAAGAACAAATTTTCAACAC 13444
QY 502 TCTTATACCTTTTCTCTTACAACTCGTTTCGGCTTCATCTGGAATTTTTCAGCCTCTATCTTA 561
Db 13445 TCTTATACCTTTTCTCTTACAACTCGTTTCGGCTTCATCTGGAATTTTTCAGCCTCTATCTTA 13504
QY 562 CTAAACGCTGATTAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGATA 621
Db 13505 CTAAACGCTGATTAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGATA 13564
QY 622 AGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 681
Db 13565 AGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 13624
QY 682 TCGCGTGTGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGACACCTGGCCATA 741
Db 13625 TCGCGTGTGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGACACCTGGCCATA 13684
QY 742 TCGTGGTGCATCATGGCCGAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAACG 801
Db 13685 TCGTGGTGCATCATGGCCGAGCTTTTCATCCCGATATGCAACCGGGTAAAGTTTCAACG 13744
QY 802 GAGACTTTATCTGACAGACAGACGTGCTGCGCAGGGGATCACCATCCGTCGCGCGGCG 861
Db 13745 GAGACTTTATCTGACAGACAGACGTGCTGCGCAGGGGATCACCATCCGTCGCGCGGCG 13804
QY 862 GTGTCAATAATATCACTCTGTATCATCCAAACAGACAGATACGGCTCTCTCTTTATAG 921
Db 13805 GTGTCAATAATATCACTCTGTATCATCCAAACAGACAGATACGGCTCTCTCTTTATAG 13864
QY 922 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCTAT 981
Db 13865 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCTAT 13924
QY 982 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGTTTCCAGCGTTGCGC 1041
Db 13925 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGTTTCCAGCGTTGCGC 13984
QY 1042 ACGCAGACACGGGCTTCTATCTGATGGTGTGCTTACAGACCGGAGATATTGACATC 1101
Db 13985 ACGCAGACACGGGCTTCTATCTGATGGTGTGCTTACAGACCGGAGATATTGACATC 14044
QY 1102 ATATATGCTCTGAGCAACTGATAGCTGTGCTGTCTCAACTGTCTGCTGTATATAGCTGCTTC 1161
Db 14045 ATATATGCTCTGAGCAACTGATAGCTGTGCTGTCTCAACTGTCTGCTGTATATAGCTGCTTC 14104
QY 1162 ATAGCACACCTCTTTTGTACATACCTACTTCCGGGTAGTGCAGTCAACGCTCTCATTTTCCCAA 1221
Db 14105 ATAGCACACCTCTTTTGTACATACCTACTTCCGGGTAGTGCAGTCAACGCTCTCATTTTCCCAA 14164
QY 1222 AAGTTGGCCACGGGCTTCCCGGTATCAACAGGGAACACAGGATTTTATTTATTTCTGCGAAG 1281

Db 14165 AAGTTGGCCAGGGCTTCCGGTATCAACAGGGACACAGGATTTATTTATTTCTCGAAG 14224
QY 1282 TGATCTTCGGTCAACAGGTATTTATTCGGCGCAAAAGTGCCTGGGTGATCTGCCAACTTA 1341
Db 14225 TGATCTTCGGTCAACAGGTATTTATTCGGCGCAAAAGTGCCTGGGTGATCTGCCAACTTA 14284
QY 1342 GTTCGACTACAGGTCATTAATACCATCTAAGTAGTTCATTCATAGTCACTGGATATGTTCT 1401
Db 14285 GTTCGACTACAGGTCATTAATACCATCTAAGTAGTTCATTCATAGTCACTGGATATGTTCT 14344
QY 1402 GTTTTACAGTATTAATGCTAGTCTCTTTTATGCAAAATCTAAATTTAATATATTTGATATTT 1461
Db 14345 GTTTTACAGTATTAATGCTAGTCTCTTTTATGCAAAATCTAAATTTAATATATTTGATATTT 14404
QY 1462 ATATCAATTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTTCGCAATTAAGAAAGCAT 1521
Db 14405 ATATCAATTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTTCGCAATTAAGAAAGCAT 1521
QY 1522 TGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAATCAATTTTGC 1581
Db 14448 ----- 14447
QY 1582 CATCCAGCTCAGCTCCTCGAGGAATTCGTACCCCA-ATTCGTAGGAAATTAATTTT 1640
Db 14448 -----TCTCGAGCAATTCGGTACCCAGCTTGGTAAGGAAATAATTTT 14492
QY 1641 TCTTTTTCCTTTTAGTATTAATAGTTAAGTATGATCTTAATTTAGTATGATTAATAATA 1700
Db 14493 TCTTTTTCCTTTTAGTATTAATAGTTAAGTATGATCTTAATTTAGTATGATTAATAATA 14552
QY 1701 TAGTGTATTAATTTGCAAAATAATTTAATAATATTTGTTTACATAAACAACATAGT 1760
Db 14553 TAGTGTATTAATTTGCAAAATAATTTAATAATATTTGTTTACATAAACAACATAGT 14612
QY 1761 AATGTAATAAATAATGCAAGTATGTTAAGACGAAGAAGATAAAGTTGAGAGTAAGT 1820
Db 14613 AATGTAATAAATAATGCAAGTATGTTAAGACGAAGAAGATAAAGTTGAGAGTAAGT 14672
QY 1821 ATATTTATTTATGATTTGATCGACATGTAAGTATGATATACGCCGTGTAAGGTTTC 1880
Db 14673 ATATTTATTTATGATTTGATCGACATGTAAGTATGATATACGATTAATGATTAAT 14725
QY 1881 CAATCTTCCACATAATGAATAAGATCACTACCGGGCGTATTTTGTAGTATCGAGATT 1940
Db 14726 ----- 14725
QY 1941 TTCCAGGAGCTAAGGAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT 2000
Db 14726 ----- 14725
QY 2001 ATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTCACTGCTCAATGTACCTA 2060
Db 14726 ----- 14725
QY 2061 TAACGAGCCGTTCCAGCTGGATATTTACGGCTTTTAAAGCCGTAAAGAAAAAATAGCA 2120
Db 14726 ----- 14725
QY 2121 CAAGTTTATCCGGCTTTTATTCACATTTCTGCGCGCTGATGATGCTCATCCGGAATT 2180
Db 14726 ----- 14725
QY 2181 CCGTATGGCAATGAAGACGGTGAGCTGGTATGGATATGGATAGTGTTCACCGCTTGTACAC 2240
Db 14726 ----- 14725
QY 2241 CGTTTCCATGAGCAAACTGAACGTTTTCATCGCTCTGGAGTGAAATACCAACGAGATT 2300
Db 14726 ----- 14725
QY 2301 CCGCAGTTTCTACACATATATCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCTA 2360
Db 14726 ----- 14725

QY 2361 TTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTCTCAGCCAAATCCCTGGGTGAGTTT 2420
Db 14726 ----- 14725
QY 2421 CACCAGTTTGTATTTAAACGTGGCCAATATGGAACAATCTCTCGCCCCCGTTTTCACCAT 2480
Db 14726 ----- 14725
QY 2481 GGGCAAAATATTATACGCAAGGCGACAAGGTGCTGATGCGGTGGGATTCAGGTTCAATCA 2540
Db 14726 ----- 14725
QY 2541 TGCCGCTCTGTGATGCTTCCATGTCCGAGCAATGCTTAATGAATTAACAACAGTACTCGGA 2600
Db 14726 ----- 14725
QY 2601 TGAGTGGCAGGGGGGGGTAATCGCTGGATCCGGCTTACTPAAAAAGCCAGATAACAGTA 2660
Db 14726 ----- 14725
QY 2661 TGCGTATTTGCGCGCTGATTTTGGGTATAGAATATATCTGATATGTCGGGCCCATTA 2720
Db 14726 -----TATTTGTTTAAATCATTA 14742
QY 2721 ATAGTAATTTCTAGCTGGTTTGATGAATTAATAATCAATGATGAATAAATCTATAGTAAAAAT 2780
Db 14743 ATAGTAATTTCTAGCTGGTTTGATGAATTAATAATCAATGATGAATAAATCTATAGTAAAAAT 14802
QY 2781 AAGAATAAATAAATAAATAATATTTTATGATTAATAGTATTTTATTAATAATAATAAT 2840
Db 14803 AAGAATAAATAAATAAATAATATTTTATGATTAATAATAGTATTTTATTAATAATAATAAT 14862
QY 2841 ATCTATACCATTTACTAATAATTTTAAAGTTTAAAGTTTAAATAATTTTCTTGAATAATCC 2900
Db 14863 ATCTATACCATTTACTAATAATTTTAAAGTTTAAAGTTTAAATAATTTTCTTGAATAATCC 14922
QY 2901 AATCTGTTGTTAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTAAACAATAA 2960
Db 14923 AATCTGTTGTTAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTAAACAATAA 14982
QY 2961 TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACATAATCTAATGCTAAATAAC 3020
Db 14983 TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACATAATCTAATGCTAAATAAC 15042
QY 3021 AAGGCAAGAGCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTTTC 3080
Db 15043 AAGGCAAGAGCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTTTC 15102
QY 3081 TAAATAATATCTTGTAGTTTTTATTAACCTTCTAATGGAATGACTATTAATAATAAGATTA 3140
Db 15103 TAAATAATATCTTGTAGTTTTTATTAACCTTCTAATGGAATGACTATTAATAATAAGATTA 15162
QY 3141 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTTGTTATCATGATCTT 3200
Db 15163 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTTGTTATCATGATCTT 15222
QY 3201 ACATTTGGGATTTGATTACAGTTGCGAAATTTGGGTTTCGAAATCGAATAAGCTTG-----GAT 3254
Db 15223 ACATTTGGGATTTGATTACAGTTGCGAAATTTGGGTTTCGAAATCGAATAAGCTTGCGCTGCACT 15282
QY 3255 CCTCTAGAGAGCTGCAAGCTGGATGGCAATAATAGATTTTATTTGACTGATAGTGACCTG 3314
Db 15283 TATCATCATCATATAGACACACGAAATAAAGTAATCAGATTATCAGTTTAAAGCTATGTA 15342
QY 3315 TTGTTTGGCAACAA----- 3328
Db 15343 ATATTTGCGCCATAACCAATCAATTAATAAATAATAGATCAGTTTAAAGAAAGATCAAGCTC 15402
QY 3329 ----- 3328
Db 15403 AAAAAATAAAGAGAAAAAGGGTCTTACCAAGAAAAATGAAGGAGAAAAAATAGAAAAAT 15462

CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 51.6%; Score 2510.6; DB 6; Length 17458;
Best Local Similarity 77.2%; Pred. No. 0;
Matches 3628; Conservative 0; Mismatches 29; Indels 1040; Gaps 6;
QY 82 GCGAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 141
DB 13025 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 13084
QY 142 AAATTAGATTGTCATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 201
DB 13085 AAATTAGATTGTCATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 13144
QY 202 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACGACGAGCCTTCCAAA 261
DB 13145 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACGACGAGCCTTCCAAA 13204
QY 262 TGTCTTCGGGTGATGCTGCAACTTAGTCGACCGACAGCCTTCGAAATGTTCTTCTCAA 321
DB 13205 TGTCTTCGGGTGATGCTGCAACTTAGTCGACCGACAGCCTTCGAAATGTTCTTCTCAA 13264
QY 322 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTAAATATCATAAAA 381
DB 13265 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTAAATATCATAAAA 13324
QY 382 AGAAATTAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 441
DB 13325 AGAAATTAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13384
QY 442 ATTATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCATCAAGAACAAATTCACAC 501
DB 13385 ATTATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCATCAAGAACAAATTCACAC 13444
QY 502 TCTTATACCTTTCTTTACAAGTCGTTTGGGCTTCATCTGGAATTTTCAGGCTCTATATCTTA 561
DB 13445 TCTTATACCTTTCTTTACAAGTCGTTTGGGCTTCATCTGGAATTTTCAGGCTCTATATCTTA 13504
QY 562 CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTATA 621
DB 13505 CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTATA 13564
QY 622 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 661
DB 13565 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 13624
QY 682 TCAGGCTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGCACACTGGCCATA 741
DB 13625 TCAGGCTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGCACACTGGCCATA 13684
QY 742 TCAGTGTGTATCATCGCCGACGCTTTCTATCCCGATATGACACCGGCTAAAGTTACCGG 801
DB 13685 TCAGTGTGTATCATCGCCGACGCTTTCTATCCCGATATGACACCGGCTAAAGTTACCGG 13744
QY 802 GAGACTTTATCTGACACGACGCTGACCTGCGCAGGGGGATCACCATCCGTCGCCGGGC 861
DB 13745 GAGACTTTATCTGACACGACGCTGACCTGCGCAGGGGGATCACCATCCGTCGCCGGGC 13804

QY 862 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACCGCTCTCTCTTTTATAG 921
DB 13805 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACCGCTCTCTCTTTTATAG 13864
QY 922 GTGTAAACCTTAAACTGCATTTCCACAGTCCCTGCTTCGTGACGAAAGAGCGCTTCAT 981
DB 13865 GTGTAAACCTTAAACTGCATTTCCACAGTCCCTGCTTCGTGACGAAAGAGCGCTTCAT 13924
QY 982 TTCATAAACCGCGGACCTCAGCAATCCCTCTCTGTATTTCCGCTTTCGAGCTTCCGC 1041
DB 13925 TTCATAAACCGCGGACCTCAGCAATCCCTCTCTGTATTTCCGCTTTCGAGCTTCCGC 13984
QY 1042 ACGCAGACGACGCGCTTCATCTGCATGTTGCTTACACAGCGGAGATATTGACATC 1101
DB 13985 ACGCAGACGACGCGCTTCATCTGCATGTTGCTTACACAGCGGAGATATTGACATC 14044
QY 1102 ATATATGCTTTGAGCAACTGATAGTGTGCTGCTCAACTGTCACCTGTAATACGCTGCTC 1161
DB 14045 ATATATGCTTTGAGCAACTGATAGTGTGCTGCTCAACTGTCACCTGTAATACGCTGCTC 14104
QY 1162 ATAGCACACCTCTTTTGGACATATCTCGGCTAGTGCAGATCAACGCTCTCATTTTCGCCAA 1221
DB 14105 ATAGCACACCTCTTTTGGACATATCTCGGCTAGTGCAGATCAACGCTCTCATTTTCGCCAA 14164
QY 1222 AAGTTGGCCCGAGGCTTCCCGGTATCAACAGGACACGAGATTTATTTATCTGCGAAG 1281
DB 14165 AAGTTGGCCCGAGGCTTCCCGGTATCAACAGGACACGAGATTTATTTATCTGCGAAG 14224
QY 1282 TGATCTTCCGTACAGGTTATTTATTCGGCGCAAGTGCCTGCGGTGATGCTGCCAATCTTA 1341
DB 14225 TGATCTTCCGTACAGGTTATTTATTCGGCGCAAGTGCCTGCGGTGATGCTGCCAATCTTA 14284
QY 1342 GTCCACTACAGGTCATTAATACCATCTTAAGTAGTTCATGCTAGCTGCGATATGTTGT 1401
DB 14285 GTCCACTACAGGTCATTAATACCATCTTAAGTAGTTCATGCTAGCTGCGATATGTTGT 14344
QY 1402 GTTTTACAGTATTAATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT 1461
DB 14345 GTTTTACAGTATTAATGATGCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT 14404
QY 1462 ATATCATTTTACGTTTCTGTTTCAGCTTTCTTGTACAAAGTGGCATTTATAAAGAACAT 1521
DB 14405 ATATCATTTTACGTTTCTGTTTCAGCTTTCTTGTACAAAGTGG----- 14447
QY 1522 TGCTTATCAATTTTGTTCAGAACGACAGGTCATATCAGTCAAAATAAAATCATTTATTTGC 1581
DB 14448 ----- 14447
QY 1582 CATCCAGCTGCGAGCTCCTCGAGGAATTCGGTACCCCAATTCGGTAAAGGAAATAATTTATTTT 1641
DB 14448 -----TCTCGAGGAATTCGGTACC-----AAGTGAAGGAAATAATTTATTTT 14489
QY 1642 CTTTTTCTTTTACGTATTAATAATAGTTAAGTGTCTTAATAGTATGATTAATAATAAT 1701
DB 14490 CTTTTTCTTTTACGTATTAATAATAGTTAAGTGTCTTAATAGTATGATTAATAATAAT 14549
QY 1702 AGTGTGTAATAATGTAAGAAAAATAATTTATAAATAATTTGTTTACATAAAACAACATAGTA 1761
DB 14550 AGTGTGTAATAATGTAAGAAAAATAATTTATAAATAATTTGTTTACATAAAACAACATAGTA 14609
QY 1762 ATGTAAAAAATATGACAAAGTGTGTGAACGAGGAGATATAAAGTTGAGAGTAAGTA 1821
DB 14610 ATGTAAAAAATATGACAAAGTGTGTGAACGAGGAGATATAAAGTTGAGAGTAAGTA 14669
QY 1822 TATTATTTTATGATTAATGATTTGATCGAACATGTAAGATGATATACCGCGGTGAAGGTTCC 1881
DB 14670 TATTATTTTATGATTAATGATTTGATCGAACATGTAAGATGATATACAGCATTA----- 14721
QY 1882 AACTTTTCCATTAATGAAATAGATCATCTACCGGCGGTATTTTTTTGAGTTATCGAGATTT 1941
DB 14722 ----- 14721
QY 1942 TCAGGAGCTAAGGAAAGCTTAAATGGAGAAAAAATCATCTGGATATACACCGCTTGATATA 2001

Db	14722	-----	14721
QY	2002	TCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTAT	2061
Db	14722	-----	14721
QY	2062	AACAGACGGTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTAAAGAAAAATAAGCAC	2121
Db	14722	-----	14721
QY	2122	AAGTTTTATCCGGCCTTTATTACATCTCTTGCCCGCTTGATGAATGCTCATCCGGAATTC	2181
Db	14722	-----	14721
QY	2182	CGTATGGCAATGAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCCTGTTTACACC	2241
Db	14722	-----	14721
QY	2242	GTITTCATGAGCAAACTGAACGTTTTTCATCGCTCTGGAGTGAATACCAACGACGATTTC	2301
Db	14722	-----	14721
QY	2302	CGGCACTTTTACACATATATTTCGAAGATGTGGCTGTACGGTGAAACCTGGCCTAT	2361
Db	14722	-----	14721
QY	2362	TTCCCTAAAGGGTTATTGAGAAATATGTTTTTCGCTCAGCCAAATCCCTGGGTGAGTTTC	2421
Db	14722	-----	14721
QY	2422	ACCAGTTTTGATTTAAACGTGGCCATATGGACAACTTCTTGCCCGCCGTTTTTCACCATG	2481
Db	14722	-----	14721
QY	2482	GGCAATATTATACGAAGCGGCAAGGTGCTGANGCCGTGGCGATTGAGGTTTCATCAT	2541
Db	14722	-----	14721
QY	2542	GCCGCTGTGATGGCTTCCATGTCGGCAGNATGCTTAATGAATTACAAACAGTACTGCGAT	2601
Db	14722	-----	14721
QY	2602	GAGTGCAGGGGGGGGTAATCGCGTGGATCGGCTTACTAAAGCCAGATAACAGTAT	2661
Db	14722	-----	14721
QY	2662	GGGTATTTGGCGCTGATTTTTGGGGTATGAAGATATATACTGATATGTGCGGGCCCATAA	2721
Db	14722	-----	14739
QY	2722	TAGTAATTTCTAGCTGGTTGATCAATTAATATCAATGATAAATAACTATAGTAAATAATA	2781
Db	14740	TAGTAATTTCTAGCTGGTTGATGAATTAATAICATATGATAAATAACTATAGTAAATAATA	14799
QY	2782	AGAATAAAATAAATAAATAATTTTTTTATGATTAATAAGTTTATATATAATAATAATA	2841
Db	14800	AGAATAAAATAAATAAATAATTTTTTTATGATTAATAAGTTTATATATAATAATAATA	14859
QY	2842	TCTATACCATTACTAAATATTTTATGATTAATAAGTTTATATATAATAATAATAATA	2901
Db	14860	TCTATACCATTACTAAATATTTTATGATTAATAAGTTTATATATAATAATAATAATA	14919
QY	2902	ATCTGCTTGAATTTATCAATAAATAAATAATTAATAAATAAGTTTAAAGTAAACAAATAAT	2961
Db	14920	ATCTGCTTGAATTTATCAATAAATAAATAATTAATAAATAAGTTTAAAGTAAACAAATAAT	14979
QY	2962	ATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTCTAATAACA	3021
Db	14980	ATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTCTAATAACA	15039
QY	3022	AAGCGAAGATCTATCATTTTTATATAGTATTTTTTCAATCAACATTTCTTATTAATTTCT	3081

Db	15040	AAGCGCAAGATCTATCATTTTTATATAGTATTTTTCAATCAACATTTCTTATTAATTTCT	15099
QY	3082	AAATAATACCTGTAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3141
Db	15100	AAATAATACCTGTAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	15159
QY	3142	TCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTATCAATGATCTTA	3201
Db	15160	TCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTATCAATGATCTTA	15219
QY	3202	CATTTGATTTGATTTACAGTTGGGAAATTTGGTTGAAATTCATTAAGCTTGGATCTCTAG	3261
Db	15220	CATTTGATTTGATTTACAGTTACTTA-----CCTTAAGCTTGGATCTCTAG	15265
QY	3262	AGAGCTGCAGCTGGATGCAAAATATATTTTTGATGATGACCTGTTGCTTG	3321
Db	15266	A-----	15266
QY	3322	CAACAAATTTGATAAGCAATGCTTTCTTATAATGCAACTTTGTACAAGAAAGCTGAACGA	3381
Db	15267	-----CCACTTTGTACAAGAAAGCTGAACGA	15292
QY	3382	GAAACGTAATATGATATAAATATCAATATATTTAATTAATTAATTAATTAATTAATTAATTAAT	3441
Db	15293	GAAACGTAATATGATATAAATATCAATATATTTAATTAATTAATTAATTAATTAATTAATTAAT	15352
QY	3442	ACATAATCTGTAAACACAAACATATCCAGTCACTATGAATCAACTACTTATGATGTTAT	3501
Db	15353	ACATAATCTGTAAACACAAACATATCCAGTCACTATGAATCAACTACTTATGATGTTAT	15412
QY	3502	AGTGACCTGTAGTCACTAAGTTGGCAGATCACCCGAGCACCTTTGGCCGGAATAATA	3561
Db	15412	AGTGACCTGTAGTCACTAAGTTGGCAGATCACCCGAGCACCTTTGGCCGGAATAATA	15472
QY	3562	CCTGTGACGGAGATCACTTCGCAGAAATAATAATAATCTCTGTCTCCCTGTTGATACCCGG	3621
Db	15473	CCTGTGACGGAGATCACTTCGCAGAAATAATAATAATCTCTGTCTCCCTGTTGATACCCGG	15532
QY	3622	AAGCCCTGGCCCAACTTTTGGCGAAATGAGACGTTGATCGSACTACCCATTTCAACAAC	3681
Db	15533	AAGCCCTGGCCCAACTTTTGGCGAAATGAGACGTTGATCGS-----ATTTCAACAAC	15584
QY	3682	TCTTATACCTTTCTCTTACAGTCGTTGGCTTCACTGGAATTTTCAGCTCTATACATTA	3741
Db	15585	TCTTATACCTTTCTCTTACAGTCGTTGGCTTCACTGGAATTTTCAGCTCTATACATTA	15644
QY	3742	CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA	3801
Db	15645	CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA	15704
QY	3802	AGGGAGCCTGACATTTATATCCCGAGAAACATCAGGTTAATCGGCTTTTGTATGTCATTT	3861
Db	15705	AGGGAGCCTGACATTTATATCCCGAGAAACATCAGGTTAATCGGCTTTTGTATGTCATTT	15764
QY	3862	TGCGGTGCTGAGATCAGCCTCTTCCCGATAACGAGACCGGACACTGGCCATA	3921
Db	15765	TGCGGTGCTGAGATCAGCCTCTTCCCGATAACGAGACCGGACACTGGCCATA	15824
QY	3922	TGCGGTGCTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAACG	3981
Db	15825	TGCGGTGCTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAACG	15884
QY	3982	GAGACTTTATCGACAGCAGCTGCACTGGCCAGGGGATCACCATCGCTGCGCCGGG	4041
Db	15885	GAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCGCTGCGCCGGG	15944
QY	4042	GTGTCAATATATCACTCTGTATCCCAACAGACGATTAAGGCTCTCTCTTTTATAG	4101
Db	15945	GTGTCAATATATCACTCTGTATCCCAACAGACGATTAAGGCTCTCTCTTTTATAG	16004
QY	4102	GTGTAAACCTTAACTTGAATTTTCCAGTCCCTGTTCTCGTCAGCAAAAAGACGCTTAT	4161
Db	16005	GTGTAAACCTTAACTTGAATTTTCCAGTCCCTGTTCTCGTCAGCAAAAAGACGCTTAT	16064

QY	4162	TTCAATAAACCGGGCGACCTCAGC	ATCCCTTCCTGATTTTC	CGCTTCCAGCGTTCCGGC	4221
Db	16065	TTCAATAAACCGGGCGACCTCAGC	ATCCCTTCCTGATTTTC	CGCTTCCAGCGTTCCGGC	16124
QY	4222	ACGCAGACGACGGGCTTCATTTCT	GCATGTTGTGCTTACCAGACGGG	AGATATTGACATC	4281
Db	16125	ACGCAGACGACGGGCTTCATTTCT	GCATGTTGTGCTTACCAGACGGG	AGATATTGACATC	16184
QY	4282	ATATATGCCCTTGAGCAACGTAG	CTGTCGCTGTCAACTGTCACTGT	GAATACGCTGCTTC	4341
Db	16185	ATATATGCCCTTGAGCAACGTAG	CTGTCGCTGTCAACTGTCACTGT	GAATACGCTGCTTC	16244
QY	4342	ATAGCACACCTCTTTTGGACATCT	CTGTTCTTGATGCAGATGATTTT	CACGACTATGA	4401
Db	16245	ATAGCACACCTCTTTTGGACATCT	CTGTTCTTGATGCAGATGATTTT	CACGACTATGA	16304
QY	4402	CACTAGCGTATATGAATAGGTAG	ATGTTTTTATTTTGTGCACACAAA	AAGGCTCGGAC	4461
Db	16305	CACTAGCGTATATGAATAGGTAG	ATGTTTTTATTTTGTGCACACAAA	AAGGCTCGGAC	16364
QY	4462	CTCTTTTCTCTATTTCTTTTTTAT	GATTTAAATACGCGATTTGAGG	ACAAATAGCGAGTAGGCT	4521
Db	16365	CTCTTTTCTCTATTTCTTTTTTAT	GATTTAAATACGCGATTTGAGG	ACAAATAGCGAGTAGGCT	16424
QY	4522	GGATACGACGATCCGTTTGGAGA	GAACAATTTGGAAAGGCTGCGTG	CGACTAAGTTGGCA	4581
Db	16425	GGATACGACGATCCGTTTGGAGA	GAACAATTTGGAAAGGCTGCGTG	CGACTAAGTTGGCA	16484
QY	4582	GCATCACCGGAAGAACATTTGG	AAGGCTGCTCGCTCGACTACAGG	TCACTAATACCATCTA	4641
Db	16485	GCATCACCGGAAGAACATTTGG	AAGGCTGCTCGCTCGACTACAGG	TCACTAATACCATCTA	16544
QY	4642	AGTAGTTGATTCATAGTACGAT	ATGTTGTGTTTTTACAGTATATG	TATGTAGTCTGTTTTT	4701
Db	16545	AGTAGTTGATTCATAGTACGAT	ATGTTGTGTTTTTACAGTATATG	TATGTAGTCTGTTTTT	16604
QY	4702	TATGCAAAATCTAAATTTAATAT	TGCATATTTATATCATTTTTACG	TTTTCTCGTTCAGCTT	4761
Db	16605	TATGCAAAATCTAAATTTAATAT	TGCATATTTATATCATTTTTACG	TTTTCTCGTTCAGCTT	16664
QY	4762	TTTTGTACAAAGTTGGC	4778		
Db	16665	TTTTGTACAAACTTGC	16681		

RESULT 5	
ABQ82130/c	
ID	ABQ82130 standard; DNA; 18691 BP.
XX	
XX	
AC	ABQ82130;
XX	
XX	
DT	11-DEC-2002 (first entry)
XX	
DE	Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
XX	
XX	
KW	Chimeric nucleic acid construct; recombinational cloning; silencing;
KW	recombination site; double stranded RNA; plant; ds.

OS Synthetic.
XX WO200259294-A1.
PN
XX
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU000073.
PF
XX
XX 26-JAN-2001; 2001US-0264067P.
PR
PR 29-NOV-2001; 2001US-0333743P.
XX
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX
PI Wesley S. Waterhouse P, Helliwell C;

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 13; Page 62-72; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 18691 BP: 4R37 A: 4621 C: 4607 G: 4626 T: 0 U: 0 Other:

Query Match	30.1%;	Score 1462.6;	DB 6;	Length 18691;
Best Local Similarity	59.4%;	Pred. No. 4.2e-194;		
Matches 2920;	Conservative	0;	Mismatches 1889;	Indels 104; Gaps 22;
QY	1	CGGGCCCCAAATAAGTATTTATTTTGACTGATAGTACCTGTTCGTTGCAACAAATTGA	60	
Db	17898	CGGGCCCCAAATAAGTATTTATTTTGACTGATAGTGAACCTGTCGTTGCAACAAATTGA	17839	
QY	61	TGAGCAATGCTTTTTTATAATGCCAACTTTGTGTAACAAAAGCTGAACGAGAAACGTAAAA	120	
Db	17838	TGAGCAATGCTTTTTTATAATGCCAACTTTGTGTACAAAAGCTGAACGAGAAACGTAAAA	17779	
QY	121	TGATATAAATATCAATATATAATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACTG	180	
Db	17778	TGATATAAATATCAATATATAATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACTG	17719	
QY	181	TAAAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTACCTGTGA	240	
Db	17718	TAAAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTACCTGTGA	17659	
QY	241	GTGACGGACAGCCTTCGAAATGTTCTTCGGGTGATGCTGCCAATTAGTCGACCGACAG	300	
Db	17658	GTGACGGACAGCCTTCGAAATGTTCTTCGGGTGATGCTGCCAATTAGTCGACCGACAG	17599	
QY	301	CCTTCCAAATGTCTTCTCAAACGGAAATCGTGGTATCCAGGCTACTCGCTATTGTCCTCA	360	
Db	17598	CCTTCCAAATGTCTTCTCAAACGGAAATCGTGGTATCCAGGCTACTCGCTATTGTCCTCA	17539	
QY	361	ATGCGGTATTAATCATATAAAAGAATAAAGAAAGAGGTGGAGCCTCTTTTGTGTG	420	
Db	17538	ATGCGGTATTAATCATATAAAAGAATAAAGAAAGAGGTGGAGCCTCTTTTGTGTG	17479	
QY	421	ACAAAATAAAACATCTACTCTTTCATATACGCTAGTGTCACTAGTCCTGAAAAATCATCTG	480	
Db	17478	ACAAAATAAAACATCTACTCTTTCATATACGCTAGTGTCACTAGTCCTGAAAAATCATCTG	17419	
QY	481	CATCAAGAACAAATTTCCACAACCTTTATCTTTTCTCTTACAAAGTCGTTCCGCTTCATCTG	540	

Db 17418 CATCAAGAACAGAAGTATGTCAAAAGAGAGTGTGCTATGAA---GCAGGCTATTACAGTG 17362
Qy 541 GATTTTCAGCCTCTATACCTTACTAAACGFGATAAAAGTTTCTGTAAATTTCTACTGTATCGA 600
Db 17361 ACAGTTGACAGCGACGCTATCAGTTGTCTCAAGGCATATATGATGTCATATCTCCGGTC 17302
Qy 601 CCTGCAGACTGGCTGTGTATTAAGGAGGCTGACATTTATATTTCCCAAGACATCAGGTTA 660
Db 17301 TGGTAAGCACACCAATGAGAGATGAAGCCCGCTGCTGGTGCC---GAACGCTGGAAG 17245
Qy 661 ATGGGCTTTTATGCTCATTTTCGGGCTGGCTGAGATCAGCCACTTTCTTCCCGGATAACG 720
Db 17244 CGAATAATCAGAAAGGATGGCTGAGTGCCTGGCTTTTATGAAATGAACGCTCTTTTG 17185
Qy 721 GAGACGGGCACTGGCCATATCGGTGTCATCATGCGGCAGCTTTTATCCCGATATGCG 780
Db 17184 CTGACGAGAACAGG-----ACTGGTGAATGTCAGTTTAAAGTTTACACCTTATAAAGA 17131
Qy 781 ACCACGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGG 840
Db 17130 GAGAGCGGTTATCGTCTGTTGTGGANGTACAGAGTGATATTTATGACACGCCCGGGCA 17071
Qy 841 ATCACCATCCGTGCGCGGCGGTGTCATAATATCACTGTACATCCACAACACAGCA 900
Db 17070 CGGATGGTGATCCCTCTGCCAGTGCAGCTGCTGTAGATAAAGTCTCCCGTGAACCT 17011
Qy 901 TAAAGGCTCTCTCTTTATAGTGTAACCTTTAACTGCACTTTTACC-----AGTCCCT 954
Db 17010 TACCGGCTGGTCATATCGGGATGAAGCTGGCGCATGATCACACCGCATATGGCCAGT 16951
Qy 955 GTTCTGTCAGCAAAAGAGCGGTTCAATTAACCGGGGACCTCAGCCATCCCTTC 1014
Db 16950 GTGCGGCTCGTTATCGGGAGAGTGGCTGATCTCAGCACCGCGAAATGACATC 16891
Qy 1015 CTGATTTTCGGCTTCCAGCGTTC---GGCAGCAGACGAGCGGCTTCATCTGCAAGG- 1070
Db 16890 AAAACGCGCATTAACCTGATGTTCTGGGAATATAAATGTCAGGCTCCCTTATACACAG 16831
Qy 1071 --TTGTCCTTACAGACCGGAGATATGATCATATATAGCTTGAGCACTGATAGCTG 1128
Db 16830 CAGTCTCAGGTCGATACAGTAGAATATACAGAACTTTATACGTTTGTAGATATAGA 16771
Qy 1129 TCGCTCTCACTGCTGCTAATACGCTGCTCATAGCACACCTCTTTTGTGACATACCTC 1188
Db 16770 GGCTGAATCCAGATGAACCGACGACGTGTAAAGAGAAAGTAAAGAGTTGTGAAT 16711
Qy 1189 GGTAGTGGCGATCAAGCTCTCATTTTGCAGAAAGTTGGCCAGGCTTCCGGTATCA 1248
Db 16710 GGGTAGTGGCGATCAAGCTCTCATTTTGGCAAAAGTTGGCCAGGCTTCCCGGTATCA 16651
Qy 1249 ACAGGACACCGAGTTTATTTATCTGCAAGTGTATCTTCCGTCACAGGTATTTATCG 1308
Db 16650 ACAGGACACCGAGTTTATTTATCTGCGAGTGTATCTTCCGTCACAGGTATTTATCG 16591
Qy 1309 GCGCAAGTGGCTGGGTGATGCTGCCAATTTAGTGCATACAGGTCACTTAATACCATCT 1368
Db 16590 GCGCAAGTGGCTGGGTGATGCTGCCAATTTAGTGCATACAGGTCACTTAATACCATCT 16531
Qy 1369 AAGTAGTGTATCATAGTGTATGATGTTGTTTACAGTATATGAGTCTGTTTT 1428
Db 16530 AAGTAGTGTATCATAGTGTATGATGTTGTTTACAGTATATGAGTCTGTTTT 16471
Qy 1429 TTATGCAAAATCTAATTTAAT 1488
Db 16470 TTATGCAAAATCTAATTTAATATATATATATATATATATATATATATATATATATAT 16411
Qy 1489 TTCTTGTACAAAGTTGGCATTTAAGAAAGCAITTTGCTTATCAATTTGTTGCAACGAAACAG 1548
Db 16410 TTCTTGTACAAAGTTGGCATTTAAGAAAGCAITTTGCTTATCAATTTGTTGCAACGAAACAG 16351
Qy 1549 GTCACTATCAGTCAAAATATAATCATTTATTTGCCATCCAGTGTGAGTCTC---GTGAGGAAT 1607
Db 16350 GTCACTATCAGTCAAAATATAATCATTTATTTGCCATCCAGTGTGAGTCTC---GTGAGGAAT 16291

Qy 1608 TCGTACCCCAATTTGGTAAGGAA-----TAATATATTTCTTTTCTCTTTTAG 1656
Db 16290 CAAGCTTATCGAATTTCCGAACCCCAATTTCCCACTGTAATCAATCAATGTAAATCAAT 16231
Qy 1657 TATAAATAGTAAAGTGTAAATAGTATGATTAATAAATATAGTGTATATATAT 1716
Db 16230 GATAACACAATGACATGATCTATCATGTTTACCTTTGTTTATTCATGTCGACTAATTCAT 16171
Qy 1717 GAAAAATATATTAATAATATATTTTACATAAACAACATAGTAATGTAAATAATATG 1776
Db 16170 TAATTAATAGTCAATCCATTTAGAAAGTTAAATAAACAACATAGTAATTTTGAATAAT 16111
Qy 1777 ACAAGTGTATGTAAGCAAGAGATAAAAGTTGAGAG-----TAAGTATATTA 1826
Db 16110 AAGAAATGTTGTTGAAATAATATCTATATAAATAGATAGATCTTCCGCTTTGTTATATTA 16051
Qy 1827 TTTTAAATGAATTTGATCGAACTGTAAGATGATATACGGCGGTAAAGGTTCCAACT 1886
Db 16050 GCATTTAGATTTATGTTTGTACATTTAGATTTACTGTTCTTATTTAGTATTTATTTCT 15991
Qy 1887 TCACCAATGAATAAGATCACTACCGGCGTATTTTTCAGTTATCGAGATTTTCAGG 1946
Db 15990 ACTTTAGCTTGTAT-----TAATATTTTGTTTATTTGACAAATTAACAAGCAGATTTGAAT 15935
Qy 1947 AGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCA 2006
Db 15934 TTCTAAACAATAATTTATTAACCTTTAACTAAATAATTTAGTATGATATAGATATTTA 15875
Qy 2007 ATGGCATCGTAAGAAACAATTTTGGCGATTTTCACTGAGTGTCTCAATGTACTATTAACA 2066
Db 15874 ATTATATAATAAATTAATTAATCATAAAAAATATTTTAAATTTTATTTTCTTTT 15815
Qy 2067 GACCTTTCAGCTGGATATACGGCTTTTAAAGACCGTAAAGAAAAATAAGACACAAGTT 2126
Db 15814 TACTATAGTATTTTATCATTTGATATTTAATTTCTCAACACGCTAGATTTACTATATG 15755
Qy 2127 TTATCCGGCTTTATTTCACTTTTCCCGCTGATGATGCTCATCCGGAATTCGAT 2186
Db 15754 GCCCGACATATCAGTATATATTTCTTATACCGCAAAATCAGCGCAAAATACGCATCTG 15695
Qy 2187 GCAATGAAGACGCTGAGTGTGATATGAGTATGTTTCACTGCTTTTGA---CACCGTT 2244
Db 15694 TTATCTGGCTTTTGTAGTACCGGATCCAGCGAATTAOGCCCGCTCCCATCTATCGCA 15635
Qy 2245 TTCCATGACAACTGAACGTTTTCATGCTCTGGAGTGAATACACACGAGTTTCCG 2304
Db 15634 GTACTGTTGATTTCAATTAAGCATTTCTCCGACATGGAGCCATCACAGACGCAATGAT 15575
Qy 2305 CAGTTTCTACATATATTTCCGAAGTGTGGCGGTGTACGGTGAATAACCTGGCTATTTTC 2364
Db 15574 AACCTGAATCGCCAGCGCATCAGCACCTTTGTCGCTTCCGTATATATTTTGGCCATG 15515
Qy 2365 CTTAAAGGTTTATTTGAGATATATTTTTCGCTCAGCCCAATCCCTGGGTGAGTTTCAC 2424
Db 15514 GAAAAAGGCGGAGAAAGTTGTCCATATGGCCAGTTTAAATCAAAACTGTTGAACT 15455
Qy 2425 AGTTTGTATTAACCGTGCCCAATATGGAACAACCTTCCGCCCCGCTTTTCCACATGG 2484
Db 15454 CACCCAGGATTTGGCTGAGACCGAACAACATATTTCAATAAACCTTTTAGGGAATATG 15395
Qy 2485 AAATATTAACGCAAGGCGACAGGTGTGATGTCGCTGGCGATTCAGGTTTCAATGCGC 2544
Db 15394 CAGTTTTCACCGTAACACGCCACATCTTTCGCAATATATGTTAGAACTCCGGAATC 15335
Qy 2545 GTCTGTGTGCTTCCATCTCGGCAGATGCTTAATGAATTAACAAGTACTGCGATGAG 2604
Db 15334 GTCTGTGTATTTCACTCAGAGCGATGAAACGTTTTCAGTTTGTCTATGGAACG---GTG 15277
Qy 2605 TGGCAGGCGGGGCTTAATCGGCTGATCGGCTTACTAAAAAGCCAGATAACAGTATGCG 2664
Db 15276 TAACAAGGTTGAACACTATCTCCCATATCACCAAGCTCACCGCTTCTTTCATTTGCCATACGGAAT 15217

QY 2665 TATTTGCGGCTGATTTTTCGGGTATAAGAAATATATACTGATATGTCGGGCCCAATAATAG 2724
Db 15216 TCCGATGAGCATTCATCAGCGGGCGAAGATGTAATAAGCCGGATAAACTTGTGC 15157
QY 2725 TAAATCTAGCTGGTTTGATGAATTAATAATCAATGATAAATAATCTATAGTAAAAATAAGA 2784
Db 15156 TTAATTTTCTTTACGGCTCTTTAAAAAGCGGTAATATCCAGCTGAACGGCTCGGTTATAG 15097
QY 2785 ATAAATTAATTAATAATAATTTTATGATTAATAGTTTATTAATTAATAATAATAATCT 2844
Db 15096 GTACATTGAGCACTGACTGAATGCGCTCAAAATGTTCTTTAGCATGCCATTGGGATATA 15037
QY 2845 ATACCAATTAATAATAATTTTAGTTTAAAAAGTTAAATAATTAATTTGTTAGAAATTCGAATC 2904
Db 15036 TCAACGGTGGTATATCCAGTGATTTTCTCCATTTAGCTTCTCTAGCTCTCTGAAAT 14977
QY 2905 TCGTTGTAATTTATCAATAAACAATAATTA---ATAACAGCTAABAGTAACAAATAA 2960
Db 14976 CTGATAAATCAAAAAATAGCCCGGTAGTATCTTTATTTCAATTATGGTGAAGTTGGAA 14917
QY 2961 TATCAAACTAATAGAACAGTAACTTAATGTAACAAAAATAATCAATCAATGCTAATAATAAC 3020
Db 14916 CTTCTTACCGCGGTATATCACTTACATGTTGCTGATCAAAATTCATTAABAAATAATACT 14857
QY 3021 AAAGCGCAAGATCTATCATTTTATATAGTATTAATTTCAATCAACAAATCTTATTAATTTT 3080
Db 14856 TA-----CTCTCAACTTTTAACTTCTTCTGCTTACACATCACTTTGTCAATATTTT 14807
QY 3081 TAAATAATCTCTAGTTTATTAACCTTAACTTGAATGATGACTTATTAATTAATAATGAATTA 3140
Db 14806 TTAATTTATCTAGTTTATGTAACAATAATATTTTAATAATTTTATTTTCAAAATATA 14747
QY 3141 GTCGAACATGAATAAACAAGGTAACTATGATGATCATGTCATTTGTTATCATGATCTT 3200
Db 14746 ACACTATATTTATTAATCACTAATTAACATCACTTAACTATTTTATCTAAAAAGGA 14687
QY 3201 ACATTTGGATGATTAAGTTGGGAATTTGGTTTGGAAATCGATAAGCTTGGATCTCTTA 3260
Db 14686 AAAAAGAAATAAT-----ATTTCTTACCAATTTGGGGTACCGAAATCTCTCGA 14638
QY 3261 GAGAGCTGACCTGGATGGCAATAATGATTTTATTTTACTGATGATGACCTGTTCTGTT 3320
Db 14637 G-GAGCTGACCTGGATGGCAATAATGATTTTATTTTACTGATGATGACCTGTTCTGTT 14579
QY 3321 GCAACAAATTTGATTAAGCAATCTTTCTTATTAATGCCAACTTTGTACAAAGACGTAACG 3380
Db 14578 GCAACAAATTTGATTAAGCAATCTTTCTTATTAATGCCAACTTTGTACAAAGACGTAACG 14519
QY 3381 AGAAACGTAAATGATATTAATATCAATATTAATTAATTAATTTTGTATTAATAAACAAGAC 3440
Db 14518 AGAAACGTAAATGATATTAATATCAATATTAATTAATTAATTTTGTATTAATAAACAAGAC 14459
QY 3441 TACATAATCTGTAATAACAACAATATCCAGTCACTATGAATCACTACTTTAGATGGTAT 3500
Db 14458 TACATAATCTGTAATAACAACAATATCCAGTCACTATGAATCACTACTTTAGATGGTAT 14399
QY 3501 TAGTGACCTGTAGTCGATAGTTGGCAGCATCACCGCAGCATCTTTCGGCGCGCAATTAAT 3560
Db 14398 TAGTGACCTGTAGTCGATAGTTGGCAGCATCACCGCAGCATCTTTCGGCGCGCAATTAAT 14339
QY 3561 ACCTGTGACGGAGATCACTTCGAGAAATAATAATCTGTTGCTGCTGTTGATACCGG 3620
Db 14338 ACCTGTGACGGAGATCACTTCGAGAAATAATAATCTGTTGCTGCTGTTGATACCGG 14279
QY 3621 GAAGCCCTGGGCAACTTTTGGCGAAATAGACGCTTGATCGGCACTACCCATTTTCAAA 3680
Db 14278 GAAGCCCTGGGCAACTTTTGGCGAAATAGACGCTTGATCGGCACTACCCAGATATGT 14219
QY 3681 CTCTTATCTTTCTCTTACAAGTCGTTCCGGCTTCACTGGAATTTTACGGCTCTATCTT 3740
Db 14218 CAAAAGAGGTGTGCTATGAA---GCAGGGTATTAACAGTGACAGTTTGACAGCAGCATTA 14162
QY 3741 ACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTTGCAGACTGGCTGTAT 3800

Db 14161 TCATTTGCTCAAGCATATATGATGTCAATATCTCCGGTCTGTAAGCAACAACCATGCAG 14102
QY 3801 AAGGAGCCTGACATTTATATTTCCCAAGAACATCAGGTTAATAGCGTTTATTTGATGTCTAT 3860
Db 14101 AATGAAGCCCTGCTCTGCGTGCC---GAACGCTGGAAGCGAANAATCAGNAAGGATG 14045
QY 3861 TTCCGGGCTGTAGATCAGCACTTTCTTCCCGATTAACGAGACCGGCACACTGGCCAT 3920
Db 14044 GCTGAGGTCGCGCCGTTTATTAATAAGAACGGCTCTTTTGTCTGACGAGAACAGG--- 13990
QY 3921 ATCGTGTGTCATCATGCGCCAGCTTTTCACTCCCGATATGACCAACCGGTTAAAGTTACG 3980
Db 13989 -ACTGCTGAATGCAAGTTTAAAGTTTACACCTATAAAGAGAGAGCGCTTATCGTCTGT 13931
QY 3981 GGAGACTTTATCTGACAGACAGCTGCACTGCCAGGGGATACCATCCGTCGCCCGG 4040
Db 13930 TGTGATCTACAGAGTGATATTTATGACACGCCCGCGGCGAGGATGGTGATCCCCCTCGC 13871
QY 4041 CGTGTCAATATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATA 4100
Db 13870 CAGTCCACGTCGTGTGATGATAAAGTCTCCCGTGAACTTTTACCGGTGGTGATATCGG 13811
QY 4101 GGTGTAAACCTTAAACTGCAATTTCAACA-----GTCCCTGTTCTCGTCAGCAAAAGAGC 4154
Db 13810 GGATGAAGCTGGCGCATGATGACCAACGATATGCGAGTGTGCGGTCTCCGTTATCGG 13751
QY 4155 CGTTCAATTTAAATAAAGCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGC 4214
Db 13750 GGAAGAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAACCTGAT 13691
QY 4215 GTTC---GSCGCGACAGACGGGCTTCACTCTGATG---TTGTGCTTACCAGACCGG 4268
Db 13690 GTTCTGGGAATTAATGTTGAGGCTCCCTTATACACSCCAGTCTGCAAGTCGATACAG 13631
QY 4269 AGATATTTGATCATATATATGCTTGGAGCAACTGATAGCTGTGCTGTCACTGTACTGT 4328
Db 13630 TAGAAATTAACAGAACTTTTATCAGCTTTAGTAAGTATAGAGGCTGAAAAATCCAGATGAAG 13571
QY 4329 AATACGCTGCTCATAGACACCTCTTTTGTACATCTTCTGTTCTTGTATGAGATGAT 4388
Db 13570 CCGAACGACTTGTGAAGAGAAAAGTATAAGAGTTGTGAAATGTTCTTGTATGAGATGAT 13511
QY 4389 TTCAAGACTATGACACTAGCGTATATGAATAGTAGATGCTTTTATTTTGTTCACAAAA 4448
Db 13510 TTCAAGACTATGACACTAGCGTATATGAATAGTAGATGCTTTTATTTTGTTCACAAAA 13451
QY 4449 ARGAGCTGCGACCTCTTTTCTTATTTCTTTTATGATTAATACGGCATTTGAGGACAA 4508
Db 13450 ARGAGCTGCGACCTCTTTTCTTATTTCTTTTATGATTAATACGGCATTTGAGGACAA 13391
QY 4509 TAGCGAGTGGCTGGATACGACATTCGGTTTTCAGAAACAATTTGGAAGGCTGTCCGTC 4568
Db 13390 TAGCGAGTGGCTGGATACGACATTCGGTTTTCAGAAACAATTTGGAAGGCTGTCCGTC 13331
QY 4569 GACTAAGTTGGCAGCATCACCCGAAAGAACATTTGGAAGGCTGTCCGTCGACTACAGTCA 4628
Db 13330 GACTAAGTTGGCAGCATCACCCGAAAGAACATTTGGAAGGCTGTCCGTCGACTACAGTCA 13271
QY 4629 CTAATACCATCTAAGTAGTTGATTCATAGTACCTGAGTATGTTGTTTACAGATTTAT 4688
Db 13270 CTAATACCATCTAAGTAGTTGATTCATAGTACCTGAGTATGTTGTTTACAGATTTAT 13211
QY 4689 GTAGTCTGTTTATGCAAAATCTAATTTAATATATTTATATTTATATCATTTTACGTT 4748
Db 13210 GTAGTCTGTTTATGCAAAATCTAATTTAATATTTATATTTATATCATTTTACGTT 13151
QY 4749 TCTCGTTCAGCTTTTGTACAAAGTTGGCAATTAATAAAGCAATTCGCTCATCAATTTGT 4808
Db 13150 TCTCGTTCAGCTTTTGTACAAAGTTGGCAATTAATAAAGCAATTCGCTCATCAATTTGT 13091
QY 4809 TGCAACGACAGGTCACTATCATCAAGTCAAAATAAATCATTTATTTGGGCGCCGAG 4861

Db 13090 TCGAACGAAAGGTCACATCATGTCGCAAAATAAAATCAATATTGCGGCCGAG 13038

RESULT 6
AAC55521
ID AAC55521 standard; DNA; 4470 BP.
XX AAC55521;
AC AAC55521;
XX
DT 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR201 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO20052027-A1.
XX
XX 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-012388P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GP, Cheo D;
PI
XX
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
PS Example 9; Fig 49; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
Query Match 24.5%; Score 1193; DB 3; Length 4470;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CGGGCCCCCAATATGATTTTATTTGACTGATAGTACCTGTTCGTCACAAATTTGA 60
|||||

Db 21 CGGGCCCCCAATATGATTTTATTTGACTGATAGTACCTGTTCGTCACAAATTTGA 80
QY 61 TGAGCAATGCTTTTATTAATGCAACTTTGTACAAAAAGCTGAAACGAGAAACGTAATA 120
Db 81 TGAGCAATGCTTTTATTAATGCAACTTTGTACAAAAAGCTGAAACGAGAAACGTAATA 140
QY 121 TGATATAAATATCAATATATTAATTTAGATTTTCATATAAAACAGACTACATATACTG 180
Db 141 TGATATAAATATCAATATATTAATTTAGATTTTCATATAAAACAGACTACATATACTG 200
QY 181 TAAACACACACATATCCAGTCACTATGAATCAACTACTTAGATGATTTAGTGCCTGTA 240
Db 201 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGATTTAGTGCCTGTA 260
QY 241 GTGACGACGAGCCTTCCAAATGTTCTCGGGTGTAGTCTGCAACTTAGTGCACGACAG 300
Db 261 GTGACGACGAGCCTTCCAAATGTTCTCGGGTGTAGTCTGCAACTTAGTGCACGACAG 320
QY 301 CTTTCCAAATGTTCTTCTCAACGGAATCGTCTGATCCAGCCTACTCGCTATTTGCTTCA 360
Db 321 CTTTCCAAATGTTCTTCTCAACGGAATCGTCTGATCCAGCCTACTCGCTATTTGCTTCA 380
QY 361 ATGCGGTATTAATATCATATAAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTTGTGTG 420
Db 381 ATGCGGTATTAATATCATATAAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTTGTGTG 440
QY 421 ACATAATATAACATCTACCTATTTCATATAGCTAGTGTGATGCTCTGTAATAATCATCTG 480
Db 441 ACATAATATAACATCTACCTATTTCATATAGCTAGTGTGATGCTCTGTAATAATCATCTG 500
QY 481 CATCAAGAACCAATTTTCACTATATCTTTCTTCTTACAAGTCTGTTGGGCTTCATCTG 540
Db 501 CATCAAGAACCAATTTTCACTATATCTTTCTTCTTACAAGTCTGTTGGGCTTCATCTG 560
QY 541 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGATCGA 600
Db 561 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGATCGA 620
QY 601 CTGACAGACTGGCTGTGTATTAAGGAGGCTGACATTTATATTTCCCGAGAACATCAGTTA 660
Db 621 CTGACAGACTGGCTGTGTATTAAGGAGGCTGACATTTATATTTCCCGAGAACATCAGTTA 680
QY 661 ATGGGGTTTTGATGTCATTTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAAGC 720
Db 681 ATGGGGTTTTGATGTCATTTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAAGC 740
QY 721 GAGACCGGCACACTGGCCATATCGGTGTGTCATCTGCGGAGCTTTTCATCCCGGATGTC 780
Db 741 GAGACCGGCACACTGGCCATATCGGTGTGTCATCTGCGGAGCTTTTCATCCCGGATGTC 800
QY 781 ACCACCGGTAAGTTTCAGGGAGACTTTTATCTGACAGCAGACGTGCACTGGCCAGGGGG 840
Db 801 ACCACCGGTAAGTTTCAGGGAGACTTTTATCTGACAGCAGACGTGCACTGGCCAGGGGG 860
QY 841 ATCACCATCCGTCGCGCGGGGGTGTCAATAATATCACTGTATCATCCACAAACAGACGA 900
Db 861 ATCACCATCCGTCGCGCGGGGGTGTCAATAATATCACTGTATCATCCACAAACAGACGA 920
QY 901 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGATTTTACCAGTCTCTGTTCTC 960
Db 921 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGATTTTACCAGTCTCTGTTCTC 980
QY 961 GTGACGAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 981 GTGACGAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1040
QY 1021 TTTCCGCTTTCCAGCGTTTCGGCAGCAGCGGGCTTCATTCTGTCATGGTTGTGCTTAC 1080
Db 1041 TTTCCGCTTTCCAGCGTTTCGGCAGCAGCGGGCTTCATTCTGTCATGGTTGTGCTTAC 1100
QY 1081 CAGACCGGAGATTTGACATCATATATGCTTTGAGCAATGTAGTCTGCGCTGTCAACT 1140
Db 1101 CAGACCGGAGATTTGACATCATATATGCTTTGAGCAATGTAGTCTGCGCTGTCAACT 1160

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QY 1141 GTCACCTGAATACGCTCTTCATAGCACACCTCTTTTGTGACATATTCGGGTA 1193
DB 1161 GTCACCTGAATACGCTCTTCATAGCACACCTCTTTTGTGACATATTCGGGTA 1213

RESULT 7
ID AB258767 standard; DNA; 4470 BP.
XX AC AB258767;
XX DT 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR201 nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX PN WO200295055-A2.
XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US015947.
XX PR 21-MAY-2001; 2001US-0291973P.
XX PA (INVI-) INVITROGEN CORP.
XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX DR WPI; 2003-129436/12.
XX PT Inserting a population of nucleic acids into a second target molecule for
XX PT selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid.
XX PS Disclosure; Fig 26B-C; 273pp; English.
XX CC The invention relates to inserting a population of nucleic acids into a
XX CC second target molecule. The method involves (a) mixing a first population
XX CC of nucleic acid comprising one or more recombination sites with a target
XX CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX CC the first population to recombine with the first target nucleic acid
XX CC molecules to form a second population; (c) mixing the second population
XX CC of nucleic acid with a second target nucleic acid; and (d) causing some
XX CC or all of the nucleic acid molecules of the second population to
XX CC recombine with some or all of the second target nucleic acid molecules to
XX CC form a third population of nucleic acid. The method is useful for
XX CC selecting and isolating nucleic acid molecules. The present sequence
XX CC represents the destination plasmid pDONR201 nucleotide sequence
XX SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.5%; Score 1193; DB 7; Length 4470;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTGACTGATGACCTCTTCGTTGCAACAAATGGA 60
DB 21 CGGGCCCCAAATAATGATTTTATTTGACTGATGACCTCTTCGTTGCAACAAATGGA 80
QY 61 TGAGCAATGCTTTTATATGCACTTTGTTGACAAAAGCTGAACGAGAAACGTAAAA 120
DB 81 TGAGCAATGCTTTTATATGCACTTTGTTGACAAAAGCTGAACGAGAAACGTAAAA 140
QY 121 TGATATAATATCAATATATTAATAGATTTTGTGATAAAAACAGACTACATATCTG 180
DB 141 TGATATAATATCAATATATTAATAGATTTTGTGATAAAAACAGACTACATATCTG 200
QY 181 TAAACACAAATATCCAGTCACTATGAATCACTACTTAGATGGTATTAGTGACCTGTA 240
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DB 201 TAAACACAAATATCCAGTCACTATGAATCACTTAGATGGTATTAGTGACCTGTA 260
QY 241 GTCGACCGACAGCCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTGCAACGACAG 300
DB 261 GTCGACCGACAGCCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTGCAACGACAG 320
QY 301 CTTTCCAAATGTTCTTCTCAAACGGAATGCTGTATCCAGCCTACTCGCTATTGTCTCA 360
DB 321 CTTTCCAAATGTTCTTCTCAAACGGAATGCTGTATCCAGCCTACTCGCTATTGTCTCA 380
QY 361 ATGCCCTATTAAATCATATAAAGAAATAGAAAGAGGTGCGAGCTCTTTTGTGTG 420
DB 381 ATGCCCTATTAAATCATATAAAGAAATAGAAAGAGGTGCGAGCTCTTTTGTGTG 440
QY 421 ACAAATAAATAACATCTACTATTATACGCTAGTGTATAGTCTGAAATATCTG 480
DB 441 ACAAATAAATAACATCTACTATTATACGCTAGTGTATAGTCTGAAATATCTG 500
QY 481 CATCAAGAACAAATTCAGAACTCTTATCTTTCTCTTCAAGTCTGTTGGCTTCACTG 540
DB 501 CATCAAGAACAAATTCAGAACTCTTATCTTTCTCTTCAAGTCTGTTGGCTTCACTG 560
QY 541 GATTTTCAGCCTCTATCTACTTAAACGCTGATAAAGTCTTCTGTAATTTCTACTGTATCGA 600
DB 561 GATTTTCAGCCTCTATCTACTTAAACGCTGATAAAGTCTTCTGTAATTTCTACTGTATCGA 620
QY 601 CTTGACAGCTGGCTGTATTAAGGAGCCTGACATTTATATCCAGAAACATCAGGTTA 660
DB 621 CTTGACAGCTGGCTGTATTAAGGAGCCTGACATTTATATCCAGAAACATCAGGTTA 680
QY 661 ATGGCGTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720
DB 681 ATGGCGTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 740
QY 721 GAGACCGGCACACTGGGCCATATCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGC 780
DB 741 GAGACCGGCACACTGGGCCATATCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGC 800
QY 781 ACCACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGG 840
DB 801 ACCACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGG 860
QY 841 ATCACCATCGTCGCGCGGCTGTCAATAATATCACTCTGTATCATCCACAAACAGACGA 900
DB 861 ATCACCATCGTCGCGCGGCTGTCAATAATATCACTCTGTATCATCCACAAACAGACGA 920
QY 901 TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTACAGTCCCTGTCTC 960
DB 921 TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTACAGTCCCTGTCTC 980
QY 961 GTCAGCAAAAGAGCCGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTCAT 1020
DB 981 GTCAGCAAAAGAGCCGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTCAT 1040
QY 1021 TTCCGCTTTTCAGCGTTCCGACGACGACGACGCGGCTTCAATTTGATAGTTGTGCTTAC 1080
DB 1041 TTCCGCTTTTCAGCGTTCCGACGACGACGACGCGGCTTCAATTTGATAGTTGTGCTTAC 1100
QY 1081 CAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTGCTGTCAACT 1140
DB 1101 CAGACCGGAGATATTGACATCATATATGCGCTTGAGCAACTGATAGCTGTGCTGTCAACT 1160
QY 1141 GTCACTGTATACGCTCTTCAATAGCACACCTCTTTTGTGACATCTTCCGGTA 1193
DB 1161 GTCACTGTATACGCTCTTCAATAGCACACCTCTTTTGTGACATCTTCCGGTA 1213

RESULT 8
ADAS0329 standard; DNA; 4892 BP.
XX ID ADAS0329
XX AC ADAS0329;
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XX DT 20-NOV-2003 (first entry)
XX DE Plasmid vector pMK2010 DNA sequence.
XX KW site-specific recombination; array construction; reporter gene fusion;
XX KW mutagenesis; protein production; protein characterisation;
XX KW plasmid pMK2010; ds.
XX OS Synthetic.
XX PN WO2003064623-A2.
XX PD 07-AUG-2003.
XX PF 31-JAN-2003; 2003WO-US03176.
XX PR 31-JAN-2002; 2002US-0354063P.
XX PS (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX PI Kahn ML, House BL, Mortimer MW;
XX DR WPI; 2003-679497/64.
XX PT Moving an insert nucleic acid between vectors using site-specific
XX PT recombination in vivo, useful for studying the biology of the organism,
XX PT including array construction, reporter gene fusions, mutagenesis and
XX PS protein production.
XX PS Claim 41; Page 47-51; 52pp; English.
XX CC The invention comprises a method for moving an insert nucleic acid
XX CC molecule between vectors, the method involves moving an insert nucleic
XX CC acid from one vector to another using site-specific recombination. The
XX CC method of the invention is useful for studying the biology of an
XX CC organism, including array construction, reporter gene fusions,
XX CC mutagenesis, protein production and characterisation. The present DNA
XX CC sequence represents the plasmid vector pMK2010 of the invention.
XX SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
Query Match 24.5%; Score 1193; DB 8; Length 4892;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCCCAAATAATGATTTTATTTTGAAGTGTGACCTGCTGCTGCAACAAATGA 60
DB 21 CGGGCCCCAAATAATGATTTTATTTTGAAGTGTGACCTGCTGCTGCAACAAATGA 80
QY 61 TGAGCAATGCTTTTATTAATGCGCACTTTGTACAAAAGCTGAACGAGAAAGTAAAA 120
DB 81 TGAGCAATGCTTTTATTAATGCGCACTTTGTACAAAAGCTGAACGAGAAAGTAAAA 140
QY 121 TGATATAATATCAATATTAATTAATTAATTTGCTATTAATAAAGAGCTACATTAATCTG 180
DB 141 TGATATAATATCAATATTAATTAATTAATTTGCTATTAATAAAGAGCTACATTAATCTG 200
QY 181 TAAACACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 240
DB 201 TAAACACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 260
QY 241 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAG 300
DB 261 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAG 320
QY 301 CTTTCCAAATGTTCTTCTCAACAGCAATGCTGATCCAGCTACTGCTATTGTCCTCA 360
DB 321 CTTTCCAAATGTTCTTCTCAACAGCAATGCTGATCCAGCTACTGCTATTGTCCTCA 380
QY 361 ATGCCGTATTAAATCATAAAAAGAAATAAGAAAAAGAGGTGCGACCTCTTTTGTGTG 420
DB 381 ATGCCGTATTAAATCATAAAAAGAAATAAGAAAAAGAGGTGCGACCTCTTTTGTGTG 440

QY 421 ACAAAATAAAAAATCTACTACTATTCATATACGCTAGTGTATAGTCTCTGAAATCATCTG 480
DB 441 ACAAAATAAAAAATCTACTACTATTCATATACGCTAGTGTATAGTCTCTGAAATCATCTG 500
QY 481 CATCAAGAACAAATTTCCAAACTCTTATATCTTTCTTACAAAGTCCCTCGGCTTCACTG 540
DB 501 CATCAAGAACAAATTTCCAAACTCTTATATCTTTCTTACAAAGTCCCTCGGCTTCACTG 560
QY 541 GATTTTTCAGCCTCTATATCTTACTTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
DB 561 GATTTTTCAGCCTCTATATCTTACTTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGA 620
QY 601 CTTGCGAGCTGCTGTATTAAGGGAGCTGACATTTATATCCCGACAGACATCAGGTTA 660
DB 621 CTTGCGAGCTGCTGTATTAAGGGAGCTGACATTTATATCCCGACAGACATCAGGTTA 680
QY 661 ATGGCGTTTGTATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAAAG 720
DB 681 ATGGCGTTTGTATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAAAG 740
QY 721 GAGACCGGCACACTGGCCATATCGTGGTCAATCGGCGAGCTTATCTGACAGAGAGTGCACGTGGCGGGG 840
DB 741 GAGACCGGCACACTGGCCATATCGTGGTCAATCGGCGAGCTTATCTGATATCACTCTGTATCACTCAAAACAGACGA 920
QY 901 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTC 960
DB 921 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTC 980
QY 961 GTCAGCAAAAGAGCGGTTCAATTAACCGGGGACCTCAGCCATCCCTTCTCTGATT 1020
DB 981 GTCAGCAAAAGAGCGGTTCAATTAACCGGGGACCTCAGCCATCCCTTCTCTGATT 1040
QY 1021 TTCCGCTTTCCAGCTTCCGCGACGACAGACGAGCGGCTTCAATCTGCAATGGTGTGCTTAC 1080
DB 1041 TTCCGCTTTCCAGCTTCCGCGACGACAGACGAGCGGCTTCAATCTGCAATGGTGTGCTTAC 1100
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAAGCACTGATAGCTGCTGCTCAACT 1140
DB 1101 CAGACCGGAGATATTGACATCATATATGCTTGAAGCACTGATAGCTGCTGCTCAACT 1160
QY 1141 GTCACTGTATACGCTCTCTCATAGCACACCTCTTTTTCATCTACTTTCGGGTA 1193
DB 1161 GTCACTGTATACGCTCTCTCATAGCACACCTCTTTTTCATCTACTTTCGGGTA 1213
RESULT 9
AAC55525
ID AAC55525 standard; DNA; 4939 BP.
XX AC AAC55525;
XX DT 11-JAN-2001 (first entry)
XX DE Donor plasmid pDONR205 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
XX OS Synthetic.
XX PN WO200052027-A1.
XX

XX WC00052027-AL.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US005432.
XX PR 02-VAR-1999; 99US-0122389P.
XX PR 23-VAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX
XX Disclosure; Fig 97; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (1), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is used
XX in the exemplification of the present invention
XX
XX Query Match 24.5%; Score 1193; DB 3; Length 5584;
XX Best Local Similarity 100.0%; Pred. No. 1e-156;
XX Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CGGGCCCCCAATGATTTTATTTTGGCTGATGACCTGTTGGTTCGACCAAAATTGA 60
XX 5564 CGGGCCCCCAATGATTTTATTTTGGCTGATGACCTGTTGGTTCGACCAAAATTGA 5505
XX
XX 61 TGAGCAATGCTTTTATTAAGCCAACTTTTGACAAAAGCTGAACGAGAAACCTTAAA 120
XX 5504 TGAGCAATGCTTTTATTAAGCCAACTTTTGACAAAAGCTGAACGAGAAACCTTAAA 5445
XX
XX 121 TGATATAATATCAATATATTAATTTAGTATTTTGCATATAAAACAGACTACATATAC 180
XX 5444 TGATATAATATCAATATATTAATTTAGTATTTTGCATATAAAACAGACTACATATAC 5385
XX
XX 181 TAAACACACATATCCAGTCTACTATGAATCAACTACTTAGATGGTATTAGTGA 240
XX 5384 TAAACACACATATCCAGTCTACTATGAATCAACTACTTAGATGGTATTAGTGA 5325
XX
XX 241 GTGACCGCAGAGCTTCCAAATGTTCTTGGGTGATGCTGGCAACTTAGTCGACGACAG 300
XX 5324 GTGACCGCAGAGCTTCCAAATGTTCTTGGGTGATGCTGGCAACTTAGTCGACGACAG 5265
XX 301 CCTTCCAAATGTTCTTCTCAACGGGAATCGTGGTATCCAGCCTACTCGCTATTGCTCA 360

DB 5264 CTTTCCAAATGTTCTTCTCAACGGGAATCGTGGTATCCAGCCTACTCGCTATTGCTCA 5205
QY 361 ATGCGGTATTAATCATATAAAAGAAATAGAAAAGAGGTGGAGCCTCTTTTGTGTG 420
DB 5204 ATGCGGTATTAATCATATAAAAGAAATAGAAAAGAGGTGGAGCCTCTTTTGTGTG 5145
QY 421 ACATAATAAAAACATCTACCTATTTCATATAGCTAGTGTATAGTCTTGAATAATCATCTG 480
DB 5144 ACATAATAAAAACATCTACCTATTTCATATAGCTAGTGTATAGTCTTGAATAATCATCTG 5085
QY 481 CATCAAGAACAAATTTCAAACTCTTATATCTTTTCTTACAAAGTCTTGGCTTCACTG 540
DB 5084 CATCAAGAACAAATTTCAAACTCTTATATCTTTTCTTACAAAGTCTTGGCTTCACTG 5025
QY 541 GATTTTCAGCCTCTATATCTTAAACGCTGATAAGTTTCTGTAATTTCTAGCTATCGA 600
DB 5024 GATTTTCAGCCTCTATATCTTAAACGCTGATAAGTTTCTGTAATTTCTAGCTATCGA 4965
QY 601 CTGCGAGACTGCTGTGTATTAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTA 660
DB 4964 CTGCGAGACTGCTGTGTATTAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTA 4905
QY 661 ATGGCGCTTTTGTATGTCTATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720
DB 4904 ATGGCGCTTTTGTATGTCTATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 4845
QY 721 GAGACCGGCACACTGGCCATATCGGTGGTGTCTATCGGCCAGCTTTCATCCCGATATGC 780
DB 4844 GAGACCGGCACACTGGCCATATCGGTGGTGTCTATCGGCCAGCTTTCATCCCGATATGC 4785
QY 781 ACCACCGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGG 840
DB 4784 ACCACCGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGG 4725
QY 841 ATCACCATCCGTCGCGCGGCGGTGTCAATAATATCACTGTATCATCCAAACAGACGA 900
DB 4724 ATCACCATCCGTCGCGCGGCGGTGTCAATAATATCACTGTATCATCCAAACAGACGA 4665
QY 901 TAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTC 960
DB 4664 TAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTC 4605
QY 961 GTCAGCAAAAGAGCGCTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 1020
DB 4604 GTCAGCAAAAGAGCGCTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 4545
QY 1021 TTCCGCTTTCCAGCGTTTCGCGACGACAGACGAGCGGCTTCAATTCGTGATGGTGTGCTTAC 1080
DB 4544 TTCCGCTTTCCAGCGTTTCGCGACGACGACGAGCGGCTTCAATTCGTGATGGTGTGCTTAC 4495
QY 1081 CAGACCGGAGATATGACATCATATATGCTTGAAGCAACTGATAGCTGTGCTCTCAACT 1140
DB 4484 CAGACCGGAGATATGACATCATATATGCTTGAAGCAACTGATAGCTGTGCTCTCAACT 4425
QY 1141 GTCACTGTAAATACGCTGCTTCATAGCAGACCTCTTTTGTGACATCTTCGGGTA 1193
DB 4424 GTCACTGTAAATACGCTGCTTCATAGCAGACCTCTTTTGTGACATCTTCGGGTA 4372

RESULT 11
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX nucleic acid isolation; ds.
XX

OS	Synthetic.	
XX	WO200295055-A2.	
PN	28-NOV-2002.	
XX	21-MAY-2002; 2002WO-US015947.	
XX	21-MAY-2001; 2001US-0291973P.	
PF	(INVI-) INVITROGEN CORP.	
XX	Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;	
XX	WPI; 2003-129436/12.	
XX	Inserting a population of nucleic acids into a second target molecule for	
PT	selecting and isolating nucleic acid molecules by mixing the second	
PT	population of nucleic acid with a second target nucleic acid.	
XX	Disclosure; Fig 18B-C; 273pp; English.	
XX	The invention relates to inserting a population of nucleic acids into a	
XX	second target molecule. The method involves (a) mixing a first population	
CC	of nucleic acid comprising one or more recombination sites with a target	
CC	nucleic acid; (b) causing some or all of the nucleic acid molecules of	
CC	the first population to recombine with the first target nucleic acid	
CC	molecules to form a second population; (c) mixing the second population	
CC	of nucleic acid with a second target nucleic acid; and (d) causing some	
CC	or all of the nucleic acid molecules of the second population to	
CC	recombine with some or all of the second target nucleic acid molecules to	
CC	form a third population of nucleic acid. The method is useful for	
CC	selecting and isolating nucleic acid molecules. The present sequence	
CC	represents the donor plasmid pDONR207 nucleotide sequence	
XX	Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;	
SQ	Query Match 24.5%; Score 1193; DB 7; Length 5584;	
	Best Local Similarity 100.0%; Pred. No. 1e-156;	
	Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGGGCCCCCAATAATGATTTTATTTTGACTGATAGTACCTGTTGCTGCAACAAATTGA 60	
DB	5564 CGGGCCCCCAATAATGATTTTATTTTGACTGATAGTACCTGTTGCTGCAACAAATTGA 5505	
QY	61 TGAGCAATGCTTTTTTATATGCCAACTTTGTACAAAAGCTGAACGAAACCTTAAA 120	
DB	5504 TGAGCAATGCTTTTTTATATGCCAACTTTGTACAAAAGCTGAACGAAACCTTAAA 5445	
QY	121 TGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAACAGACTACATAATCTG 180	
DB	5444 TGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAACAGACTACATAATCTG 5385	
QY	181 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGCCTGTA 240	
DB	5384 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGCCTGTA 5325	
QY	241 GTGACCGCAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTTAGTCGACGACAG 300	
DB	5324 GTGACCGCAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTTAGTCGACGACAG 5265	
QY	301 CCTTCCAAATGTTCTTCTCAACGGGAATGTCCTGATCCAGCCTACTCGCTATTGTCTCA 360	
DB	5264 CCTTCCAAATGTTCTTCTCAACGGGAATGTCCTGATCCAGCCTACTCGCTATTGTCTCA 5205	
QY	361 ATCCCGTATTAAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 420	
DB	5204 ATCCCGTATTAAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 5145	
QY	421 ACAAAATAAAACATCTACCTATTATATACGCTAGTGTACATAGTCTGAAATCATCTG 480	
DB	5144 ACAAAATAAAACATCTACCTATTATACGCTAGTGTATAGTCTGAAATCATCTG 5085	

QY	481	CATCAGAACAAATTTCAAACTCTTATACCTTTTCTTTCTTAAAGTCGTTCCGGCTTCATCTG	540
DB	5084	CATCAGAACAAATTTCAAACTCTTATACCTTTTCTTTCTTAAAGTCGTTCCGGCTTCATCTG	5025
QY	541	GATTTTCAGCCTCTATATCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA	600
DB	5024	GATTTTCAGCCTCTATATCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA	4965
QY	601	CTGCGAGACTGGCTGTGTATAGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	660
DB	4964	CTGCGAGACTGGCTGTGTATAGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	4905
QY	661	ATGGCGTTTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG	720
DB	4904	ATGGCGTTTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG	4845
QY	721	GAGACCGGCACATCGGCCATATCGGTGGTTCATGCGCCAGCTTTCATCCCGATATGC	780
DB	4844	GAGACCGGCACATCGGCCATATCGGTGGTTCATGCGCCAGCTTTCATCCCGATATGC	4785
QY	781	ACCACCGGTAAAGTTTACGGGAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGG	840
DB	4784	ACCACCGGTAAAGTTTACGGGAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGG	4725
QY	841	ATCACCATCCGTCGCCCGCGCTGTCAATAATATCACTCTGTACATCCACAAACAGACGA	900
DB	4724	ATCACCATCCGTCGCCCGCGCTGTCAATAATATCACTCTGTACATCCACAAACAGACGA	4665
QY	901	TACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTCACCAGTCCCTGTTCTC	960
DB	4664	TACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTCACCAGTCCCTGTTCTC	4605
QY	961	GTACAGAAAAAGAGCCGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTCTGATT	1020
DB	4604	GTACAGAAAAAGAGCCGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTCTGATT	4545
QY	1021	TTCCGCTTTCCAGGTTTCGGCAGCAGACGAGCGGCTTCAATCTGCAATGTTGCTTAC	1080
DB	4544	TTCCGCTTTCCAGGTTTCGGCAGCAGACGAGCGGCTTCAATCTGCAATGTTGCTTAC	4485
QY	1081	CAGACCGGAGATATGACATCATATATGCTTGAAGCACTGATAGCTGTGCTCTCAACT	1140
DB	4484	CAGACCGGAGATATGACATCATATATGCTTGAAGCACTGATAGCTGTGCTCTCAACT	4425
QY	1141	GTCACTGTAAATACCGCTGCTTCATAGCACACCTCTTTTGTACATCTTCGGGTA	1193
DB	4424	GTCACTGTAAATACCGCTGCTTCATAGCACACCTCTTTTGTACATCTTCGGGTA	4372

RESULT 12
ABZ59768
ID ABZ59768 standard; DNA; 4428 BP.
XX
AC ABZ59768;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX
OS nucleic acid isolation; ds.
XX
XX Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US015947.
XX
XX 21-MAY-2001; 2001US-0291973P.
XX
XX (INVI-) INVITROGEN CORP.

XX	Brasch WA, Cheo D, Li X, Esposito D, Byrd DRN;	661	ATGGCGTTTGTGATGTCATTTTCGGCTGGCTGAGATCAGCCACTTCTTCCCGATAACG	720
PI	WPI; 2003-129436/12.	1518	ATGGCGTTTGTGATGTCATTTTCGGCTGGCTGAGATCAGCCACTTCTTCCCGATAACG	1577
XX	Inserting a population of nucleic acids into a second target molecule for	721	GAGACCGGCACACTGCGGCATATCGGTGGTCAATCATCGGCAGCTTTTCATCCCGATATGC	780
PT	selecting and isolating nucleic acid molecules by mixing the second	1578	GAGACCGGCACACTGCGGCATATCGGTGGTCAATCATCGGCAGCTTTTCATCCCGATATGC	1637
PT	population of nucleic acid with a second target nucleic acid.	781	ACCACCGGTAAAGTTTCAAGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGG	840
XX	Disclosure; Fig 27B-C; 273pp; English.	1638	ACCACCGGTAAAGTTTCAAGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGG	1697
XX	The invention relates to inserting a population of nucleic acids into a	841	ATCACCATCGTCCGCGGCGTGTCAATAATATCACTGTATCATCCACAAAACAGACGA	900
CC	second target molecule. The method involves (a) mixing a first population	1698	ATCACCATCGTCCGCGGCGTGTCAATAATATCACTGTATCATCCACAAAACAGACGA	1757
CC	of nucleic acid comprising one or more recombination sites with a target	901	TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCACTTTCACCGTCCCTGTTCTC	960
CC	nucleic acid; (b) causing some or all of the nucleic acid molecules of	1758	TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCACTTTCACCGTCCCTGTTCTC	1817
CC	the first population to recombine with the first target nucleic acid	961	GTACGCAAAAGAGCGGTTTCATTAATAAACCGGCGAGCTCAGCCATCCCTTCCCTGATT	1020
CC	molecules to form a second population; (c) mixing the second population	1818	GTACGCAAAAGAGCGGTTTCATTAATAAACCGGCGAGCTCAGCCATCCCTTCCCTGATT	1877
CC	of nucleic acid with a second target nucleic acid; and (d) causing some	1021	TTCCGCTTTCAGCGTTTCGGCACGACGACGCGGCTTCATTCTGCTATGTTGTGCTTAC	1080
CC	or all of the nucleic acid molecules of the second population to	1878	TTCCGCTTTCAGCGTTTCGGCACGACGACGCGGCTTCATTCTGCTATGTTGTGCTTAC	1937
CC	recombine with some or all of the second target nucleic acid molecules to	1081	CAGACCGGAGATATGACATCATATATGCTTGAAGCAACTGATAGCTGCTGCTGCACT	1140
CC	form a third population of nucleic acid. The method is useful for	1938	CAGACCGGAGATATGACATCATATATGCTTGAAGCAACTGATAGCTGCTGCTGCACT	1997
CC	selecting and isolating nucleic acid molecules. The present sequence	1141	GTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTA	1193
CC	represents the destination plasmid pDONR212 nucleotide sequence	1998	GTCACTGTATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTA	2050
XX	Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;	RESULT 13		
SQ	Query Match 24.4%; Score 1186.6; DB 7; Length 4428;	ABZ58769		
	Best Local Similarity 99.7%; Pred. No. 7.9e-156;	ID	ABZ58769 standard; DNA; 4627 BP.	
	Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	XX	ABZ58769;	
QY	1 CGGGCCCCAATAATGATTTTATTTGACTGATAGTGACCTGTCGTTGCAACAAATGA	AC	XX	
DB	858 CGGGCCCCAATAATGATTTTATTTGACTGATAGTGACCTGTCGTTGCAACAAATGA	DT	01-MAY-2003 (first entry)	
QY	61 TGAGCAATGCTTTTATAAAGCCAACTTTGTACAAAAAAGCTGAACGAGAAAAAGTAAAA	XX	Destination plasmid pDONR212 (P) nucleotide sequence.	
DB	918 TGAGCAATGCTTTTATAAAGCCAACTTTGTACAAAAAAGCTGAACGAGAAAAAGTAAAA	XX	Nucleic acid insertion; recombination; nucleic acid selection;	
QY	121 TGATATAAATATCAATATATTAATAATGATTTTGTGATATAAATAAAGCACTATATCTG	XX	nucleic acid isolation; ds.	
DB	978 TGATATAAATATCAATATATTAATAATGATTTTGTGATATAAATAAAGCACTATATCTG	OS	Synthetic.	
QY	181 TAAACACACACATATCCAGTCACTATGATCACTTATGATGATTTAGTGACCTGTA	XX	WO200295055-A2.	
DB	1038 TAAACACACACATATCCAGTCACTATGATCACTTATGATGATTTAGTGACCTGTA	XX	28-NOV-2002.	
QY	241 GTGACCGCAGACCTTCCAAATGTTCTTGGGTGATGCTGCGCAACTAGTCGACCGACAG	XX	21-MAY-2002; 2002WO-US015947.	
DB	1098 GTGACCGCAGACCTTCCAAATGTTCTTGGGTGATGCTGCGCAACTAGTCGACCGACAG	XX	21-MAY-2001; 2001US-0291973P.	
QY	301 CTTTCCAAATGTTCTTCCAAACGGAATGCTGATCCAGCCTACTCGCTATTGTCCTCA	XX	(INVI-) INVITROGEN CORP.	
DB	1158 CTTTCCAAATGTTCTTCCAAACGGAATGCTGATCCAGCCTACTCGCTATTGTCCTCA	XX	Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;	
QY	361 ATGCGGTATTAATCATAAAAAGAAATAAGAAAGAGGTGCGAGCTCTTTTGTGTG	PI	WPI; 2003-129436/12.	
DB	1218 ATGCGGTATTAATCATAAAAAGAAATAAGAAAGAGGTGCGAGCTCTTTTGTGTG	XX	Inserting a population of nucleic acids into a second target molecule for	
QY	421 ACAAAATAAATACTACTCTATTCATATACGCTAGTGTCAATGCTGCTGAAATCATCTG	XX	selecting and isolating nucleic acid molecules by mixing the second	
DB	1278 ACAAAATAAATACTACTCTATTCATATACGCTAGTGTCAATGCTGCTGAAATCATCTG	XX	population of nucleic acid with a second target nucleic acid.	
QY	481 CATCAAGAACAAATTCACAACTTTATCTTTCTTACAAAGTCTGTCGCTTCACTCG	XX	Disclosure; Fig 28B-C; 273pp; English.	
DB	1338 CATCAAGAACAAATTCACAACTTTATCTTTCTTACAAAGTCTGTCGCTTCACTCG	XX		
QY	541 GATTTTCAGCTCTATCTACTTACTTAAAGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGA	XX		
DB	1398 GATTTTCAGCTCTATCTACTTACTTAAAGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGA	XX		
QY	601 CTGACAGATGGCTGTATAGGGAGCCTGACATTTATATCCCGAAGCAATCAGGTTA	XX		
DB	1458 CTGACAGATGGCTGTATAGGGAGCCTGACATTTATATCCCGAAGCAATCAGGTTA	XX		

CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.4%; Score 1186.6; DB 7; Length 4627;
Best Local Similarity 99.7%; Pred. No. 7.9e-156;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTGACTGATAGTGCACCTGTTGCTTGCACCAAAATGA 60
Db 9 CGGGCCCCAAATAATGATTTTATTTGACTGATAGTGCACCTGTTGCTTGCACCAAAATGA 68

QY 61 TGAGCAATGCTTTTATATATGCGCAACTTTGTACAAAAGAGCTGAACAGAAACGTAAAA 120
Db 69 TGAGCAATGCTTTTATATATGCGCAACTTTGTACAAAAGAGCTGAATGCGAAACGTAAAA 128

QY 121 TGAATATAATCAATATATTAATTAATGATTTTGCATATAAAACAGACTACATATACTG 180
Db 129 TGAATATAATCAATATATTAATTAATGATTTTGCATATAAAACAGACTACATATACTG 188

QY 181 TAAACACAAACATATCCAGTCACTATGATGAATCAACTTACTTAGATGATTAAGTACCTGTA 240
Db 189 TAAACACAAACATATCCAGTCACTATGATGAATCAACTTACTTAGATGATTAAGTACCTGTA 248

QY 241 GTGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAAGTCTAGTGCAGCGACAG 300
Db 249 GTGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAAGTCTAGTGCAGCGACAG 308

QY 301 CCTTCCAAATGTTCTTCCTCAACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCA 360
Db 309 CCTTCCAAATGTTCTTCCTCAACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCA 368

QY 361 ATGCGGTATTAATCATAAAAGAAATAGAAAAGAGAGTGCGAGCCTCTTTTGTGTG 420
Db 369 ATGCGGTATTAATCATAAAAGAAATAGAAAAGAGAGTGCGAGCCTCTTTTGTGTG 428

QY 421 ACATAATAAACAATCTACCTATTTCATATACGCTAGTGTCAAGTCTGAAATCATCTG 480
Db 429 ACATAATAAACAATCTACCTATTTCATATACGCTAGTGTCAAGTCTGAAATCATCTG 488

QY 481 CATCAAGAACAAATTCACAACTCTTATACATTTTCTTACAAAGTGTTCGGCTTCATCTG 540
Db 489 CATCAAGAACAAATTCACAACTCTTATACATTTTCTTACAAAGTGTTCGGCTTCATCTG 548

QY 541 GATTTTCAGCCTTATCTACTTAACCGTGAATAGTTCTGTAATTTCTACTGTATCA 600
Db 549 GATTTTCAGCCTTATCTACTTAACCGTGAATAGTTCTGTAATTTCTACTGTATCA 608

QY 601 CTTGACAGCTGGTGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTGA 660
Db 609 CTTGACAGCTGGTGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTGA 668

QY 661 ATGCGGTTTTGATGCTCAATTTTCGGTGTGCTGAGATCAGCACTTCTCCCGATAACG 720
Db 669 ATGCGGTTTTGATGCTCAATTTTCGGTGTGCTGAGATCAGCACTTCTCCCGATAACG 728

QY 721 GAGACCGGCACACTGGCCATATCGGTGTCATCATGCGCAGCTTTCATCCCGATATGC 780
Db 729 GAGACCGGCACACTGGCCATATCGGTGTCATCATGCGCAGCTTTCATCCCGATATGC 788

QY 781 ACCACCGGTTAAAGTTTCAACGGGAGCTTTATCTGACAGCAGAGCTGCACTGGCCAGGGG 840

Db 789 ACCACCGGTTAAAGTTTCAACGGGAGAGCTTTATCTGACAGCAGCTGCACTGGCCAGGGG 848
QY 841 ATCAACATCGTGGCCCGGGGTGTCAATATATACATCTGTACATCCACAAACAGACGA 900
Db 849 ATCAACATCGTGGCCCGGGGTGTCAATATATACATCTGTACATCCACAAACAGACGA 908
QY 901 TAAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACCAAGTCCCTGTTCTC 960
Db 909 TAAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACCAAGTCCCTGTTCTC 968
QY 961 GTACAGCAAAAGAGCGGTTCAATTTCAATAAACCGGCGAGCTCAGCATCCCTGCTGATT 1020
Db 969 GTACAGCAAAAGAGCGGTTCAATTTCAATAAACCGGCGAGCTCAGCATCCCTGCTGATT 1028
QY 1021 TTCCGCTTTCCAGCGTTCGGCACGACGACGCGGCTTCATTTCTGATGGTTGTGCTTAC 1080
Db 1029 TTCCGCTTTTCACGCGTTCGGCACGACGACGCGGCTTCATTTCTGATGGTTGTGCTTAC 1088
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1140
Db 1089 CAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1148
QY 1141 GTCACTGTAAATAGCTGCTTCAATAGCACACCTCTTTTGCATACATCTCGGGA 1193
Db 1149 GTCACTGTAAATAGCTGCTTCAATAGCACACCTCTTTTGCATACATCTCGGGA 1201

RESULT 14
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX
AC ABZ58770;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212(R) nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW Nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
XX WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule for
XX selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid.
XX
XX Disclosure; Fig 29B-C; 273pp; English.
XX
XX The invention relates to inserting a population of nucleic acids into a
XX second target molecule. The method involves (a) mixing a first population
XX of nucleic acid comprising one or more recombination sites with a target
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX the first population to recombine with the first target nucleic acid
XX molecules to form a second population; (c) mixing the second population
XX of nucleic acid with a second target nucleic acid; and (d) causing some
XX or all of the nucleic acid molecules of the second population to
XX recombine with some or all of the second target nucleic acid molecules to
XX form a third population of nucleic acid. The method is useful for
XX selecting and isolating nucleic acid molecules. The present sequence

CC represents the destination plasmid pDONR212(R) nucleotide sequence	
XX	Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;
XX	Query Match 24.4%; Score 1186.6; DB 7; Length 4627;
XX	Best Local Similarity 99.7%; Pred. No. 7.9e-156;
XX	Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 CGGGCCCCAAATATGATTTTATTTTGAAGTACAGTACCTGTTGCTTGCACAAATATGA 60
DB	9 CGGGCCCCAAATATGATTTTATTTTGAAGTACAGTACCTGTTGCTTGCACAAATATGA 68
QY	61 TGAGCAATGCTTTTATTAATGCCAACTTTGACAAAAAGCTGAACGAGAAACGTAATA 120
DB	69 TGAGCAATGCTTTTATTAATGCCAACTTTGACAAAAAGCTGATATCGAAACGTAATA 128
QY	121 TGATTAATATCAATATATTAATTTAGATTTTGCATATAAAGACAGACTACATATAC 180
DB	129 TGATTAATATCAATATATTAATTTAGATTTTGCATATAAAGACAGACTACATATAC 188
QY	181 TAAACACAAATATCCAGTCACTATGAATCACTACTTAGATGGTATTTAGTACCTGTA 240
DB	189 TAAACACAAATATCCAGTCACTATGAATCACTACTTAGATGGTATTTAGTACCTGTA 248
QY	241 GTCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCACCGACAG 300
DB	249 GTCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCACCGACAG 308
QY	301 CCTTCCAAATGTTCTTCCAAAGGAATCGTGTATCCAGCTTACTCGCTATTTGCTTCA 360
DB	309 CCTTCCAAATGTTCTTCCAAAGGAATCGTGTATCCAGCTTACTCGCTATTTGCTTCA 368
QY	361 ATGCCCTATTAAATCATATAAAGAAATAGAAAAAGAGTGCAGCTCTTTTGTGTG 420
DB	369 ATGCCCTATTAAATCATATAAAGAAATAGAAAAAGAGTGCAGCTCTTTTGTGTG 428
QY	421 ACAAATATAAATCACTTACTATATACGTAGTGTGTCATAGTCTGAAATCATCTG 480
DB	429 ACAAATATAAATCACTTACTATATACGTAGTGTGTCATAGTCTGAAATCATCTG 488
QY	481 CATCAAGAACAAATTCACAACTCTTATCTTTCTTCTTCAAGTCTGCTTCTATCTG 540
DB	489 CATCAAGAACAAATTCACAACTCTTATCTTTCTTCTTCAAGTCTGCTTCTATCTG 548
QY	541 GATTTTCAGCTCTATATCTTACTAAAGTGAATAAAGTTTCTGTAATTTCTACTGTATCGA 600
DB	549 GATTTTCAGCTCTATATCTTACTAAAGTGAATAAAGTTTCTGTAATTTCTACTGTATCGA 608
QY	601 CTTGCAGACTGGCTGTATTAAGGAGCGCTGACATTTATATTTCCCAAGACATCAGGTTA 660
DB	609 CTTGCAGACTGGCTGTATTAAGGAGCGCTGACATTTATATTTCCCAAGACATCAGGTTA 668
QY	661 ATGCGCTTTTGTATGTCATTTTCCGGTGGCTGAGATCAGCACTTCTTCCCGGATTAACG 720
DB	669 ATGCGCTTTTGTATGTCATTTTCCGGTGGCTGAGATCAGCACTTCTTCCCGGATTAACG 728
QY	721 GAGACCGGACACTGGCCATATCGGTGTATATGCGGACAGCTTATCCCGGATATGC 780
DB	729 GAGACCGGACACTGGCCATATCGGTGTATATGCGGACAGCTTATCCCGGATATGC 788
QY	781 ACCACCGGTAAGTTTCAGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGG 840
DB	789 ACCACCGGTAAGTTTCAGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGG 848
QY	841 ATCAACATCTCGTCCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 900
DB	849 ATCAACATCTCGTCCGCGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 908
QY	901 TAAAGGCTCTCTCTTTTATAGTGTAACCTTAACTGATTTACAGAGTCCCTGTTCTC 960
DB	909 TAAAGGCTCTCTCTTTTATAGTGTAACCTTAACTGATTTACAGAGTCCCTGTTCTC 968
QY	961 GTCAGCAAAAGAGCGCTTCAATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTCTGATT 1020
DB	969 GTCAGCAAAAGAGCGCTTCAATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTCTGATT 1028
QY	1021 TTCCGCTTTCCAGCGTTCCGACGACGACGACGAGCGGCTTCAATCTGCAATGTTGCTTAC 1080
DB	1029 TTCCGCTTTCCAGCGTTCCGACGACGACGACGAGCGGCTTCAATCTGCAATGTTGCTTAC 1088
QY	1081 CAGACCGGAGATTTGACATCATATATGCTTGTAGCAACTGATAGCTGTGCTGTCAACT 1140
DB	1089 CAGACCGGAGATTTGACATCATATATGCTTGTAGCAACTGATAGCTGTGCTGTCAACT 1148
QY	1141 GTCACCTGTAATACCGCTCTTCATAGCACACCTCTTTTGTGACATCTTGGGTA 1193
DB	1149 GTCACCTGTAATACCGCTCTTCATAGCACACCTCTTTTGTGACATCTTGGGTA 1201
RESULT 15	
AAC55524	
ID	AAC55524 standard; DNA; 4165 BP.
XX	AC AAC55524;
XX	DT 11-JAN-2001 (first entry)
XX	Donor plasmid pDONR204 nucleotide sequence.
DE	Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW	mutant; recombinational cloning; entry vector; destination vector;
KW	gene product targeting; fusion tag cleavage; ds.
OS	Bacteriophage lambda.
OS	Synthetic.
XX	WO200052027-A1.
XX	08-SEP-2000.
XX	02-MAR-2000; 2000WO-US005432.
XX	02-MAR-1999; 99US-0122389P.
PR	23-MAY-1999; 99US-0126049P.
PR	28-MAY-1999; 99US-0136744P.
XX	(LIFE-) LIFE TECHNOLOGIES INC.
XX	Hartley JL, Brasch WA, Temple GF, Cheo D;
PI	WPI; 2000-543948/49.
DR	Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
XX	Example 9; Fig 52; 459pp; English.
XX	The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins,

CC changing copy number, changing replicons, cloning into phages and		
CC cloning (I), (II), (III), host cells and vectors can be used in the		
CC production of polypeptides and antibodies. The present sequence is used		
CC in the exemplification of the present invention		
XX		
SQ	Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 0 U; 1 Other;	
	Query Match 22.0%; Score 1068.2; DB 3; Length 4165;	
	Best Local Similarity 98.8%; Pred. No. 2e-139;	
	Matches 1088; Conservative 0; Mismatches 8; Indels 5; Gaps 1;	
QY	3278 GGCAATATATGATTTTATTTGATGATGACCTGTTGGTGCACAAATTTGATAAGC 3337	
DB	2108 GGCAATATATGATTTTATTTGATGATGACCTGTTGGTGCACAAATTTGATAAGC 2167	
QY	3338 AATGCTTTCTTATAATGCCAATTTTGTACAGAAAGCTGAACGAGAAACGTTAAATGATA 3397	
DB	2168 AATGCTTTTATTAATGCCAATTTTGTACAGAAAGCTGAACGAGAAACGTTAAATGATA 2227	
QY	3398 TAAATATCAATATATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACCTGTAAAA 3457	
DB	2228 TAAATATCAATATATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACCTGTAAAA 2287	
QY	3458 CACAACATATCCAGTCACTATGAATCAACTTACTTAGATGGTATTAGTGAACCTGTAGTCGA 3517	
DB	2288 CACAACATATCCAGTCACTATGAATCAACTTACTTAGATGGTATTAGTGAACCTGTAGTCGA 2347	
QY	3518 CTAAAGTTGGCAGCATCACCGACGACCTTTGCGCGCGAATAAATACCTGTGACGGAAGATC 3577	
DB	2348 CTAAAGTTGGCAGCATCACCGACGACCTTTGCGCGCGAATAAATACCTGTGACGGAAGATC 2407	
QY	3578 ACTTGGCAGAAATAAATAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCCACT 3637	
DB	2408 ACTTGGCAGAAATAAATAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCCACT 2467	
QY	3638 TTTGGCGAAATAGACGCTTGTATCGGCACTACCCATTTTCAACCTCTTTATATCTTTCTCT 3697	
DB	2468 TTTGGCGAAATAGACGCTTGTATCGGCACTACCCATTTTCAACCTCTTTATATCTTTCTCT 2522	
QY	3698 TACAAGTCGTTGCGGCTTCATCTGGATTTTTCAGCCTCTATCTTACTAAACGTGATAAAGT 3757	
DB	2523 TACAAGTCGTTGCGGCTTCATCTGGATTTTTCAGCCTCTATCTTACTAAACGTGATAAAGT 2582	
QY	3758 TTTCTGTAATTTCTATGTATCGAATCGAGTGTGCTGTGATTAAGGAGCTGACATTT 3817	
DB	2583 TTTCTGTAATTTCTATGTATCGAATCGAGTGTGCTGTGATTAAGGAGCTGACATTT 2642	
QY	3818 ATATTCCCGACAGACATCAGGTTAATGCGGTTTGTATGATGTCATTTTCGGGTTGGCTGAGAT 3877	
DB	2643 ATATTCCCGACAGACATCAGGTTAATGCGGTTTGTATGATGTCATTTTCGGGTTGGCTGAGAT 2702	
QY	3878 CAGCCACTTTCTCCCGATAACGAGAACCGGACACTGGCCCATATCGGTGGTCAATGC 3937	
DB	2703 CAGCCACTTTCTCCCGATAACGAGAACCGGACACTGGCCCATATCGGTGGTCAATGC 2762	
QY	3938 GCGAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTTCACGGGAGCTTTTATCTGACA 3997	
DB	2763 GCGAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTTCACGGGAGCTTTTATCTGACA 2822	
QY	3998 GCGAGCTGTCATCTGGCCAGGGGATCACCATCCGTCGCGCGGCGTGTCAATAATATCAC 4057	
DB	2823 GCGAGCTGTCATCTGGCCAGGGGATCACCATCCGTCGCGCGGCGTGTCAATAATATCAC 2882	
QY	4058 TCTGTATACATCCAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACT 4117	
DB	2883 TCTGTATACATCCAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACT 2942	
QY	4118 GCATTTCCAGTCCCTGTTCTGTGACGAAAGAGCGGTTTCAATTAATAACCGGGCG 4177	
DB	2943 GCATTTCCAGTCCCTGTTCTGTGACGAAAGAGCGGTTTCAATTAATAACCGGGCG 3002	
QY	4178 ACCTCAGCCATCCCTTCTGATTTTTCGGCTTTCCAGGCTTTCGGCACGACGACGCGGCT 4237	

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Job time : 1223.77 secs

Wed May 12 08:20:57 2004

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 209,917 Seconds
(without alignments)
12850.857 Million cell updates/sec

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Scoring table: IDENTITY_NVC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	759.2	15.6	5838	2	US-08-850-880-3
C 2	759.2	15.6	5838	2	US-08-944-916-3
C 3	759.2	15.6	5838	2	US-08-814-877-3
C 4	759.2	15.6	5838	4	US-09-272-432A-3
C 5	759.2	15.6	9737	4	US-09-479-122-22
C 6	759.2	15.6	9737	4	US-09-479-122-23
C 7	759.2	15.6	9737	4	US-09-479-122-28
C 8	759.2	15.6	9737	4	US-09-484-997-22
C 9	759.2	15.6	9737	4	US-09-484-997-23
C 10	759.2	15.6	9737	4	US-09-484-997-28
C 11	759.2	15.6	9737	4	US-09-481-355-22
C 12	759.2	15.6	9737	4	US-09-481-355-23
C 13	759.2	15.6	9737	4	US-09-481-355-28
C 14	759.2	15.6	9737	4	US-09-481-822-22
C 15	759.2	15.6	9737	4	US-09-481-822-23
C 16	759.2	15.6	9737	4	US-09-481-822-28
C 17	759.2	15.6	9737	4	US-09-455-659A-22
C 18	759.2	15.6	9737	4	US-09-455-659A-23
C 19	759.2	15.6	9737	4	US-09-455-659A-28
C 20	759.2	15.6	9737	4	US-09-484-996-22
C 21	759.2	15.6	9737	4	US-09-484-996-23
C 22	759.2	15.6	9737	4	US-09-484-996-28
C 23	759.2	15.6	9737	4	US-09-479-123-22
C 24	759.2	15.6	9737	4	US-09-479-123-23
C 25	759.2	15.6	9737	4	US-09-479-123-28
C 26	759.2	15.6	9871	4	US-09-479-122-24
C 27	759.2	15.6	9871	4	US-09-484-997-24

C 28	759.2	15.6	9871	4	US-09-481-355-24
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C 43	752.8	15.5	3225	4	US-09-358-856C-2
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ALIGNMENTS

RESULT 1
US-08-850-880-3/c
; Sequence 3, Application US/08850880
; Patent No. 5925545
; GENERAL INFORMATION:
; APPLICANT: Reznikoff, William S
; APPLICANT: Gorysin, Igor Y
; APPLICANT: Zhou, Hong
; TITLE OF INVENTION: System for In Vitro Transposition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,880
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.94142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608/251-9166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5838 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pRZ11
; FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 1..19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..1267
; OTHER INFORMATION: /function= "tetracycline"

Wed May 12 08:20:57 2004

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; OTHER INFORMATION: resistance"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2301..2960)
; OTHER INFORMATION: /function= "chloramphenicol"
; OTHER INFORMATION: resistance"
; FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 4564..4582
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4715..5530
; OTHER INFORMATION: /function= "kanamycin resistance"
; US-08-850-880-3
Query Match 15.6%; Score 759.2; DB 2; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 2471 GACAACTTCTCGCCCGCTTTTCCCAATGGGCAAAATATATATACGCAAGGCGCAAGGTG 2412
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; US-08-944-916-3/c
; Sequence 3, Application US/08944916
; Patent No. 5948622
; GENERAL INFORMATION:
; APPLICANT: Reznikoff, William S
; APPLICANT: Goryshin, Igor Y
; APPLICANT: York, Dona L
; APPLICANT: Zhou, Hong
; TITLE OF INVENTION: System for In Vitro Transposition
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,916
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/814,877
; FILING DATE: 09-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/850,880
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.94916
; TELEPHONE: 608/251-5000
; TELEFAX: 608/251-9166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5838 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pRZ11
; FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 1..19
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; LOCATION: 77..1267
; OTHER INFORMATION: /function= "tetracycline
; OTHER INFORMATION: resistance"
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; NAME/KEY: CDS
; LOCATION: complement (2301..2960)
; OTHER INFORMATION: /function= "chloramphenicol
; OTHER INFORMATION: resistance"
; FEATURE:
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; LOCATION: 4564..4582
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; LOCATION: 4715..5530
; OTHER INFORMATION: /function= "kanamycin resistance"
; US-08-944-916-3
Query Match 15.6%; Score 759.2; DB 2; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;

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US-08-814-877-3/c									
Sequence 3, Application US/08814877									
Patent No. 5965443									
GENERAL INFORMATION:									
APPLICANT: Goryshin, Igor V									
APPLICANT: Reznikoff, William S									
TITLE OF INVENTION: System for In Vitro Transposition									
NUMBER OF SEQUENCES: 6									
CORRESPONDENCE ADDRESS:									
ADDRESSEE: Quarles & Brady									
STREET: 1 South Pinckney Street									
CITY: Madison									
STATE: WI									
COUNTRY: USA									
ZIP: 53703									
COMPUTER READABLE FORM:									
MEDIUM TYPE: Floppy disk									

COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS	SOFTWARE: PatentIn Release #1.0, Version #1.30	CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/814,877	FILING DATE:	CLASSIFICATION: 435	ATTORNEY/AGENT INFORMATION:	NAME: Berson, Bennett J	REGISTRATION NUMBER: 37094	REFERENCE/DOCKET NUMBER: 960296.94142	TELECOMMUNICATION INFORMATION:	TELEPHONE: 608/251-5000	TELEFAX: 608-251-9166	INFORMATION FOR SEQ ID NO: 3:	SEQUENCE CHARACTERISTICS:	LENGTH: 5838 base pairs	TYPE: nucleic acid	STRANDEDNESS: double	TOPOLOGY: circular	MOLECULE TYPE: other nucleic acid	DESCRIPTION: /desc = "Plasmid DNA"	IMMEDIATE SOURCE:	CLONE: PRZTL1	FEATURE:	NAME/KEY: insertion_seq	LOCATION: 1..19	NAME/KEY: CDS	LOCATION: 77..1267	OTHER INFORMATION: /function= "tetracycline resistance"	FEATURE:	NAME/KEY: CDS	LOCATION: complement (2301..2960)	OTHER INFORMATION: /function= "chloramphenicol resistance"	FEATURE:	NAME/KEY: insertion_seq	LOCATION: 4564..4582	NAME/KEY: CDS	LOCATION: 4715..5530	OTHER INFORMATION: /function= "kanamycin resistance"	US-08-814-877-3																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Query Match										15.6%	Score 759.2;	DB 2;	Length 5838;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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Matches										764;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	1852	TAAGATGATATACGGCGGTAAAGAGTTTCCAACTTTCCACATAATGAATAAGATCACTA	1911																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						</

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814.877
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.94142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid DNA"
IMMEDIATE SOURCE:
CLONE: PRZTL1
FEATURE:
NAME/KEY: insertion_seq
LOCATION: 1..19
FEATURE:
NAME/KEY: CDS
LOCATION: 77..1267
OTHER INFORMATION: /function= "tetracycline resistance"
FEATURE:
NAME/KEY: CDS
LOCATION: 4715..5530
OTHER INFORMATION: /function= "kanamycin resistance"
US-08-814-877-3

Query Match 15.6%; Score 759.2; DB 2; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1852	TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACATAATGAATAAGATCACTA	1911
Db	3071	TGAGACGCTTGATCGGCAGCTAGAGGTTCCAACTTTCCACATAATGAATAAGATCACTA	3012
Qy	1912	CCGGCGCTATTTTGGATTATCGAGATTTTCAGAGCTTAAGAGCTAAATGGAGAAA	1971
Db	3011	CCGGCGCTATTTTGGATTATCGAGATTTTCAGAGCTTAAGAGCTAAATGGAGAAA	2952
Qy	1972	AAATCACTGGATATACACCGTTGATATATCCATGGCATCGTAAGAAACATTTTGAG	2031
Db	2951	AAATCACTGGATATACACCGTTGATATATCCATGGCATCGTAAGAAACATTTTGAG	2892
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Db	2891	GCATTTCACTGCTGCTCAATGTACTATATAACACGACCGTTTCAGCTGGATATTACGGCC	2832
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QY 2511 CTGATGCGGTGGGATTCAGGTTTCATCGCTCTGTGATGGTTCCATGTCGGCAGA 2571
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QY 2572 ATGCTTAATGAATTACACAGTACTGCGATGAGTGGCGAGGGCGGGCGGCTAAT 2623
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RESULT 4

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US-09-272-432A-3/c
; Sequence 3, Application US/09272432A
; Patent No. 6437109
; GENERAL INFORMATION:
; APPLICANT: Reznikoff, William S
; APPLICANT: Goryshin, Igor Y
; APPLICANT: Zhou, Hong
; TITLE OF INVENTION: System for In Vitro Transposition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,432A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.96277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5838 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pr2TL1
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FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 1..19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..1267
; OTHER INFORMATION: /function= "tetracycline resistance"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2301..2960)
; OTHER INFORMATION: /function= "chloramphenicol resistance"
; FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 4564..4582
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4715..5530
; OTHER INFORMATION: /function= "kanamycin resistance"
; US-09-272-432A-3

Query Match 15.6%; Score 759.2; DB 4; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;
Matches 764; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACCATTAATGAAATAAGATCACTA 1911
Db 3071 TGAGACGTTGATCGGCACGTAAAGAGTTCCAACTTTCCACCATTAATGAAATAAGATCACTA 3012
QY 1912 CCGGGCGTATTTTTTGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAA 1971
Db 3011 CCGGGCGTATTTTTTGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAGGAAGCTAAGGA 2952
QY 1972 AAATCACTGGATATACCCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2031
Db 2951 AAATCACTGGATATACCCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2892
QY 2032 GCATTTTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGTGGATATTACGGCC 2091
Db 2891 GCATTTTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGTGGATATTACGGCC 2832
QY 2092 TTTTAAAGACCGTAAAGAAAATTAAGCAAGTTTATCCGGCTTTTATTCACATTTCTT 2151
Db 2831 TTTTAAAGACCGTAAAGAAAATTAAGCAAGTTTATCCGGCTTTTATTCACATTTCTT 2772
QY 2152 GCCCGCTGATGAATGCTCATCCGAAATTCGGTATGGCAATGAAAGACGGTGAAGTGTG 2211
Db 2771 GCCCGCTGATGAATGCTCATCCGAAATTCGGTATGGCAATGAAAGACGGTGAAGTGTG 2712
QY 2212 ATATGGGATAGTGTTCACCCCTTGTTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 2271
Db 2711 ATATGGGATAGTGTTCACCCCTTGTTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 2652
QY 2272 TCGCTCTGGAGTGAATACCAAGAGATTCGGGAGTTTCTACACATATATTCGCAAGAT 2331
Db 2651 TCGCTCTGGAGTGAATACCAAGAGATTCGGGAGTTTCTACACATATATTCGCAAGAT 2592
QY 2332 GTGGCGTGTACGGTGAACCTGGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTT 2391
Db 2591 GTGGCGTGTACGGTGAACCTGGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTT 2532
QY 2392 TTCCTCTCAGCCCAATCCCTGGGTGAGTTTCCACAGTTTTCGATTTTAAACGTGGCAATG 2451
Db 2451 TTCCTCTCAGCCCAATCCCTGGGTGAGTTTCCACAGTTTTCGATTTTAAACGTGGCAATG 2472
QY 2452 GACAACTTCTTCGGCCCGGTTTCCACCATGGGCAAAATATTATACGCAAGGCGCAAGGTG 2511
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QY 2511 CTGATGCGGTGGGATTCAGGTTTCATCGCTCTGTGATGGTTCCATGTCGGCAGA 2571
Db 2411 CTGATGCGGTGGGATTCAGGTTTCATCGCTCTGTGATGGTTCCATGTCGGCAGA 2352
QY 2572 ATGCTTAATGAATTACACAGTACTGCGATGAGTGGCGAGGGCGGGCGGCTAAT 2623
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Db 2351 ATGCTTAATGAATTACAAACAGTACTGCGATGAGTGGCGAGGGGGGGGTAAT 2300
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RESULT 5
US-09-479-122-22/c
; Sequence 22, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-22
Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1852 TAAGATGATATACGGCCGGTAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 1911
Db 3094 TGAGACGTTGATCGGCACGTAAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 3035
Qy 1912 CCGGCGGTATTTTGGTATTCGAGATTTTCAGGAGCTAAGGAGCTAAATGGAGAAA 1971
Db 3034 CCGGCGGTATTTTGGTATTCGAGATTTTCAGGAGCTAAGGAGCTAAGGAGCTAAGGAGAAA 2975
Qy 1972 AAAATCACTGGATATACCAACCGTTGATATCCCAATGCGATCGTAAAGAACATTTTCAG 2031
Db 2974 AAAATCACTGGATATACCAACCGTTGATATCCCAATGCGATCGTAAAGAACATTTTCAG 2915
Qy 2032 GCATTTCACTGAGTTCGCTCAATGTACCTATAACCAAGCGTTCACTGATATACGCGC 2091
Db 2914 GCATTTCACTGAGTTCGCTCAATGTACCTATAACCAAGCGTTCACTGATATACGCGC 2855
Qy 2092 TTTTAAAGACCGTAAAGAAAATTAAGCAAGTTTATCCGGCCTTTATTCACATTCCT 2151
Db 2854 TTTTAAAGACCGTAAAGAAAATTAAGCAAGTTTATCCGGCCTTTATTCACATTCCT 2795
Qy 2152 GCGCGCCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGTGAGCTGGTG 2211
Db 2794 GCGCGCCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGTGAGCTGGTG 2735
Qy 2212 ATATGGGATAGTGTTCACCGTTGTACACCGTTTCCATGAGCAAACTGAACAGTTTCA 2271
Db 2734 ATATGGGATAGTGTTCACCGTTGTACACCGTTTCCATGAGCAAACTGAACAGTTTCA 2675

Qy 2272 TCCTCTGGAGTGAATACACGAGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
Db 2674 TCCTCTGGAGTGAATACACGAGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2615
Qy 2332 GTGGCGGTGTACCGTGAATAACCTGGCCCTATTTCCCTAAAGGTTTATTTGAGAATATGTTT 2391
Db 2614 GTGGCGGTGTACCGTGAATAACCTGGCCCTATTTCCCTAAAGGTTTATTTGAGAATATGTTT 2555
Qy 2392 TTCTCTCAGCCAAATCCCTGGGTGAGTTTCCAGTGTTCACAGTTTTCATTTAAACGTTGGCAATATG 2451
Db 2554 TTCTCTCAGCCAAATCCCTGGGTGAGTTTCCAGTGTTCACAGTTTTCATTTAAACGTTGGCAATATG 2495
Qy 2452 GACAACTTCTTCGCCCCCGTTTTCACCATGGCAAAATATTATAGCAAGCGCAAGGTG 2511
Db 2494 GACAACTTCTTCGCCCCCGTTTTCACCATGGCAAAATATTATAGCAAGCGCAAGGTG 2435
Qy 2512 CTGATGCCGTGGCGATTCAGGTTTCATCCGCTCTGTGATGGCTTCCATGTGGCGAGA 2571
Db 2434 CTGATGCCGTGGCGATTCAGGTTTCATCCGCTCTGTGATGGCTTCCATGTGGCGAGA 2375
Qy 2572 ATGCTTAATGAATTACAAACAGTACTGCGATGAGTGGCAGCGGGGGGCTAAT 2623
Db 2374 ATGCTTAATGAATTACAAACAGTACTGCGATGAGTGGCAGCGGGGGGCTAAT 2323

RESULT 6

US-09-479-122-23/c
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-23

Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1852 TAAGATGATATACGGCCGGTAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 1911
Db 3094 TGAGACGTTGATCGGCACGTAAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 3035
Qy 1912 CCGGCGGTATTTTGGTATTCGAGATTTTCAGGAGCTAAGGAGCTAAGGAGCTAAGGAGAAA 1971

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Db 3034 CCGGGCGTATTTTGGTATTCAGAGATTTTCAGAGCTAAGGAGCTAAATGGAGAA 2975
Qy 1972 AAAATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2031
Db 2974 AAAATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2915
Qy 2032 GCATTTCACTGATGCTCAATGATACCTATACACAGACCGTTTCAGCTGGATATTTACGGCC 2091
Db 2914 GCATTTCACTGATGCTCAATGATACCTATACACAGACCGTTTCAGCTGGATATTTACGGCC 2855
Qy 2092 TTTTAAAGACCGTAAAGAAAATTAAGCACAAGTTTATCCGGCTTTATTCACATCTT 2151
Db 2854 TTTTAAAGACCGTAAAGAAAATTAAGCACAAGTTTATCCGGCTTTATTCACATCTT 2795
Qy 2152 GCGGCGCTGATGATGCTCATCCGGAATTCGGATGCGAATGAAAGACGGTGAGCTGGTG 2211
Db 2794 GCGGCGCTGATGATGCTCATCCGGAATTCGGATGCGAATGAAAGACGGTGAGCTGGTG 2735
Qy 2212 ATATGGGATAGTTTACCCCTGTTTACACCGTTTTCATGCGCAATGAAAGACGGTTTCA 2271
Db 2734 ATATGGGATAGTTTACCCCTGTTTACACCGTTTTCATGCGCAATGAAAGACGGTTTCA 2675
Qy 2272 TCGCTCTGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
Db 2674 TCGCTCTGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2615
Qy 2332 GTGGCGTTTACGGTGAAGAACTGCGCTTATTTCCCTAAAGGGTTTATTCAGAAATATGTT 2391
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Qy 2392 TCGCTCTCAGCAATCCCTGGTGGTGGTTTACACGTTTGTATTTAAAGCTGGCCAAATG 2451
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Qy 2572 ATGCTTAATGAATTAACACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2623
Db 2374 ATGCTTAATGAATTAACACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2323
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RESULT 7

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US-09-479-122-28/c
; Sequence 28, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/359,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-28
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Query Match

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Best Local Similarity 15.6%; Score 759.2; DB 4; Length 9737;
Matches 764; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 1912 CCGGCGCTATTTTGGTATTCGAGATTTTCAGGAGCTAAGGAGCTAAATGGAGAAA 1971
Db 3034 CCGGCGCTATTTTGGTATTCGAGATTTTCAGGAGCTAAGGAGCTAAATGGAGAAA 2975
Qy 1972 AAAATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2031
Db 2974 AAAATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2915
Qy 2032 GCATTTCACTGATGCTCAATGATACCTATAACACGACCGTTTCAGCTGGATATTTACGGCC 2091
Db 2914 GCATTTCACTGATGCTCAATGATACCTATAACACGACCGTTTCAGCTGGATATTTACGGCC 2855
Qy 2092 TTTTAAAGACCGTAAAGAAAATTAAGCACAAGTTTATCCGGCTTTATTCACATCTT 2151
Db 2854 TTTTAAAGACCGTAAAGAAAATTAAGCACAAGTTTATCCGGCTTTATTCACATCTT 2795
Qy 2152 GCGGCGCTGATGATGCTCATCCGGAATTCGGATGCGAATGAAAGACGGTGAGCTGGTG 2211
Db 2794 GCGGCGCTGATGATGCTCATCCGGAATTCGGATGCGAATGAAAGACGGTGAGCTGGTG 2735
Qy 2212 ATATGGGATAGTTTACCCCTGTTTACACGTTTTCATGAGCAAACTGAACCGTTTCA 2271
Db 2734 ATATGGGATAGTTTACCCCTGTTTACACGTTTTCATGAGCAAACTGAACCGTTTCA 2675
Qy 2272 TCGCTCTGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
Db 2674 TCGCTCTGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2615
Qy 2332 GTGGCGTTTACGGTGAAGAACTGCGCTTATTTCCCTAAAGGGTTTATTCAGAAATATGTT 2391
Db 2614 GTGGCGTTTACGGTGAAGAACTGCGCTTATTTCCCTAAAGGGTTTATTCAGAAATATGTT 2555
Qy 2392 TCGCTCTCAGCAATCCCTGGTGGTGGTTTACACGTTTGTATTTAAAGCTGGCCAAATG 2451
Db 2554 TCGCTCTCAGCAATCCCTGGTGGTGGTTTACACGTTTGTATTTAAAGCTGGCCAAATG 2495
Qy 2452 GACAACTTTTGGCCCGCTTTTCCACCATGGGCAAAATATATACGCAAGGGGCAAGGTG 2511
Db 2494 GACAACTTTTGGCCCGCTTTTCCACCATGGGCAAAATATATACGCAAGGGGCAAGGTG 2435
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Qy 2572 ATGCTTAATGAATTAACACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2623
Db 2374 ATGCTTAATGAATTAACACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2323
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RESULT 8

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US-09-484-997-22/c
; Sequence 22, Application US/09484997
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; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-22

Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCCGTTAGAGTTCCAACTTTCACCATATGAATAAGATCACTA 1911
DB 3094 TGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACCATATGAATAAGATCACTA 3035
QY 1912 CCGGCGGTATTTTGGATTTCAGAGTTTCAGAGGCTAAGAGCTAAGAGCTAAGAGCTA 1971
DB 3034 CCGGCGGTATTTTGGATTTCAGAGTTTCAGAGGCTAAGAGCTAAGAGCTAAGAGCTA 2975
QY 1972 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2031
DB 2974 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2915
QY 2032 GCATTTCACTGATGATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2091
DB 2914 GCATTTCACTGATGATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2855
QY 2092 TTTTAAAGACCGTAAAGAACTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2151
DB 2854 TTTTAAAGACCGTAAAGAACTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2795
QY 2152 GCCCGCTGATGAATGCTATCCGGAATTCGATGGAATGAAGAGCGGTGAGTGTG 2211
DB 2794 GCCCGCTGATGAATGCTATCCGGAATTCGATGGAATGAAGAGCGGTGAGTGTG 2735
QY 2212 ATATCGGATAGTTTTCAGCTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2271
DB 2734 ATATCGGATAGTTTTCAGCTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2675
QY 2272 TCGCTCTGGAGTGAATATACCAACCGTTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2331
DB 2674 TCGCTCTGGAGTGAATATACCAACCGTTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2615
QY 2332 GTGGCGGTGTTACGGTGAAACCTGGCCCTATTTCCCTAAAGGGTTTATTCAGAGATATGTTT 2391
DB 2391 GTGGCGGTGTTACGGTGAAACCTGGCCCTATTTCCCTAAAGGGTTTATTCAGAGATATGTTT 2915

; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-23/c

Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCCGTTAGAGTTTCACCATATGAATAAGATCACTA 1911
DB 3094 TGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACCATATGAATAAGATCACTA 3035
QY 1912 CCGGCGGTATTTTGGATTTCAGAGTTTCAGAGGCTAAGAGCTAAGAGCTAAGAGCTA 1971
DB 3034 CCGGCGGTATTTTGGATTTCAGAGTTTCAGAGGCTAAGAGCTAAGAGCTAAGAGCTA 2975
QY 1972 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2031
DB 2974 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2915
QY 2032 GCATTTCACTGATGATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2091
DB 2914 GCATTTCACTGATGATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAACTTTTGG 2855
QY 2092 TTTTAAAGACCGTAAAGAACTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2151
DB 2854 TTTTAAAGACCGTAAAGAACTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2795
QY 2152 GCCCGCTGATGAATGCTATCCGGAATTCGATGGAATGAAGAGCGGTGAGTGTG 2211
DB 2794 GCCCGCTGATGAATGCTATCCGGAATTCGATGGAATGAAGAGCGGTGAGTGTG 2735
QY 2212 ATATCGGATAGTTTTCAGCTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2271
DB 2734 ATATCGGATAGTTTTCAGCTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2675
QY 2272 TCGCTCTGGAGTGAATATACCAACCGTTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2331
DB 2674 TCGCTCTGGAGTGAATATACCAACCGTTTTCAGAGTTTTCAGAGGCTTATTCAGAGCTTATTCAGAG 2615
QY 2332 GTGGCGGTGTTACGGTGAAACCTGGCCCTATTTCCCTAAAGGGTTTATTCAGAGATATGTTT 2391
DB 2391 GTGGCGGTGTTACGGTGAAACCTGGCCCTATTTCCCTAAAGGGTTTATTCAGAGATATGTTT 2915
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Qy 2032 GCATTCAGTCAGTGTCTCAATGTACCTATTAACACAGACCGTTTCAGCTGGATATTAACGGCC 2091
Db 2914 GCATTCAGTCAGTGTCTCAATGTACCTATTAACACAGACCGTTTCAGCTGGATATTAACGGCC 2855
Qy 2092 TTTTAAAGACCGTAAGAAAAAATAGACAAAGTTTATCCGGCTTTTATTCACATCTTT 2151
Db 2854 TTTTAAAGACCGTAAGAAAAAATAGACAAAGTTTATCCGGCTTTTATTCACATCTTT 2795
Qy 2152 GCCGCCCTGATGAATGCTATCCGGAATTCGGTATGGCAATGMAAGACGGTGAAGCTGGTG 2211
Db 2794 GCCGCCCTGATGAATGCTATCCGGAATTCGGTATGGCAATGMAAGACGGTGAAGCTGGTG 2735
Qy 2212 ATATGGGATAGTGTACCTCTGTATACACCTTTTCCATGAGCAATGMAAGACGGTGAAGCTGGTG 2271
Db 2734 ATATGGGATAGTGTACCTCTGTATACACCTTTTCCATGAGCAATGMAAGACGGTGAAGCTGGTG 2675
Qy 2272 TCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
Db 2674 TCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2615
Qy 2332 GTGGCGTGTACGGTGAAGAACTGGCTATTTCCCTAAAGGTTTATTTGAAATATGTTT 2391
Db 2614 GTGGCGTGTACGGTGAAGAACTGGCTATTTCCCTAAAGGTTTATTTGAAATATGTTT 2555
Qy 2392 TTCTGTCTCAGCAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAAGCTGGCCAAATG 2451
Db 2554 TTCTGTCTCAGCAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAAGCTGGCCAAATG 2495
Qy 2452 GACAACTTCTTCGCCCGCTTTTCCATGGGCAAAATATTAACGAAAGGCGCAAGGTTG 2511
Db 2494 GACAACTTCTTCGCCCGCTTTTCCATGGGCAAAATATTAACGAAAGGCGCAAGGTTG 2435
Qy 2512 CTGATGCCGCTGGGATTCAGTTTCATCGCTGTGTGATGGCTTCCATGTGGGAGA 2571
Db 2434 CTGATGCCGCTGGGATTCAGTTTCATCGCTGTGTGATGGCTTCCATGTGGGAGA 2375
Qy 2572 ATGCTTAATGAATACAAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2623
Db 2374 ATGCTTAATGAATACAAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2323

RESULT 10

US-09-484-997-28/c
; Sequence 28, Application US/09484997
; Patent No. 6524818

GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; TITLE OF INVENTION: ENDOGENOUS GENES

; FILE REFERENCE: 0221-0003J

; CURRENT APPLICATION NUMBER: US/09/484,997

; PRIORITY FILING DATE: 2000-01-18

; PRIORITY FILING DATE: 09/27/82

; PRIORITY FILING DATE: 1999-03-26

; PRIORITY FILING DATE: 09/15/99, 643

; PRIORITY FILING DATE: 1998-09-24

; PRIORITY FILING DATE: 08/94/1,223

; PRIORITY FILING DATE: 1997-09-26

; PRIORITY FILING DATE: 09/26/3,814

; PRIORITY FILING DATE: 1999-03-08

; PRIORITY FILING DATE: 09/253,022

; PRIORITY FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO 28

; LENGTH: 9737

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (8347)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified_base

; LOCATION: (8499)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-484-997-28

Query Match 15.6%; Score 759.2; DB 4; Length 9737;

Best Local Similarity 99.0%; Pred. No. 1.4e-141;

Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1852 TAAGATGATATACGGCGGTAAAGAGTTTCCAACTTTTCCACATATTAAGAAATAGATCACTA 1911

Db 3094 TGAGAGTTGATCGGCACGTAAGAGTTTCCAACTTTTCCACATATTAAGAAATAGATCACTA 3035

Qy 1912 CCGGGCGTATTTTGGAGTTATCGAGATTTTTCAGGAGCTTAAGAACTAAATGGAGAAA 1971

Db 3034 CCGGGCGTATTTTGGAGTTATCGAGATTTTTCAGGAGCTTAAGAACTAAATGGAGAAA 2975

Qy 1972 AAATCACTGATATACCACTGTTGATATCCCAATGGCATCGTAAAGAACTTTTGAG 2031

Db 2974 AAATCACTGATATACCACTGTTGATATCCCAATGGCATCGTAAAGAACTTTTGAG 2915

Qy 2032 GCATTTTCAGTCAGTGTCTCAATGTAATTAACACAGACCGTTTTCAGCTGGATATTAACGGCC 2091

Db 2914 GCATTTTCAGTCAGTGTCTCAATGTAATTAACACAGACCGTTTTCAGCTGGATATTAACGGCC 2855

Qy 2092 TTTTAAAGACCGTAAAGAAAAATAGACAAAGTTTATCCGGCTTTTATTCACATCTTT 2151

Db 2854 TTTTAAAGACCGTAAAGAAAAATAGACAAAGTTTATCCGGCTTTTATTCACATCTTT 2795

Qy 2152 GCCGCCCTGATGAATGCTATCCGGAATTCGGTATGGCAATGMAAGACGGTGAAGCTGGTG 2211

Db 2794 GCCGCCCTGATGAATGCTATCCGGAATTCGGTATGGCAATGMAAGACGGTGAAGCTGGTG 2735

Qy 2212 ATATGGGATAGTGTTCACCTTGTTCACCGCTTTTCCATGAGCAAACTGAAAGCTTTTCA 2271

Db 2734 ATATGGGATAGTGTTCACCTTGTTCACCGCTTTTCCATGAGCAAACTGAAAGCTTTTCA 2675

Qy 2272 TCGCTCTGGAGTGAATACCAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2331

Db 2674 TCGCTCTGGAGTGAATACCAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2615

Qy 2332 GTGGCGTGTTCAGGTGAAAAACCTGGCTATTTCCCTAAAGGTTTATTTGAAATATGTTT 2391

Db 2614 GTGGCGTGTTCAGGTGAAAAACCTGGCTATTTCCCTAAAGGTTTATTTGAAATATGTTT 2555

Qy 2392 TTCTGTCTCAGCAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAAGCTGGCCAAATG 2451

Db 2554 TTCTGTCTCAGCAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAAGCTGGCCAAATG 2495

Qy 2452 GACAACTTCTTCGCCCGCTTTTCCATGGGCAAAATATTAACGAAAGGCGCAAGGTTG 2511

Db 2494 GACAACTTCTTCGCCCGCTTTTCCATGGGCAAAATATTAACGAAAGGCGCAAGGTTG 2435

Qy 2512 CTGATGCCGCTGGGATTCAGTTTCATCGCTGTGTGATGGCTTCCATGTGGGAGA 2571

Db 2434 CTGATGCCGCTGGGATTCAGTTTCATCGCTGTGTGATGGCTTCCATGTGGGAGA 2375

Qy 2572 ATGCTTAATGAATACAAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2623

Db 2374 ATGCTTAATGAATACAAACAGTACTGCGATGAGTGGCGGGGGCGGTAAT 2323

RESULT 11

US-09-481-355-22/c

; Sequence 22, Application US/09481355

; Patent No. 6524824

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; TITLE OF INVENTION: ENDOGENOUS GENES

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; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-22

Query Match          15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAGAGGTTCCAACTTTCACCATTAAGTAAGATCACTA 1911
DB 3094 TGAGAGTTGATCGGCACGTAAGAGTTCCAACTTTCACCATTAAGTAAGATCACTA 3035
QY 1912 CCGGGCGTATTTTGGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 1971
DB 3034 CCGGGCGTATTTTGGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 2975
QY 1972 AAAATCAGTGATATACCAACCGTTGATATATCCAAATGCGATCGTAAGAAATTTGAG 2031
DB 2974 AAAATCAGTGATATACCAACCGTTGATATATCCAAATGCGATCGTAAGAAATTTGAG 2915
QY 2032 GCATTTCACTGCTGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2091
DB 2914 GCATTTCACTGCTGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2855
QY 2092 TTTTAAAGACCGTAAAGAAAAAAGCAAGTTTATCCGGCTTTTATTCACATTTCTT 2151
DB 2854 TTTTAAAGACCGTAAAGAAAAAAGCAAGTTTATTCGGCTTTTATTCACATTTCTT 2795
QY 2152 GCGGCGCTGATGATGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2211
DB 2794 GCGGCGCTGATGATGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2735
QY 2212 ATATGGGATGATGCTTACCGCTTGTATACCGTATTTCCATGAGCAAACTGAAAGCTTTTCA 2271
DB 2734 ATATGGGATGATGCTTACCGCTTGTATACCGTATTTCCATGAGCAAACTGAAAGCTTTTCA 2675
QY 2272 TCGCTCTGAGTGAATPACCAAGATTTTCGGGAGTTTCTACATATATTTTCGAAAGAT 2331
DB 2674 TCGCTCTGAGTGAATPACCAAGATTTTCGGGAGTTTCTACATATATTTTCGAAAGAT 2615
QY 2332 GTGGCGGTGTACGGTGAAACCTGGCTATTTCCCTAAAGGGTTTATTTGAGAAATATGTTT 2391
DB 2614 GTGGCGGTGTACGGTGAAACCTGGCTATTTCCCTAAAGGGTTTATTTGAGAAATATGTTT 2555
QY 2392 TTCGCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTGTATTTAAACCTGGCCCAATAG 2451
DB 2554 TTCGCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTGTATTTAAACCTGGCCCAATAG 2495
QY 2452 GACAACTTCTTCGCCCGCTTTTTCACCATGGGCAATATATATACGAAGCGCAAGGTG 2511

; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23/c
; Sequence 23, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23

Query Match          15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAGAGGTTCCAACTTTCACCATTAAGTAAGATCACTA 1911
DB 3094 TGAGAGTTGATCGGCACGTAAGAGTTCCAACTTTCACCATTAAGTAAGATCACTA 3035
QY 1912 CCGGGCGTATTTTGGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 1971
DB 3034 CCGGGCGTATTTTGGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 2975
QY 1972 AAAATCAGTGATATACCAACCGTTGATATATCCAAATGCGATCGTAAGAAATTTGAG 2031
DB 2974 AAAATCAGTGATATACCAACCGTTGATATATCCAAATGCGATCGTAAGAAATTTGAG 2915
QY 2032 GCATTTCACTGCTGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2091
DB 2914 GCATTTCACTGCTGCTCAATGATACCTATTAACCAAGCTTTCAGTTCGATATACGGCC 2855
QY 2092 TTTTAAAGACCGTAAAGAAAAAAGCAAGTTTATCCGGCTTTTATTCACATTTCTT 2151
DB 2854 TTTTAAAGACCGTAAAGAAAAAAGCAAGTTTATTCGGCTTTTATTCACATTTCTT 2795
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Wed May 12 08:20:57 2004

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Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAATGATATATACCGCGGTAGAGGTTCCAACTTTTCCACATATTAAGAAATAGTCACTA 1911
Db 3094 TGAGACGTTGATCGGCGAGTAAAGAGTTTCCAACTTTTCCACATATTAAGAAATAGTCACTA 3035
QY 1912 CCGGCGGTATTTTGTAGTTATCGAGATTTTTCAGAGCTAAGAGCTAAATGGAGAA 1971
Db 3034 CCGGCGGTATTTTGTAGTTATCGAGATTTTTCAGAGCTAAGAGCTAAATGGAGAA 2975
QY 1972 AAAATCACTGGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAAATTTTCAG 2031
Db 2974 AAAATCACTGGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAAATTTTCAG 2915
QY 2032 GCATTTCACTGATGTTGCTCAATGTACCTATACACGAGCCGTTTCAGTGGATATACGGCC 2091
Db 2914 GCATTTCACTGATGTTGCTCAATGTACCTATACACGAGCCGTTTCAGTGGATATACGGCC 2855
QY 2092 TTTTAAAGACCGTAAAGAAATTAAGCAAGTTTATCCGGCTTTTATCCGGCTTTTATCCATTCT 2151
Db 2854 TTTTAAAGACCGTAAAGAAATTAAGCAAGTTTATCCGGCTTTTATCCGGCTTTTATCCATTCT 2795
QY 2152 GCCCGCTGATGATGATGCTCATCGGAATTCGGTATGCGCAATGAAGACCGGTGAGCTGGTG 2211
Db 2794 GCCCGCTGATGATGATGCTCATCGGAATTCGGTATGCGCAATGAAGACCGGTGAGCTGGTG 2735
QY 2212 ATATGGATAGTGTTCACCCCTTGTACACCGTTTTCATGAGCAAACTGAAACGTTTTC 2271
Db 2734 ATATGGATAGTGTTCACCCCTTGTACACCGTTTTCATGAGCAAACTGAAACGTTTTC 2675
QY 2272 TCCTCTGGAGTGAATACACGAGGATTTCCCGAGTTTCTACATATATATCGCAAGAT 2331
Db 2674 TCCTCTGGAGTGAATACACGAGGATTTCCCGAGTTTCTACATATATATCGCAAGAT 2615
QY 2332 GTGGCGTTTACGGTGAAACCTGGCTATTTCCCTAAAGGGTTTATTTGAGATATGTTT 2391
Db 2614 GTGGCGTTTACGGTGAAACCTGGCTATTTCCCTAAAGGGTTTATTTGAGATATGTTT 2555
QY 2392 TTCCTCTCAGCCAAATCCCTGGTGAGTTTTCACCGTTTGTATTAACGTTGGCCAAATG 2451
Db 2554 TTCCTCTCAGCCAAATCCCTGGTGAGTTTTCACCGTTTGTATTAACGTTGGCCAAATG 2495
QY 2452 GACAACTTCTTCGCCCGGTTTTCACCATGGCAATATATATAGCAAGGCGCAAGGTG 2511
Db 2494 GACAACTTCTTCGCCCGGTTTTCACCATGGCAATATATATAGCAAGGCGCAAGGTG 2435
QY 2512 CTGATGCGGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGCTTCCATGTGGCAGA 2571
Db 2434 CTGATGCGGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGCTTCCATGTGGCAGA 2375
QY 2572 ATGCTTAATGAATTAACACAGTACTGCGATGGGCGGCGGCGTAAAT 2623
Db 2374 ATGCTTAATGAATTAACACAGTACTGCGATGGGCGGCGGCGTAAAT 2323

RESULT 13
US-09-481-355-28/c
; Sequence 28, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-481-355-28
; Query Match 15.6%; Score 759.2; DB 4; Length 9737;

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; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; -US-09-481-282-22

Query Match      15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAAAGAGCTTCCAACTTTCCACATATGAATAAGATCACTA 1911
DB 3094 TGAGAGCTTGATCGGCACGTAAGAGGTTCCAACTTTCCACATATGAATAAGATCACTA 3035
QY 1912 CCGGGCGTATTTTTCAGTTATCGAGATTTTCAGGAGCTTAAGGAAGCTAAATGGAGAA 1971
DB 3034 CCGGGCGTATTTTTCAGTTATCGAGATTTTCAGGAGCTTAAGGAAGCTAAATGGAGAA 2975
QY 1972 AAAATCACTGGATATACCAACCGTTGATATATCCAAATGGCATCGTAAAGAACATTTTGAG 2031
DB 2974 AAAATCACTGGATATACCAACCGTTGATATATCCAAATGGCATCGTAAAGAACATTTTGAG 2915
QY 2032 GCATTTTCAGTCAGTCTCAATGACCTATAACACGACCGTTCAGCTGGATATATACGGCC 2091
DB 2914 GCATTTTCAGTCAGTCTCAATGACCTATAACACGACCGTTCAGCTGGATATATACGGCC 2855
QY 2092 TTTTAAAGACCGTAAAGAAAATAAGCAAGTTTTATCCGGCCCTTTTATTCACATTTCTT 2151
DB 2854 TTTTAAAGACCGTAAAGAAAATAAGCAAGTTTTATTCGGCCCTTTTATTCACATTTCTT 2795
QY 2152 GCCCGCTGATGAATGCTCATCCGGAATTCGGATTCGGCAATGCGCAATGAAGACCGTGAGCTGGTG 2211
DB 2794 GCCCGCTGATGAATGCTCATCCGGAATTCGGATTCGGCAATGCGCAATGAAGACCGTGAGCTGGTG 2735
QY 2212 ATATGGGATAGTGTTCACCCCTTGTACACCGTTTTCATCCAGCTGATATATACGGCC 2271
DB 2735 ATATGGGATAGTGTTCACCCCTTGTACACCGTTTTCATCCAGCTGATATATACGGCC 2675
QY 2272 TCCTCTGAGTGAATACCAACGAGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
DB 2674 TCCTCTGAGTGAATACCAACGAGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2615
QY 2332 GTGGCGTTCAGGTGAACACCTGGCTATTTCCCTAAAGGTTTATGGAATATGTTT 2391
DB 2555 GTGGCGTTCAGGTGAACACCTGGCTATTTCCCTAAAGGTTTATGGAATATGTTT 2511
QY 2392 TTCCTCTCAGCAATCCCTGGGTGAGTTTACCAAGTTTTGATTTAAACGTTGGCCCAATATG 2451
DB 2451 TTCCTCTCAGCAATCCCTGGGTGAGTTTACCAAGTTTTGATTTAAACGTTGGCCCAATATG 2495
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DB 2495 GACAACTTTCTTCGCCCCGGTTTTCACCAATGGGCAAAATATATACGCAAGGCGCAAGGTG 2435
QY 2512 CTGATGCCGCTGGCGAATTCAGGTTCATCATGCCGCTCTGTGATGGCTTCCATGTCGGCAGA 2571
DB 2435 CTGATGCCGCTGGCGAATTCAGGTTCATCATGCCGCTCTGTGATGGCTTCCATGTCGGCAGA 2375
QY 2572 ATGCTTANTGAATTACACAGTACTGGATGAGTGGCGAGGGCGGGCGGTAAAT 2623
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DB 2374 ATGCTTANTGAATTACACAGTACTCGGATGATGGCGAGGGCGGGCGGTAAAT 2323
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RESULT 15
US-09-481-282-23/c
; Sequence 23, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; -US-09-481-282-23

Query Match      15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAAAGAGGTTCCAACTTTCCACATATGAATAAGATCACTA 1911
DB 3094 TGAGAGCTTGATCGGCACGTAAGAGGTTCCAACTTTCCACATATGAATAAGATCACTA 3035
QY 1912 CCGGGCGTATTTTTCAGTTATCGAGATTTTCAGGAGCTTAAGGAAGCTAAATGGAGAA 1971
DB 3034 CCGGGCGTATTTTTCAGTTATCGAGATTTTCAGGAGCTTAAGGAAGCTAAATGGAGAA 2975
QY 1972 AAAATCACTGGATATACCAACCGTTGATATATCCAAATGGCATCGTAAAGAACATTTTGAG 2031
DB 2974 AAAATCACTGGATATACCAACCGTTGATATATCCAAATGGCATCGTAAAGAACATTTTGAG 2915
QY 2032 GCATTTTCAGTCAGTCTCAATGACCTATAACACGACCGTTCAGCTGGATATATACGGCC 2091
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DB 2854 TTTTAAAGACCGTAAAGAAAATAAGCAAGTTTTATTCGGCCCTTTTATTCACATTTCTT 2795
QY 2152 GCCCGCTGATGAATGCTCATCCGGAATTCGGATTCGGCAATGCGCAATGAAGACCGTGAGCTGGTG 2211
DB 2794 GCCCGCTGATGAATGCTCATCCGGAATTCGGATTCGGCAATGCGCAATGAAGACCGTGAGCTGGTG 2735
QY 2212 ATATGGGATAGTGTTCACCCCTTGTACACCGTTTTCATCCAGCTGATATATACGGCC 2271
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QY 2452 GACAACTTTCTTCGCCCCGGTTTTCACCAATGGGCAAAATATATACGCAAGGCGCAAGGTG 2511
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QY 2512 CTGATGCCGCTGGCGAATTCAGGTTCATCATGCCGCTCTGTGATGGCTTCCATGTCGGCAGA 2571
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Search completed: May 9, 2004, 22:12:56
Job time : 214.917 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1296.16 Seconds

(without alignments)
16988.923 Million cell updates/sec

Title: US-10-055-001B-13_COPY_13040_17900

Perfect score: 4861
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3154.4	64.9	17862	15	US-10-055-001A-23
3	2563.2	52.7	17476	15	US-10-055-001A-24
4	2563.2	52.7	17476	15	US-10-385-546-7
5	2528	52.0	17681	15	US-10-055-001A-26
6	2510.6	51.6	17458	15	US-10-055-001A-25
7	1462.6	30.1	18691	15	US-10-055-001A-13
8	1193	24.5	4470	15	US-10-151-690-21
9	1193	24.5	4892	16	US-10-357-268-1
10	1193	24.5	5584	15	US-10-151-690-61
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14	876.4	18.0	4782	13	US-10-270-176-20

C 15	876.4	18.0	6742	13	US-10-270-176-19
C 16	846.2	17.4	4428	15	US-10-151-690-62
C 17	846.2	17.4	4470	15	US-10-151-690-21
C 18	846.2	17.4	4627	15	US-10-151-690-63
C 19	846.2	17.4	4627	15	US-10-151-690-64
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C 22	846.6	17.4	1846	15	US-10-023-208-63
C 23	844.6	17.4	1846	15	US-10-151-690-20
C 24	830	17.1	17862	17	US-10-097-034A-37
C 25	776.8	16.0	7278	15	US-10-097-034A-37
C 26	775.4	16.0	5558	13	US-10-241-596-137
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C 45	757.6	15.6	14468	15	US-10-295-362-19

ALIGNMENTS

RESULT 1

US-10-055-001A-13

; Sequence 13, Application US/10055001A

; Publication No. US20030049835A1

; GENERAL INFORMATION:

; APPLICANT: Waterhouse, Peter

; APPLICANT: Halliwell, Christopher A.

; TITLE OF INVENTION: Method and means for producing efficient silencing constructs

; TITLE OF INVENTION: using recombinational cloning

; FILE REFERENCE: HELIGA

; CURRENT APPLICATION NUMBER: US/10/055,001A

; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 18691

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: acceptor vector pHELLSGATE

; NAME/KEY: misc feature

; LOCATION: (7922)..(9985)

; OTHER INFORMATION: spectinomycin resistance

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (10706)..(11324)

; OTHER INFORMATION: right T-DNA border fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (11674)..(13019)

; OTHER INFORMATION: CamV35S promoter fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17890)..(17659)

; OTHER INFORMATION: attP1 recombination site (complement)


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NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccd8 selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
FEATURE:
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LOCATION: (13675)..(13980)
OTHER INFORMATION: ccd8 selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
FEATURE:
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LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
FEATURE:
NAME/KEY: misc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (497)..(1442)
OTHER INFORMATION: nptII coding region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
FEATURE:
NAME/KEY: misc feature
LOCATION: (2149)..(2706)
OTHER INFORMATION: a left T-DNA border region
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3781 CTTGCGAGACTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAACAATCAGGTTA 3840
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Db 17240 TTCCGCTTTCCAGGTTTCGGCAGCAGACGCGGCTTCACTTGTGATGTTGCTTAC 17299
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Qy 4561 TGTCCGTCCACTAAGTTGGCAGCATCACCCGAAGAACATTTTGGAGGCTGCGGTGCACT 4620
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Qy 4621 ACAGGCTACTAATACCACTAAGTAGTGAATTCATAGTGAATGTTGTTGTTTAC 4680
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Db 17720 AGTATTATGTAGTCTGTCTTTTATGCAAAATCTAATTTAATATATATGATATATATCAT 17779
Qy 4741 TTTACGTTTCTCGTTCAGCTTTTGTACAAAGTTGGCAATTTATAAAAGCATTCCTCAT 4800
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Db 17900 G 17900

RESULT 2

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; Sequence 23, Application US/10055001A
; Publication No. US20030049H35A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

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Best Local Similarity 82.6%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 16; Indels 831; Gaps 2;

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QY	481	CATCAAGAAACAATTTCAAACTCTATACCTTTCTCTTACAAGTCGTTCCGCTTCATCTG	540		14600	CAAAATAAAATCAATTTATTTGCCATCCAGCTGCAGCTCCTCGAGAAATTCGGTACCCCA	14659
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QY	541	GATTTTCAGCGCTCTATCTTACTTAAACGTCGATAAAGTTTCGTATTTCTTACTGTATCGA	600		14660	TTGGTAAGGAAATAAATATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	14719
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Db	13820	ACCACCGGTTAAAGTTTCAACGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGG	13879		1920	ATTTTGTAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTTAAATAATGGAGAAAAAATCAC	1979
QY	841	ATCACCATTCGTCGCCCGGGCTGTCAATATATCACTGTATCATCCACAAAACAGACGA	900		14914	-----	14913
Db	13880	ATCACCATTCGTCGCCCGGGCTGTCAATATATCACTGTATCATCCACAAAACAGACGA	13939		1980	TGATATATACCACCGTTGATATATCCCAATGGCATCGTAAGAACATTTTCGAGGCAATTTCA	2039
QY	901	TAAAGGCTCTCTCTTTATAGTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTC	960		14914	-----	14913
Db	13940	TAAAGGCTCTCTCTTTATAGTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTC	13999		2040	GTGAGTTGCTCAATGTACTATTAACACGACCGTTTCCAGCTGGAATATTACGGCCTTTTAA	2099
QY	961	GTACAGAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT	1020		14914	-----	14913
Db	14000	GTACAGAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT	14059		2100	GACCGTAAGAAAAATAAGCACAAAGTTTATCCGGCTTTTATTCACATTTCTGCGCGCCT	2159
QY	1021	TTCCGCTTTCCAGCGTTCCGACACAGACGCGGCTTCATTTGCAATGTTGTGCTTAC	1080		14914	-----	14913
Db	14060	TTCCGCTTTCCAGCGTTCCGACACAGACGCGGCTTCATTTGCAATGTTGTGCTTAC	14119		2160	GATGAATGCTCATCCGGAATTCGATGGCAATGAAAGACGCTGAGCTGTGATATGGGA	2219
QY	1081	CAGACCGGAGATATGACATCATATATGCTTGGACACTGATAGCTGCTGCTCACT	1140		14914	-----	14913
Db	14120	CAGACCGGAGATATGACATCATATATGCTTGGACACTGATAGCTGCTGCTCACT	14179		2220	TAGTGTTCACCCCTTGTATACACCGTTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTG	2279
QY	1141	GTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATACTTCGGGTAGTGCGGA	1200		14914	-----	14913
Db	14180	GTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATACTTCGGGTAGTGCGGA	14239		2280	GAGTGAATACACGACGATTTCCGGCAGTTTCTACATATATTCGCAAGATGTGGCGTG	2339
QY	1201	TCAACGCTCTATTTTCGCCAAAGTTGGCCCGAGGGCTTCCGGTATCAAAGGACACCA	1260		14914	-----	14913
Db	14240	TCAACGCTCTATTTTCGCCAAAGTTGGCCCGAGGGCTTCCGGTATCAAAGGACACCA	14299		2340	TTACGGTGAACCACTGCGCTTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTTCGCTC	2399
QY	1261	GGATTTATTTATCTCGGAAGTATCTTCGCTCACAGTATTTATTCGGCCCAAGTGGC	1320		14914	-----	14913
Db	14300	GGATTTATTTATCTCGGAAGTATCTTCGCTCACAGTATTTATTCGGCCCAAGTGGC	14359		2400	AGCCAATCCCTGGGTGAGTTTCCAGTTTGTATTTTAAACGTGGCCAATATGGAACAAT	2459
QY	1321	TCGGGTGATGTCGCCAACTTAGTCGACTACAGGTCACTTAATACCATCTAAGTAGTTGATT	1380		14914	-----	14913
Db	14360	TCGGGTGATGTCGCCAACTTAGTCGACTACAGGTCACTTAATACCATCTAAGTAGTTGATT	14419		2460	CTTCGCCCCGTTTTTACCATGGGCAAAATATTATACCAAGGCGACAGGTGTGTATGCC	2519
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Db	14420	CATAGTGACTGGAATATGTTGTTTACAGTATTAATGATGCTGTTTTTATGCAAAATC	14479		2520	GCTGGCGATTTCAGGTTTCATCATGCGCTCTCTGTATGGCTTCCATGTCCGCGAGATGCTTAA	2579
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QY	1501	GTGGCATTTATAAGAAAGCAATTCCTTATCAATTTTGTTCACCAACGAGGTCACTATCAGT	1560				

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Qy	2640	ACTAAAGCCAGATAACAGATATCGTATTTTGGCGCTGATTTTGGCGTATTAAGATATA	2699
Db	14914	-----	14913
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Db	14914	-----	14913
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Db	14970	ATRAATACTATAGTAAAAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAA	15029
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Db	15270	ATCAACATCTCTTAATAATTTCTTAATAATACCTTGTAGTTTATTAATACTCTTAATGGAT	15329
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Db	15330	GACTATTAATAATGAATAGTGCAGCATGAATAAACAAGGTAAACATGATAGATCATGT	15389
Qy	3180	CATTGTGTTATCATATGATCTTACATTTTGGATTTGATTTACAGTTGGGAATTTGGTTCCGAA	3239
Db	15390	CATTGTGTTATCATATGATCTTACATTTTGGATTTGATTTACAGTTGGGAATTTGGTTCCGAA	15449
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Db	15510	ACTGATAGTACCTTGTTCGTTGCAACAAATTTGATAAGCAATGCTTTCTTAATAATGCCAAC	15569
Qy	3360	TTTGTACAGAAAGCTGAAACGAGAAACCTTAAATGATATAATATCAATATAATTAATAATTA	3419
Db	15570	TTTGTACAGAAAGCTGAAACGAGAAACCTTAAATGATATAATATCAATATAATTAATAATTA	15629
Qy	3420	GATTTTGATATAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTCACTATG	3479
Db	15630	GATTTTGATATAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTCACTATG	15689
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Db	15690	AATCAACTACTTAGATGGTATTTAGTGACCTGTAGTTCGACTAAGTTGGCAGCATCAACCGA	15749
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Db	15750	CGCACTTTTCGGCGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCC	15809
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Db	15810	TGGTGTCCCTGTGTATACCGGAAGCCCTGGGCCAACTTTTGGCGAAAAATGAGCGTTGA	15869
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Db	15870	TGGGCACTACCATTTCAACAATCTATATCTTTCTTACAGTGGTTCGGCTTCATCT	15929
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Db	15990	ACCTCGACACTGGCTGTGTATAAGGAGCCTGACATTTTATATTTCCCGAAGACATCAGGTT	16049
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Db	16230	GATCACCATCGCTCGCCCGGGCGTGTCAATATATCACTCTGTACATCCACAAACAGACG	16289
Qy	4080	ATAAGCGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTCAACAGTCCCTGTTCT	4139
Db	16290	ATAAGCGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTCAACAGTCCCTGTTCT	16349
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Db	16350	CGTCAGCAAAAGAGCCGTTTCAATTTCAATAAAGCGGGGCGACCTCAGCCATCCCTTCTGAT	16409
Qy	4200	TTTTCCGCTTTCAGCGCTTCGCGACGACGAGCGGCTTCATTTCTCATGTTGTTGCTTA	4259
Db	16410	TTTTCCGCTTTCAGCGCTTCGCGACGAGCGGCTTCATTTCTCATGTTGTTGCTTA	16469
Qy	4260	CCAGACCGGAGATTAATGACATCATATATGCTTTGAGCACTGATAGCTGCTGTCACAC	4319
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Qy	4320	TGTCACGTAAATACGCTGCTTCATGACACACCTCTTTTTCACATCTCTGTTCTTGATG	4379
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Db	16590	CAGATGATTTTCAGGACTATGACACCTGATATGATAGGTAGATGTTTATTTTGT	16649
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Db	16650	CACACAAAAAGAGGCTCGCACCTCTTTTCTTTTATTTTATGATTTAATACGGCAT	16709
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Db	16710	TGAGGACAAATAGCGAGTAGCTCGATACGAGATTCGTTTGGAGAAACATTTGGAAGG	16769
Qy	4560	CTGTGCGTCCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGCTGCTGCGAC	4619
Db	16770	CTGTGCGTCCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGCTGCTGCGAC	16829
Qy	4620	TACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATGTTGTTGTTTA	4679
Db	16830	TACAGGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGATGTTGTTGTTTA	16889
Qy	4680	CAGTATTTATGAGTCTGTTTTTATGCAAAATCTAAATTTAATTTATTTATATCA	4739
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RESULT 4

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US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Hellmell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
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; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7
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Query Match 52.7%; Score 2563.2; DB 15; Length 17476;
Best Local Similarity 77.7%; Pred. No. 0;
Matches 3651; Conservative 0; Mismatches 23; Indels 1024; Gaps 5;

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Db 13205 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGAGAGCTTCCAAA 13264
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QY 322 AGGAATCGTGTATCCAGCCTACTCGCTATTTGTCTCAATGCGGTATTAATCAATAA 381
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QY 382 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAATCTACCT 441
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Db 13325 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAATCTACCT 13384
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QY 442 ATTCAATATACGTPAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTTCAAC 501
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Db 13385 ATTCAATATACGTPAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTTCAAC 13444
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QY 502 TCTTATACCTTTCTCTTACAGTCTGTCGCTTCACTCTGATTTTCAGCCTCTATCTTA 561
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QY 562 CTAACGCTGATAAAGTTTCTGTAAATTTCTATCTGTATCGACCTGCAGACTGGCTGTATA 621
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Db 13505 CTAACGCTGATAAAGTTTCTGTAAATTTCTATCTGTATCGACCTGCAGACTGGCTGTATA 13564
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Db 13565 AGGAGCCTGACATTTATATTTCCAGAAATCAGGTTAATGGCGTTTGTATCTTT 13624
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Db 13625 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGAGACCGGACACCTGGGCGATA 13684
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QY 742 TCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGCACCAACCGGGTAAAGTTCA 801
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Db 13685 TCGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGCACCAACCGGGTAAAGTTCA 13744
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|
QY 802 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATACCATTCGTCGCCCGGGC 861
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Db 13745 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATACCATTCGTCGCCCGGGC 13804
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QY 862 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATTAACGGCTCTCTCTTTTATAG 921
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|
Db 13805 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATTAACGGCTCTCTCTTTTATAG 13864
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QY 922 GTGTAAACCTTAAACTGCATTTTCCAGTCCCTGTTTCTCGTCAGCAAAAGAGCGGTTTCA 981
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Db	13865	GTGTAACCTTAAACTGCAATTTACAGTCCCTGTTCTCGTCAGCAAAAGACGGTTCAT	13924	Db	14726	-----	14725
Qy	982	TTCAATAAAGCGGGGACCTCAGCATCCCTTCCTGATTTTCGGCTTTCCAGGTTCCGC	1041	Qy	2061	TAACAGACCGTTCAGCTGGATATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCA	2120
Db	13925	TTCAATAAAGCGGGGACCTCAGCATCCCTTCCTGATTTTCGGCTTTCCAGGTTCCGC	13984	Db	14726	-----	14725
Qy	1042	ACGACAGACGCGGCTTCATTTGCGATGGTGTGCTTACAGACCGGAGATATTGACATC	1101	Qy	2121	CAAGTTTTATCGGCTTTTATTCACATTTCTGCGCGCTGATGAATGCTCATCCGGAAT	2180
Db	13985	ACGACAGACGCGGCTTCATTTGCGATGGTGTGCTTACAGACCGGAGATATTGACATC	14044	Db	14726	-----	14725
Qy	1102	ATATATGCTTGAACAACTGATAGCTGCTGCTCACTGCTCACTGATATACCGTCTTC	1161	Qy	2181	CGGTATGGCAATGAAGAAGCGTTCAGCTGGTGATATGGGATAGTGTTCACCTTGTACAC	2240
Db	14045	ATATATGCTTGAACAACTGATAGCTGCTGCTCACTGCTCACTGATATACCGTCTTC	14104	Db	14726	-----	14725
Qy	1162	ATAGCACACCTCTTTTGAATCTTCGGTAGTGGCGATCAACGCTCATTTTCGCCAA	1221	Qy	2241	CGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAAGACGATTT	2300
Db	14105	ATAGCACACCTCTTTTGAATCTTCGGTAGTGGCGATCAACGCTCATTTTCGCCAA	14164	Db	14726	-----	14725
Qy	1222	AAGTTGGCCACAGGCTTCCCGGTATCAACAGGGACACAGGATTTATTATTCTTCGGAAG	1281	Qy	2301	CGGGCAGTTTTCACACATATATTGGCAAGATGTGGGTGTACGGTGAAGAACTCGCCCTA	2360
Db	14165	AAGTTGGCCACAGGCTTCCCGGTATCAACAGGGACACAGGATTTATTATTCTTCGGAAG	14224	Db	14726	-----	14725
Qy	1282	TGATCTTCCTGTCACAGGATTTATTCGGCGCAAGTGGCTGGGTGATGCTGCCAACTTA	1341	Qy	2361	TTTCCCTAAAGGTTTATTGAGAAATGTTTTTTCGTCTCAGCCATCCCTGGGTGAGTTT	2420
Db	14225	TGATCTTCCTGTCACAGGATTTATTCGGCGCAAGTGGCTGGGTGATGCTGCCAACTTA	14284	Db	14726	-----	14725
Qy	1342	GTCGACTACAGGTCACATAACCTAAGTAGTTCATTCATAGTGCAGTGGATGTTGT	1401	Qy	2421	CACGAGTTTTGATTTAAACGTGGCCCAATATGGACAACCTTCTTCGCCCCCGTTTTCCACCAT	2480
Db	14285	GTCGACTACAGGTCACATAACCTAAGTAGTTCATTCATAGTGCAGTGGATGTTGT	14344	Db	14726	-----	14725
Qy	1402	GTTTTACAGTATTAGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATATGATTTT	1461	Qy	2481	GGCAAAATATTATACGCAAGGCGCAAGGTGCTGTATGCGCTGGCGATTCAGGTTCAATCA	2540
Db	14345	GTTTTACAGTATTAGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATATGATTTT	14404	Db	14726	-----	14725
Qy	1462	ATATCAATTTACGTTTCCTGCTCAGCTTCTCTGTACAAAAGTTGGCATTTAAGAAAGCAT	1521	Qy	2541	TGCGCTGTGATGGCTTCCATGTCGGCAGAAATGCTTAATGAATTAACAACAGTACTGCGA	2600
Db	14405	ATATCAATTTACGTTTCCTGCTCAGCTTCTCTGTACAAAAGTTGGCATTTAAGAAAGCAT	14447	Db	14726	-----	14725
Qy	1522	TGCTTATCAATTTGTTGCAAGCAAGAGTCACTATCAGTCAAAATAAATCATTTATTCG	1581	Qy	2601	TGAGTGGCAGGGGGGGCGTAATCGCTGGATCGGCTTACTAAAAGCCAGATAACAGTA	2660
Db	14448	-----	14447	Db	14726	-----	14725
Qy	1582	CATCCAGCTGCAGCTCCTCGAGGATTCGGTACCCCA-ATTGGTAAGAAATAATTATT	1640	Qy	2661	TGCGTATTTGCGGCTGATTTTTCGGGTATAAGAAATATATCTGATATGTCGGGCCCATTA	2720
Db	14448	-----	14447	Db	14726	-----	14742
Qy	1641	TCTTTTTTCTTTAGTATAAATAAGTTAAGTAGTGTAAATPAGTATGATTAATAATA	1700	Qy	2721	ATAGTAATTTCTAGCTGGTTTGATGAATTAATAATCAATGATTAATAATAGTAAAAAT	2780
Db	14493	TCTTTTTTCTTTAGTATAAATAAGTTAAGTAGTGTAAATPAGTATGATTAATAATA	14552	Db	14743	ATAGTAATTTCTAGCTGGTTTGATGAATTAATAATCAATGATTAATAATAGTAAAAAT	14802
Qy	1701	TAGTTGTTATATTTGTAATAATAATTTATATAATATATTTTACATAAACAACATAGT	1760	Qy	2781	AAGAAATAAATAAATAAATAAATAATTTTTTATGATTAATAGTGTATATATAATTAAT	2840
Db	14553	TAGTTGTTATATTTGTAATAATAATTTATATAATATATTTTACATAAACAACATAGT	14612	Db	14803	AAGAAATAAATAAATAAATAAATAATTTTTTATGATTAATAGTGTATATATAATTAAT	14862
Qy	1761	AATGTAAAAAATAATGACAAGTGTGTGAAGACGAAGAATAAAGTTGAGAGTAAGT	1820	Qy	2841	ATCTATACCATTAATAATATTTTAGTTTAAAGTTAAATTAATTTTGTAGAAAATTC	2900
Db	14613	AATGTAAAAAATAATGACAAGTGTGTGAAGACGAAGAATAAAGTTGAGAGTAAGT	14672	Db	14863	ATCTATACCATTAATAATATTTTAGTTTAAAGTTAAATTAATTTTGTAGAAAATTC	14922
Qy	1821	ATATTATTTTAAATGAATTTGATCGAACATGTGAAGATGATATACGGCCGGTGAAGGTTTC	1880	Qy	2901	AATCTGCTGTGTAATTTTATCAATAAACAATAATTTAAATTAACAAGCTAAAGTAAACAAATAA	2960
Db	14673	ATATTATTTTAAATGAATTTGATCGAACATGTGAAGATGATATACGGCCGGTGAAGGTTTC	14725	Db	14923	AATCTGCTGTGTAATTTTATCAATAAACAATAATTTAAATTAACAAGCTAAAGTAAACAAATAA	14982
Qy	1881	CAACTTTCACCAATAAGAAATAGATCACTACCGGGCGTATTTTGTAGTTATCGAGATT	1940	Qy	2961	TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACAATAATCTAATGTAATATAAAC	3020
Db	14726	-----	14725	Db	14983	TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACAATAATCTAATGTAATATAAAC	15042
Qy	1941	TTCCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT	2000	Qy	3021	AAAGGCAAGATCTCATTTTTTATATAGTATTTTCAATCAACATTTCTTTTAAATTTTC	3080
Db	14726	-----	14725	Db	15043	AAAGGCAAGATCTCATTTTTTATATAGTATTTTCAATCAACATTTCTTTTAAATTTTC	15102
Qy	2001	ATCCCAATGGCATCGTAAAGAACATTTTGGAGCAATTTTCAGTCAGTTGCTCAATGTACCTA	2060	Qy	3081	TAAATAATCTAGTATTTTATTAACCTTCTAAATGGATTTGACTATTAAATTAATGAATTA	3140
Db	14726	-----	14725	Db	15103	TAAATAATCTAGTATTTTATTAACCTTCTAAATGGATTTGACTATTAAATTAATGAATTA	15162

3141 GTCCGACATGAATAAACAAGCTAAACATGATAGATCATGTCTCATTTGTTATCATTTGATCTT 3200
15163 GTCCGACATGAATAAACAAGCTAAACATGATAGATCATGTCTCATTTGTTATCATTTGATCTT 15222
3201 ACATTTGATTTGATTTACAGTTGGGAAATGGTTTCGAAATCGAATCGAATCGGATCGCTCTTA 3260
15223 ACATTTGATTTGATTTACAGTTGGGAAATGGTTTCGAAATCGAATCGGATCGCTCTCTTA 15282
3261 GAGAGCTGCGATGCGCAAAATGAATTTATTTTGAATGATGATGATGATGATGATGATGATGAT 3320
15283 GA----- 15284
3321 GCAACAAATTTGATAGCAAACTGCTTTTATAATGCAAACTTTGTTATCAAGAAAGCTGAACG 3380
15285 -----CCACTTTTGTACAAGAAAGCTGAACG 15309
3381 AGAAGCTGAATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3440
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3441 TACATAAATCTGTAATAACACAAATATCCAGTCACTATGAATCAACTACTTACTTAGATGGTAT 3500
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3501 TAGTGACCTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3560
15430 TAGTGACCTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 15489
3561 ACCTGTGAGGAGATCACTTCGAGAAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3620
15490 ACCTGTGAGGAGATCACTTCGAGAAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15549
3621 GAAGCCCTGGGCCAACTTTTGGCGAAATGAGACGTTGATCGGCACTACCCATTTTCAAAA 3680
15550 GAAGCCCTGGGCCAACTTTTGGCGAAATGAGACGTTGATCGG-----ATTTTCAAAA 15601
3681 CTCTTAATCTTTCTTTTCAAGTCTGTTGGCTTCACTGGATTTTCAAGCTCTTACTT 3740
15602 CTCTTAATCTTTCTTTTCAAGTCTGTTGGCTTCACTGGATTTTCAAGCTCTTACTT 15661
3741 ACTTAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGAT 3800
15662 ACTTAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGAT 15721
3801 AAGGGAGCCTGACATTTATTTATTTCCCGAATCAATCAGGTTAATGCGCTTTTGTGATGAT 3860
15722 AAGGGAGCCTGACATTTATTTATTTCCCGAATCAATCAGGTTAATGCGCTTTTGTGATGAT 15781
3861 TTGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3920
15782 TTGCGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 15841
3921 ATCGGTTGCTCATGATGCGGCGAGCTTTTATCCCGATATGACACCGGCTTAAAGTTTCAAG 3980
15842 ATCGGTTGCTCATGATGCGGCGAGCTTTTATCCCGATATGACACCGGCTTAAAGTTTCAAG 15901
3981 GGAGACTTTTATCTGACAGCAGAGTGATGATGCGGCGAGGATCACCATCCGTGCGCGCGG 4040
15902 GGAGACTTTTATCTGACAGCAGAGTGATGATGCGGCGAGGATCACCATCCGTGCGCGCGG 15961
4041 CGTGCTCAATTAATCACTCTGTATCATCCACAAACAGACGATTAACGGCTCTCTCTTTTATA 4100
15962 CGTGCTCAATTAATCACTCTGTATCATCCACAAACAGACGATTAACGGCTCTCTCTTTTATA 16021
4101 GGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTGTCAGCAAAAAGAGCGCTTCA 4160
16022 GGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGTTCTGTCAGCAAAAAGAGCGCTTCA 16081
4161 TTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCGTGATTTTCCGCTTTCCAGGCTTCGG 4220
16082 TTTCAATAAACCAGGCGACCTCAGCCATCCCTTCCGTGATTTTCCGCTTTCCAGGCTTCGG 16141

4221 CACGACGACGCGCTTCATTTCTGATGTTGCTTTACACGCGGAGATATTGACAT 4280
16142 CACGACGACGCGCTTCATTTCTGATGTTGCTTTACACGCGGAGATATTGACAT 16201
4281 CATATATGCTTTGAGCAACTGATAGCTGTCCGTCACTGTCTAATACCTGCTT 4340
16202 CATATATGCTTTGAGCAACTGATAGCTGTCCGTCACTGTCTAATACCTGCTT 16261
4341 CATAGCACCTCTTTTGGACATCTTCTGTTGATGCGAGATGATTTTCCAGGACTATG 4400
16262 CATAGCACCTCTTTTGGACATCTTCTGTTGATGCGAGATGATTTTCCAGGACTATG 16321
4401 ACATAGCTATATGAATAGTAGATGTTTATTTTGTTCACACAAAAGAGCTCGCA 4460
16322 ACATAGCTATATGAATAGTAGATGTTTATTTTGTTCACACAAAAGAGCTCGCA 16381
4461 CCTCTTTTCTTATTTCTTTTATGATTTAATAGGCAATGAGGCAATAGCGAGTAGGC 4520
16382 CCTCTTTTCTTATTTCTTTTATGATTTAATAGGCAATGAGGCAATAGCGAGTAGGC 16441
4521 TGGATAGCAGCTTCCGTTTTCGAGAAACATTTTGGAGGCTGTCCGTGCACTAAAGTTGGC 4580
16442 TGGATAGCAGCTTCCGTTTTCGAGAAACATTTTGGAGGCTGTCCGTGCACTAAAGTTGGC 16501
4581 AGCATCACCCGAAAGCAATTTTGGAGGCTGTCCGTGCACTAAAGTTGGC 4640
16502 AGCATCACCCGAAAGCAATTTTGGAGGCTGTCCGTGCACTAAAGTTGGC 16561
4641 AAGTAGTTGATTCATGAGTCTGATGATGTTGTTTACAGTATGATGATGATGATGATGATGAT 4700
16562 AAGTAGTTGATTCATGAGTCTGATGATGTTGTTTACAGTATGATGATGATGATGATGATGAT 16621
4701 TTATGCAAAATCTAATTTAATATTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 4760
16622 TTATGCAAAATCTAATTTAATATTTAATATTTAATATTTAATATTTAATATTTAATATTTAAT 16681
4761 TTTTGTACAAAGTTGGC 4778
16682 TTTTGTACAAAGTTGGC 16699

RESULT 5

US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 52.0%; Score 2528; DB 15; Length 17681;

Best Local Similarity 76.5%; Pred. No. 0;

Matches 3682; Conservative 0; Mismatches 85; Indels 1043; Gaps 6;

QY 82 GCCAACTTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 141

Db 13025 GACAGTTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 13084

QY 142 AAATTAGATTTGCAATAAAAAACAGACTACATTAATCTGTAAAAACACACATATCCAGTC 201

Db	13085	AAATAGATTTTTCATATAAAAAAGACATACATAAATCTGTGAACACACATATCCAGTC	13144
QY	202	ACTATGAAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCTTCCAAA	261
Db	13145	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCTTCCAAA	13204
QY	262	TGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCAA	321
Db	13205	TGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCAA	13264
QY	322	ACGGAATCGTGTATCCAGCCTACTTCGCTATTGCTCAATGCCGTATTAATCATATAAA	381
Db	13265	ACGGAATCGTGTATCCAGCCTACTTCGCTATTGCTCAATGCCGTATTAATCATATAAA	13324
QY	382	AGAAATTAAGAAAAAGAGTGCAGCGCTCTTTTGTGTGCAAAATAAAAACATCTACCT	441
Db	13325	AGAAATTAAGAAAAAGAGTGCAGCGCTCTTTTGTGTGCAAAATAAAAACATCTACCT	13384
QY	442	ATTCAATACGCTAGTGTCTAGTCATAGTCCTGAAATCATCTGCATCAAGAACAAATTC	501
Db	13385	ATTCAATACGCTAGTGTCTAGTCATAGTCCTGAAATCATCTGCATCAAGAACAAATTC	13444
QY	502	TCCTATACCTTTCTCTTAAAGTCGTTGGCTTCACTCTGGATTTTCAGCCTCTATACTTA	561
Db	13445	TCCTATACCTTTCTCTTAAAGTCGTTGGCTTCACTCTGGATTTTCAGCCTCTATACTTA	13504
QY	562	CTAAAAGTGTATAAAGTTTCGTAAATTTTACTGTATTCGACCTGCAGCTGGCTGTATA	621
Db	13505	CTAAAAGTGTATAAAGTTTCGTAAATTTTACTGTATTCGACCTGCAGCTGGCTGTATA	13564
QY	622	AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGGCGTTTGTGATCATTT	681
Db	13565	AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGGCGTTTGTGATCATTT	13624
QY	682	TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCACCTGGCCATA	741
Db	13625	TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCACCTGGCCATA	13684
QY	742	TCGCGGTGCTGATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCA	801
Db	13685	TCGCGGTGCTGATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCA	13744
QY	802	GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCGTGCGCCGGC	861
Db	13745	GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCGTGCGCCGGC	13804
QY	862	GTGTCAATAAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTATAG	921
Db	13805	GTGTCAATAAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTATAG	13864
QY	922	GTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTGTCAGATAAAGCGTTTCAT	981
Db	13865	GTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTGTCAGATAAAGCGTTTCAT	13924
QY	982	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGCTTTCCAGGTTCCGC	1041
Db	13925	TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGCTTTCCAGGTTCCGC	13984
QY	1042	ACGACAGCAGCGGCTTCATCTGATGGTGTGCTTACCAGACCGGAGATATTGATC	1101
Db	13985	ACGACAGCAGCGGCTTCATCTGATGGTGTGCTTACCAGACCGGAGATATTGATC	14044
QY	1102	ATATATGCCCTTGAGCAACTGATAGCTGTCCTGTCAACTGTCTGATATTCGCTCTTC	1161
Db	14045	ATATATGCCCTTGAGCAACTGATAGCTGTCCTGTCAACTGTCTGATATTCGCTCTTC	14104
QY	1162	ATAGCAACCTCTTTTGTGATACCTTCGGGTAGTGGCGATACAGCTCATTTTCGCCAA	1221
Db	14105	ATAGCAACCTCTTTTGTGATACCTTCGGGTAGTGGCGATACAGCTCATTTTCGCCAA	14164
QY	1222	AGTTTCGCCCGCAGGCTTCCGGTATCAACAGGGACACCGAGTATTTATTTATCTCGAG	1281

Db	14165	AAAGTTGGCCCGCGGCTTCCGGTATCAACACAGGACACACAGGATTTATTTATTTCTGCGAAG	14224
QY	1282	TGATCTTCGTCACAGGATATTTATTCGGCGGCAAAGTGGTGGGTGATGCTGCCAACTTA	1341
Db	14225	TGATCTTCGTCACAGGATTTATTCGGCGGCAAAGTGGTGGGTGATGCTGCCAACTTA	14284
QY	1342	GTGACTACAGGTCACCTAATCACTTAAGTAGTTGATTCATAGTGACTCGATATGTTGT	1401
Db	14285	GTGACTACAGGTCACCTAATCACTTAAGTAGTTGATTCATAGTGACTCGATATGTTGT	14344
QY	1402	GTTTTACAGTATATAGTAGTCGTGTTTTTATGCAAAATCTAATTAATATATTCGATATTT	1461
Db	14345	GTTTTACAGTATATAGTAGTCGTGTTTTTATGCAAAATCTAATTAATATTCGATATTT	14404
QY	1462	ATATCAATTTACGTTTCGTTTCAGCTTCCTGTGTACAAAGTTGGCAATTAAGAAAGCAT	1521
Db	14405	ATATCAATTTACGTTTCGTTTCAGCTTCCTGTGTGTACAAAGTTGGCAATTAAGAAAGCAT	1521
QY	1522	TGCTTATCAATTTGTTGCCAAGCAACAGGTCACCTATCAGTCAAAATAAAATCATTTATTCG	1581
Db	14448	-----	14447
QY	1582	CATCCAGCTGAGCTCTTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATATTAATTT	1640
Db	14448	-----TCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATATTAATTT	14492
QY	1641	TCCTTTTTCCTTTTAGTATATAATAGTTAAGTCAGTGTATTAATAGTATGATTAATAATA	1700
Db	14493	TCCTTTTTCCTTTTAGTATATAATAGTTAAGTCAGTGTATTAATAGTATGATTAATAATA	1700
QY	1701	TAGTGTATATATGTGCAAAAAATAATTTATAAATATATGTTTACATAAAACAACATAGT	1760
Db	14553	TAGTGTATATATGTGCAAAAAATAATTTATAAATATATGTTTACATAAAACAACATAGT	14612
QY	1761	AATGTAAAAAATATCAGCAAGTGATGTGTAGACGAAGAGATATAAAGTTGAGAGTAAGT	1820
Db	14613	AATGTAAAAAATATCAGCAAGTGATGTGTAGACGAAGAGATATAAAGTTGAGAGTAAGT	14672
QY	1821	ATATTATTTTTTAATGAATTTGATCGAAATGTAAAGTATATACGGCCGGTAAGAGTTTC	1880
Db	14673	ATATTATTTTTTAATGAATTTGATCGAAATGTAAAGTATATACGGCCGGTAAGAGTTTC	14725
QY	1881	CAACTTTCACCATATGAATAAGATCATCTACGGGCGGTATTTTTTGTAGTTATCGAGATT	1940
Db	14726	-----	14725
QY	1941	TTCAGGAGCTAAGGAAGCTAAAAATCGAGAAAAAATCACTGGATATACACCGTTGATAT	2000
Db	14726	-----	14725
QY	2001	ATCCCAATGGCATCGTAAGAACAATTTTGGGCATTTTCAGTCAGTTGCTCAATGTACCTA	2060
Db	14726	-----	14725
QY	2061	TAACCAGACCGTTACGTGGATATACGGCCTTTTAAAGACCGTAAGAAAAATAAGCA	2120
Db	14726	-----	14725
QY	2121	CAAGTTTTTATCCGCCCTTTATTCACATTCCTGCGCGCTGATGATGGATAGTGTTCACCC	2180
Db	14726	-----	14725
QY	2181	CCGTATGGCAATGAAGAAGCGTGAGTGTGATATGGATAGTGTTCACCCCTGTTACAC	2240
Db	14726	-----	14725
QY	2241	CGTTTTCCATGACCAACTGAACGTTTTCATCGCTCTGGAGTGAATACACGACGATTT	2300
Db	14726	-----	14725
QY	2301	CCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGGTGTACGGTGAATAAATCGGCTTA	2360
Db	14726	-----	14725

Qy	2361	TTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTCTGCTCAGCCAATCCTGGGTGAGTTT	2420
Db	14726	-----	14725
Qy	2421	CACCAGTTTTTGATTTAAACGTCGGCCAATATGGACAACCTCTTCGCCCCCGTTTTCACCAT	2480
Db	14726	-----	14725
Qy	2481	GGGCAAAATATTATACGCAAGGCGACAGAGTGTGATGCCGTGGCGATTCAGGTTTCATCA	2540
Db	14726	-----	14725
Qy	2541	TGCCGTCGTGATGGCTTCCATGTCGGCAGATGCTTAAATGAAATTACAACAGTACTGGCA	2600
Db	14726	-----	14725
Qy	2601	TGAGTGGCAGGGCGGGCGTAATTCGGTGGATCCGGCTTACTAAAGCGCAGATAACAGTA	2660
Db	14726	-----	14725
Qy	2661	TGCGTATTTGCGCGCTGATTTTTTTCGGGTATAAGAAATATACTGATATGTCGGGCCCATTA	2720
Db	14726	-----	14742
Qy	2721	ATAGTAATTTCTAGCTGGTTTTGATGAATTAATAATCAATGATAAAAAATCACTAGTAGAAAAAT	2780
Db	14743	ATAGTAATTTCTAGCTGGTTTTGATGAATTAATAATCAATGATAAAAAATCACTAGTAGAAAAAT	14802
Qy	2781	AGAAATAAATAAATTAATAATATATTTTTTTTATGATTAATAGTTTATTATATAATTAAT	2840
Db	14803	ARGAATAAATAAATTAATAATATATTTTTTTTATGATTAATAGTTTATTATATAATTAAT	14862
Qy	2841	ATCTATACCAATTAATAATATTTTTTACGTTTAAAGGTTAATAAATATTTTGTAGAAAAATCC	2900
Db	14863	ATCTATACCAATTAATAATATTTTTTACGTTTAAAGGTTAATAAATATTTTGTAGAAAAATCC	14922
Qy	2901	AATCTCGTTGTAAATTTTCAATAAACAATAATTAATAACAAGCTAAAGTAAACAATAAA	2960
Db	14923	AATCTCGTTGTAAATTTTCAATAAACAATAATTAATAACAAGCTAAAGTAAACAATAAA	14982
Qy	2961	TATCAAACTAATAAGAAACAGTAATCTAATGTAAACAACAATTAATCTAATGCTAATAAAC	3020
Db	14983	TATCAAACTAATAAGAAACAGTAATCTAATGTAAACAACAATTAATCTAATGCTAATAAAC	15042
Qy	3021	AAAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACAATCTCTTATTAAATTC	3080
Db	15043	AAAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACAATCTCTTATTAAATTC	15102
Qy	3081	TAAATAATATCTGTAGTTTTTAATCTCTAAATGGATGACTATTAATTAATGAATTA	3140
Db	15103	TAAATAATATCTGTAGTTTTTAATCTCTAAATGGATGACTATTAATTAATGAATTA	15162
Qy	3141	GTGCAATCAATGAATAAACAAGGTAAACATGATAGATCATGTTCATTTGTTTATCATTTGATCTT	3200
Db	15163	GTGCAATCAATGAATAAACAAGGTAAACATGATAGATCATGTTCATTTGTTTATCATTTGATCTT	15222
Qy	3201	ACATTTGGATTGATTACAGTTGGGAAATTTGGGTTCGAAATCGATAAGCTTG-----GAT	3254
Db	15223	ACATTTGGATTGATTACAGTTGGGAAAGCTGGGTTTCGAAATCGATAAGCTTTGGCGTGCAGT	15282
Qy	3255	CCCTAGAGAGCTGCAGCTGGATGGCAATAATGATTTTTTTTTCATGCTAGTAGCACTG	3314
Db	15283	TATCATCATCATATAGACACACGAAATAAGTAATCAGATTATCAGTTAAAGCTATGTA	15342
Qy	3315	TTCGTTGCCAACAAA-----	3328
Db	15343	ATATTTGGCCATAACCAATCANTTAABAAAATAGATCAGTTTAAAGAAGATCAAGCTC	15402
Qy	3329	-----	3328
Db	15403	AAAAAATAAAAAAGAGAAAAAGGGTCTTAACCAAGAAAAATGAAGGAGAGAAAACTAGAAATT	15462

QY	3329	TTGATTAAGCAATGCTTTCTTTATAATAGCCAACTTTTGTAACAAGAAAGCTGAAACGAGAAACGCT	3388
DB	15463	TACCTGCAAAAGCTTGGATCCCTCTAGACACACTTTGTACAAGAAAGCTGAAACGAGAAACGCT	15522
QY	3389	AAAATGATATAAATATCAATATATAATATAATTTGTCATAAAAAAAGACTACATAAT	3448
DB	15523	AAAATGATATAAATATCAATATATAATATAATTTGTCATAAAAAAAGACTACATAAT	15582
QY	3449	ACTGTAACACACAACATATCCAGTCACTAATGAATCAACTACTTAGATGGTATTAGTGACC	3508
DB	15583	ACTGTAACACACAACATATCCAGTCACTAATGAATCAACTACTTAGATGGTATTAGTGACC	15642
QY	3509	TGTTAGTCGACTAAGTTGGCAGCATCACCGACGCACTTTGCGCCGAAATAAATACCTGTGA	3568
DB	15643	TGTTAGTCGACTAAGTTGGCAGCATCACCGACGCACTTTGCGCCGAAATAAATACCTGTGA	15702
QY	3569	CGGAAGATCACTTTGCGAGAAATAATAAATCTCTGGTGTCCCTTTGATACCGGGAAGCCCT	3628
DB	15703	CGGAAGATCACTTTGCGAGAAATAATAAATCTCTGGTGTCCCTTTGATACCGGGAAGCCCT	15762
QY	3629	GGGCCAACTTTTGGCGAAAAATGAGAGCTTGATCGGCACTACCCATTTTCAACAATCTTTATA	3688
DB	15763	GGGCCAACTTTTGGCGAAAAATGAGAGCTTGATCGG-----ATTTCACAATCTTTATA	15814
QY	3689	CTTTTCTCTTACAAGTCTTTGGCTTCATCTGGATTTTCAGGCTCTATACTTACTTAAAAAG	3748
DB	15815	CTTTTCTCTTACAAGTCTTTGGCTTCATCTGGATTTTCAGGCTCTATACTTACTTAAAAAG	15874
QY	3749	TGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTTGAGAGCTGGCTGTGTATAGGGAGC	3808
DB	15875	TGATAAAGTTTCTGTAATTTCTACTGTATCGAAGCTTGAGAGCTGGCTGTGTATAGGGAGC	15934
QY	3809	CTGACATTTATATTTCCCGAGAAATCAGGTAAATGGCGTTTGTGATGTCAATTTTCGCGGT	3868
DB	15935	CTGACATTTATATTTCCCGAGAAATCAGGTAAATGGCGTTTGTGATGTCAATTTTCGCGGT	15994
QY	3869	GGCTGAGATCAGCCATTCTTTCCCGATTAACCGAGACCGGCACATGCGCCATATCGGTGG	3928
DB	15995	GGCTGAGATCAGCCATTCTTTCCCGATTAACCGAGACCGGCACATGCGCCATATCGGTGG	16054
QY	3929	TCATCATGCGCAGCTTTTCATCCCGCATATGACCAACCGGTAAAGTTTCAAGGAGACTT	3988
DB	16055	TCATCATGCGCAGCTTTTCATCCCGCATATGACCAACCGGTAAAGTTTCAAGGAGACTT	16114
QY	3989	TATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGCGCTGTCAA	4048
DB	16115	TATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGCGCTGTCAA	16174
QY	4049	TAATATCACTCTGTATATCAACAAAGACGATTAACGGCTCTCTCTTTTATAGGTGTAAA	4108
DB	16175	TAATATCACTCTGTATATCAACAAAGACGATTAACGGCTCTCTCTTTTATAGGTGTAAA	16234
QY	4109	CCCTTAACTGCATTTCCACAGTCCCTGTCTCGTACGCAAAAGACCGGTTCATTTCAATA	4168
DB	16235	CCCTTAACTGCATTTCCACAGTCCCTGTCTCGTACGCAAAAGACCGGTTCATTTCAATA	16294
QY	4169	AACCGCGACCTCAGCCATCCCTTCCCTGATTTTCGGCTTTCCAGCTTTCCGACGACGAGA	4228
DB	16295	AACCGCGACCTCAGCCATCCCTTCCCTGATTTTCGGCTTTCCAGCTTTCCGACGACGAGA	16354
QY	4229	CGACGGCTTCATTTCTGCATGGTTGTGCTTACACAGACGGAGATATGACATCATATATG	4288
DB	16355	CGACGGCTTCATTTCTGCATGGTTGTGCTTACACAGACGGAGATATGACATCATATATG	16414
QY	4289	CCCTTGACAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTCTCATAGCAC	4348
DB	16415	CCCTTGACAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTCTCATAGCAC	16474
QY	4349	ACCTCTTTTTCATCTCTGTCTGTATGATGAGATGATTTTCAGGACTATGACACTAGC	4408
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QY	4409	GTATATGAAATAGTATGTTTTTATTTTGTTCACAAAAAAGAGGCTCGACCTCTTTT	4468


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Db 16535 GTATATGATAGTAGATGTTTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTT 16594
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QY 4529 ACGATTCGGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 4588
Db 16655 ACGATTCGGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 16714
QY 4589 CCGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCACATCTAAGTAGTT 4648
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Db 16775 GATTCATAGTACTGATATGTTGTTTACAGTATTAAGTAGTCTGTTTTTATGCAA 16834
QY 4709 AATCTAATTTAATATATGATTTATATCAATTTTACGTTTCTCGTTTACGTTTTTTGTA 4768
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QY 4769 CAAAAGTTGGC 4778
Db 16895 CAAACTGTGC 16904

RESULT 6
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 51.6%; Score 2510.6; DB 15; Length 17458;
Best Local Similarity 77.2%; Pred. No. 0;
Matches 3628; Conservative 0; Mismatches 29; Indels 1040; Gaps 6;

QY 82 GCCAACTTTTGTAACAAAAAGCTGAACAGAGAAACGTAATAATCATATAATATCAATATTT 141
Db 13025 GACAAGTTTGTAACAAAAAGCTGAACAGAGAAACGTAATAATCATATAATATCAATATTT 13084
QY 142 AAATTAGATTTTGCAAAAAAAGACACTACATATACTGTAAACACACATATCCAGTC 201
Db 13085 AAATTAGATTTTGCAAAAAAAGACACTACATATACTGTAAACACACATATCCAGTC 13144
QY 202 ACTATGAATCAACTTATAGATGTTATTTAGTGACTGTAGTCGACCGACAGCCCTTCCAAA 261
Db 13145 ACTATGAATCAACTTATAGATGTTATTTAGTGACTGTAGTCGACCGACAGCCCTTCCAAA 13204
QY 262 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAGCCCTTCCAAATGTTCTTCA 321
Db 13205 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACAGCCCTTCCAAATGTTCTTCA 13264
QY 322 ACGAATCGTGTATCCAGCCCTACTCGCTATGTCCTCAATGCGGTATTAATCATAAAA 381
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Db 13265 ACGGAATCGTGTATCTACAGCCTACTCGCTATTGTCTCAATGCCGTATTAATCATAAAA 13324
QY 382 AGAAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGA CAAAAATAAAAAATCTACTCT 441
Db 13325 AGAAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGA CAAAAATAAAAAATCTACTCT 13384
QY 442 ATTCATATACGCTAGTGTGCATAGTCTGAAATCATCTGCAATCAAGAACAAATTTCCACAC 501
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QY 682 TCGCGGTGCTGAGATCAGACCACTTTCTTCCCGATAACGAGACCGGACACACTGGCCATA 741
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QY 1222 AAGTTGGCCCGGCTTTCCGGGTATCAACAGGACACACAGGATTTTATTTTCTGCGAAG 1281
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QY 1282 TGATCTTCCGTCACAGGTATTTTATTCGGGCGAAAGTGCCTCGGGTGATGCTGCCAATCTTA 1341
Db 14225 TGATCTTCCGTCACAGGTATTTTATTCGGGCGAAAGTGCCTCGGGTGATGCTGCCAATCTTA 14284
QY 1342 GTCGACTACAGGTCACTAATAACCTAAGTAGTTGATTCATAGTACCTGGATATGTTCT 1401
Db 14285 GTCGACTACAGGTCACTAATAACCTAAGTAGTTGATTCATAGTACCTGGATATGTTCT 14344
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Db 15533 AAGCCCTGGGCCAACTTTTGGCGAAATGAGAGCTTGATCGG-----ATTTCACAAC 15584
QY 3682 TCTTATACCTTTCTCTTACAAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 3741
Db 15585 TCTTATACCTTTCTCTTACAAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 15644
QY 3742 CTAAACGTGATAAAGTTCTGTAAATTTCTACTGATCGACTGCAGACTGGCTGTGATATA 3801
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QY 3802 AGGAGAGCTGACATTTATATTTCCCGAAGCATCAGGTTAATGCGTTTTCATGTCATTT 3861
Db 15705 AGGAGAGCTGACATTTATATTTCCCGAAGCATCAGGTTAATGCGTTTTCATGTCATTT 15764
QY 3862 TCGCGGTGGCTGAGATCAGCCACTTTTCCCGGATACGGAGACCGGCACACTGGCCATA 3921
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QY 3922 TCGGTGTGATCATGCGCGAGCTTTTCATCCCGGATATGCACACCGGGTAAAGTTCAAG 3981
Db 15825 TCGGTGTGATCATGCGCGAGCTTTTCATCCCGGATATGCACACCGGGTAAAGTTCAAG 15884
QY 3982 GAGACTTTATCTGACAGCAGACGTCACCTGCCAGGGGATCACCATCCGTCGCCCGGGC 4041
Db 15885 GAGACTTTATCTGACAGCAGACGTCACCTGCCAGGGGATCACCATCCGTCGCCCGGGC 15944
QY 4042 GTGTCAATATATCACTCTGPACATCCAAACAGACGATAACGGCTCTCTCTTTTATAG 4101
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QY 4102 GTGTAAACCTTAACTGCATTTACCAAGTCCTCTCTGTCACGAAAGAGCGGTTTCAT 4161
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QY 4162 TTCAATAAAGCGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGGC 4221
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QY 4282 ATATATGCTTGAACAACTGATAGCTGCTGCTGCACTGCTCACTGTAATACGCTGCTTC 4341
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QY 4402 CACTAGCGTATGATAGGTAGATGTTTATTTTGTACACAAAAGAGGCTCCGAC 4461
Db 16305 CACTAGCGTATGATAGGTAGATGTTTATTTTGTACACAAAAGAGGCTCCGAC 16364
QY 4462 CTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTTAGGACATAGCGAGTAGGCT 4521
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QY 4522 GGATACGACGATTCGGTTTGGAGAGACATTTGGAAGCTGTCGGTCGACTAAGTTGGCA 4581
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QY 4582 GCATCACCGGAGACATTTGGAGAGGCTGTCGGTCGACTACAGGTCACATAACCATTA 4641
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QY 4702 TATCGAAATCTAATTTAATATATGATGATTTATATCAATTTTACGTTTCTCGTTACGCTT 4761

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Db 16665 TTTTGTACAAACTTGTGTC 16681
RESULT 7
US-10-055-001A-13/c
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION: Susan V.
; APPLICANT: Wesley, Susan V.
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 16691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17890)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
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; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
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; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
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; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:

[illegible]

Db 16110 AAGAAATGTTGATGAAATAATACTATATATAAATAGTAGATCTTGGCTTTGTTATATTA 16051
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Db 16050 GCATTAGATTATGTTTGTACATAGATTACTGTTTCTATTATAGTTTGATATTATTTGTT 15991
QY 1887 TCACCATAATGAATAAGATCACTACCGGGCGTATTTTGTAGTTATCGAGATTTTCAGG 1946
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QY 2961 TATCAAACTAATAGAAACAGTAAATCTAATGTAAACAAACATTAATCTAATGCTTAATATAAC 3020
Db 14916 CCTCTTACCGCGGTATATCATCTTACATGTTTCGATCAAAATTCATTAATAATAATACT 14857
QY 3021 AAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATCAACATTTTAAATTC 3080
Db 14856 TA ---CTCTCAACTTTTATCTTCTGCTTTACACATCACTTGTCATATTTT 14807
QY 3081 TAAATAAATCTTGTAGTTTATTTAACTTCTAAATGGATGACTATTTAATTAATAAATAA 3140
Db 14806 TTACATTAATAATGTTTGTATGATAACAAATAATTTATATAAATAATTTTTCACAATAA 14747
QY 3141 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTTATCATTTGATCTT 3200
Db 14746 ACAACTATATTAATAATAATCACTAAATTAACATCACTTAACATTTTATATAAAGGA 14687
QY 3201 ACATTTGGATTCATTTACAGTTTGGGAAATTTGGGTTCGAAATCGATAAGCTTGGATCTCTA 3260
Db 14686 AAAAGAAATAATTT ---ATTTCTTACCAATTTGGGTACCGAATTTCTCGA 14638
QY 3261 GAGAGCTGAGCTGGATGCAAAATAATGATTTTATTTGACTGATGAGTACCTGTTGCTT 3320
Db 14637 G-GAGCTGAGCTGGATGCAAAATAATGATTTTATTTGACTGATGAGTACCTGTTGCTT 14579
QY 3321 GCACAAATTTGATAGCAATGCTTTCTTATGATGCACTTTGTAACAAGAGCTGGAACG 3380
Db 14578 GCAACAAATTTGATAGCAATGCTTTCTTATAATGCCAATTTGTACAAGAAAGCTGAACG 14519
QY 3381 AGAAACGTAAATGATATAAATATCAATATATAATTAATTTAGATTTTGCATAAATAAACA 3440
Db 14518 AGAAGCTAAATGATATAAATATCAATATATAATTTAATTTAGATTTTGCATAAATAAACA 14459
QY 3441 TACATAAATCTGTAAACAAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 3500
Db 14458 TACATAAATCTGTAAACAAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 14399
QY 3501 TAGTGACCTGTAGTGCATTAAGTTGCGACATCACCGACGACCTTTGGCGCGAATAAAT 3560
Db 14398 TAGTGACCTGTAGTGCATTAAGTTGCGACATCACCGACGACCTTTGGCGCGAATAAAT 14339
QY 3561 ACTGTGACGGAAGATCACTTCGCGAATAAATAAATCTTGGTGTCCCTGTTGATACCGG 3620
Db 14338 ACTGTGACGGAAGATCACTTCGCGAATAAATAAATCTTGGTGTCCCTGTTGATACCGG 14279
QY 3621 GAAGCCCTGGCGAATTTTGGGAAATGAGAGCTTGTGATGCGGACCTACCCATTTTCAAA 3680
Db 14278 GAAGCCCTGGCGAATTTTGGGAAATGAGAGCTTGTGATGCGGACCTACCCGAAATGAT 14219
QY 3681 CTCTTATATCTTTCTTCAAAAGTGGTTCGGCTTCATCTGGATTTTTCAGCCCTCTATCTT 3740
Db 14218 CAAAAGAGGTGTGCTATGAA ---GCAGGTATTACAGTGAAGTGTGACGAGCAGCTA 14162
QY 3741 ACTAAAGTGAATAAGTTTCTGTAAATTTCTATGATATGACCTGACAGCTGGCTGTGAT 3800
Db 14161 TCAGTTGCTCAAGGCATATATGATGTCATATCTCCGGTCTGTAAGCAACACCATGCGAG 14102
QY 3801 AAGGAGCCGTGATTTATTTCCCGAATCAAGTAAATGAGCTTAAATGAGCTTTTTCATGTCATT 3860
Db 14101 AATGAAGCCGTGCTGCTGCTGCC ---GAACGCTGGAAGCGGAAATCAGGAAGGGATG 14045
QY 3861 TCCGCGTGGCTGAGATCAGCACTCTTCTCCCGATTAACGGGAGACCGGACACTTGGCCAT 3920
Db 14044 GCTGAGCTGCCGGTGTATTGAAATGAACGGCTCTTTTGTGTCAGCAGAACAGGG --- 13990
QY 3921 ATCGGTGGTATCATGCGCAGCTTTTCATCCCGATATACACCGGGTAAAGTTACG 3980
Db 13989 -ACTGGTGAATGACGTTTTAAGGTTTACACCTATAAAGAGAGAGCGGTTATCGTCTGTT 13931

QY 3981 GGAGACTTATCTGACAGCAGCGTGCACCTGGCCAGGGGGGATCACCATCGTCCCGGGG 4040
Db 13930 TGTGGATGACAGAGTGATATTATGACAGCCCGGGGACGGATGATCCCGCTGGC 13871
QY 4041 CGTGTCAATAATCACTCTGTACATCCAAACACAGACGATACGGCTCTCTTTTATA 4100
Db 13870 CAGTGACGCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCGGTGGTGATATCGG 13811
QY 4101 GGTGTAAACCTTAACTGCAATTTTACCA-----GTCCCTGTCTCTGTGACGAAAGAGC 4154
Db 13810 GGATGAAAGCTGGCGCATGATGACACCGATATGGCCAGTGTGCGGTCTCCGTTATCGG 13751
QY 4155 CGTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCGCTTCCAGC 4214
Db 13750 GGAAGAGTGGCTGATCTCAGCCACCGCGAAATGACATCAAAACGCCATTAACCTGAT 13691
QY 4215 GTTC--GGCAGCAGACGACGGGCTTCATCTGCAATGG---TTGTGCTTACCAGACCGG 4268
Db 13690 GTTCTGGGAATATAATGTCAGGCTCCCTTATACAGCCAGTCTGCAGGTGATACAG 13631
QY 4269 AGATATTGACATATATGCTTGTAGCAACTGATAGCTGCTGCTGTCACACTGT 4328
Db 13630 TAGAAATTTACAGAACTTTTATCAGTTTAGTAAGTATAGAGGCTGAAATCCAGATGAAG 13571
QY 4329 AATACGCTGCTTCATAGCACACCTCTTTTGGACATCTTCTGTTCTGTGATGCGATGATT 4388
Db 13570 CCGAACGACTGTAAGAGAAAGTATAAGAGTTGTGAAATGTTCTTGTGCGATGATT 13511
QY 4389 TTCAGGACTATGACACTAGCGTATATGAATAGTAGATGTTTATTTTGTGTCACAAAA 4448
Db 13510 TTCAGGACTATGACACTAGCGTATATGAATAGTAGATGTTTATTTTGTGTCACAAAA 13451
QY 4449 AAGAGGCTCCGACTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTTGAGACAA 4508
Db 13450 AAGAGGCTCCGACTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTTGAGACAA 13391
QY 4509 TAGCGAGTAGCGTGATACACGATTCGTTTGAGAGAACATTTGGAAGGCTGTCGGTC 4568
Db 13390 TAGCGAGTAGCGTGATACACGATTCGTTTGAGAGAACATTTGGAAGGCTGTCGGTC 13331
QY 4569 GACTAAGTTGGCAGCATCACCAGAACATTTTGGAGGCTGTCGGTGCAGTACAGTCA 4628
Db 13330 GACTAAGTTGGCAGCATCACCAGAACATTTTGGAGGCTGTCGGTGCAGTACAGTCA 13271
QY 4629 CTAATACCATTAAGTAGTATGATCATAGTACGATGATGTTGTTTACAGTATTAT 4688
Db 13270 CTAATACCATTAAGTAGTATGATCATAGTACGATGATGTTGTTTACAGTATTAT 13211
QY 4689 GTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTATATCATTTTACGTT 4748
Db 13210 GTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTATATCATTTTACGTT 13151
QY 4749 TCTGTTTACGTTTTTGTACAAAGTTGGCATTATAAAAGCATTTGCTCATCAATTTGT 4808
Db 13150 TCTGTTTACGTTTTTGTACAAAGTTGGCATTATAAAAGCATTTGCTCATCAATTTGT 13091
QY 4809 TGCACCAACAGGTCATCATGTCACAAATTAATCATTTTGGGCGCCGAG 4861
Db 13090 TGCACCAACAGGTCATCATGTCACAAATTAATCATTTTGGGCGCCGAG 13038

RESULT 8

US-10-151-690-21

; Sequence 21, Application US/10151690

; Publication No. US2003012455A1

; GENERAL INFORMATION:

; APPLICANT: BRASCH, MICHAEL A.

; APPLICANT: CHEO, DAVID

; APPLICANT: LI, XIAO

; APPLICANT: ESPOSITO, DOMINIC

; APPLICANT: BYRD, DEVON R.N.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI

FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 4470
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pDONR201
FEATURE:
NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attP1
FEATURE:
NAME/KEY: gene
LOCATION: (656)..(961)
OTHER INFORMATION: ccdB
FEATURE:
NAME/KEY: gene
LOCATION: (1099)..(1184)
OTHER INFORMATION: ccdA
FEATURE:
NAME/KEY: gene
LOCATION: (1303)..(1962)
OTHER INFORMATION: Cmr
FEATURE:
NAME/KEY: gene
LOCATION: (2210)..(2442)
OTHER INFORMATION: attP2
FEATURE:
NAME/KEY: gene
LOCATION: (2565)..(3374)
OTHER INFORMATION: Kmr
FEATURE:
NAME/KEY: gene
LOCATION: (3495)..(4134)
OTHER INFORMATION: Ori
US-10-151-690-21

Query Match 24.5%; Score 1193; DB 15; Length 4470;
Best Local Similarity 100.0%; Pred. No. 2.6e-188;
Matches 1193; Conservative 0; Mismatches C; Indels 0; Gaps 0;

QY 1 CGGGCCCCCAATAATGATTTTATTTTGGCTGATAGTGACCTGTTTGCACAAATTTGA 60
Db 21 CGGGCCCCCAATAATGATTTTATTTTGGCTGATAGTGACCTGTTTGCACAAATTTGA 80
QY 61 TGAGCAATGCTTTTTTATTAATGCCAACTTTGTACAAAAAAGCTGAAACGAGAAACGTAAA 120
Db 81 TGAGCAATGCTTTTTTATTAATGCCAACTTTGTACAAAAAAGCTGAAACGAGAAACGTAAA 140
QY 121 TGNATAAATATCAATATATTAATTAATTTAGATTTTGGCAAAAAACAGACTACATAATCTG 180
Db 141 TGNATAAATATCAATATATTAATTAATTTAGATTTTGGCAAAAAACAGACTACATAATCTG 200
QY 181 TAAACACACATATATCCAGTCACTATGAATCACTACTTATAGTGGTATTAGTGACCTGTA 240
Db 201 TAAACACACATATATCCAGTCACTATGAATCACTACTTATAGTGGTATTAGTGACCTGTA 260
QY 241 GTGACCGCAGCAGCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCGACAG 300
Db 261 GTGACCGCAGCAGCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCGACAG 320
QY 301 CCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCA 360
Db 321 CCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCA 380

Qy	361	ATGCCGTTATTAATCATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTGG	420
Db	381	ATGCCGTTATTAATCATAAAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTGG	440
Qy	421	ACAAATATAAAACATCTACCTATTTCATATACGCTAGTGTCTAGTCTCGAAATCATCTG	480
Db	441	ACAAATATAAAACATCTACCTATTTCATATACGCTAGTGTCTAGTCTCGAAATCATCTG	500
Qy	481	CATCAAGAACAAATTCACAACTCTTATCTTTCTCTTACAAGTCGTTCCGGTTCATCTG	540
Db	501	CATCAAGAACAAATTCACAACTCTTATCTTTCTCTTACAAGTCGTTCCGGTTCATCTG	560
Qy	541	GATTTTCAGCGCTCTATATCTTCTAABACGTCATATAAGTTTCTGTAAATTTCTACTGTATCGA	600
Db	561	GATTTTCAGCGCTCTATATCTTCTAABACGTCATATAAGTTTCTGTAAATTTCTACTGTATCGA	620
Qy	601	CCTGCAGACTGGCTGTGTATAGAAGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTA	660
Db	621	CCTGCAGACTGGCTGTGTATAGAAGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTA	680
Qy	661	ATGCGGTTTTGTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAAACG	720
Db	681	ATGCGGTTTTGTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAAACG	740
Qy	721	GAGACCGGCACATCGGCCATATCGGTGGTCATCATCGCCAGCTTTTCATCCCGATATGC	780
Db	741	GAGACCGGCACATCGGCCATATCGGTGGTCATCATCGCCAGCTTTTCATCCCGATATGC	800
Qy	781	ACCACCGGGTAAAGTTTCACGGGAGACTTATCTGACAGCAGAGCTGCACTGGCCAGGGGG	840
Db	801	ACCACCGGGTAAAGTTTCACGGGAGACTTATCTGACAGCAGAGCTGCACTGGCCAGGGGG	860
Qy	841	ATCACCATCGTCCCGCGGGGTGTCAATATATCACTGTATCCACAAACAGACGA	900
Db	861	ATCACCATCGTCCCGCGGGGTGTCAATATATCACTGTATCCACAAACAGACGA	920
Qy	901	TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTCACCAAGTCCCTGTTCTC	960
Db	921	TAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTCACCAAGTCCCTGTTCTC	980
Qy	961	GTACAGAAAAGAGCGGTTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCCTGATT	1020
Db	981	GTACAGAAAAGAGCGGTTTCATTTCAATAAAACCGGGCGACCTCAGCCATCCCTTCCTGATT	1040
Qy	1021	TTCCGCTTTCAGGCTTCGGCAGCAGACGGGCTTCATTCGATAGTGTGTGTGCTTAC	1080
Db	1041	TTCCGCTTTCAGGCTTCGGCAGCAGACGGGCTTCATTCGATAGTGTGTGTGCTTAC	1100
Qy	1081	CAGACCGGAGATATTGACATCATATATGSCCTTTGAGCAACTGATAGCTGTGCTGTCAACT	1140
Db	1101	CAGACCGGAGATATTGACATCATATATGSCCTTTGAGCAACTGATAGCTGTGCTGTCAACT	1160
Qy	1141	GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTACATACTTCGGGTA	1193
Db	1161	GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTACATACTTCGGGTA	1213

RESULT 9

US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US20030219902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; FILE REFERENCE: WSUR-1-20291
; CURRENT APPLICATION NUMBER: US/10/357,268
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2

QY 901 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTCACCAAGTCCCTGTTCTC 960
Db 4664 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTCACCAAGTCCCTGTTCTC 4605
QY 961 GTACGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 4604 GTACGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 4545
QY 1021 TTCCGCTTTCCAGCGTTCCGCGACGACGACGCGGCTTCATTCTGCATGGTTGTGCTTAC 1080
Db 4544 TTCCGCTTTCCAGCGTTCCGCGACGACGACGCGGCTTCATTCTGCATGGTTGTGCTTAC 4485
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAGCAACTGATAGCTGTCGCTGCAACT 1140
Db 4484 CAGACCGGAGATATTGACATCATATATGCTTGAGCAACTGATAGCTGTCGCTGCAACT 4425
QY 1141 GTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 1193
Db 4424 GTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 4372

RESULT 11
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match 24.4%; Score 1186.6; DB 15; Length 4428;
Best Local Similarity 99.7%; Pred. No. 3e-187;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAATAATAGATTTTATTTGCTGATGATGACCTGTTGCTGCAACAAATGA 60
Db 858 CGGGCCCCAATAATAGATTTTATTTGCTGATGATGACCTGTTGCTGCAACAAATGA 917
QY 61 TGAGCAATGCTTTTTTATAATGCGCAACTTTGTACAAAAAAGCTGAACGAGAAACGTAAAA 120
Db 918 TGAGCAATGCTTTTTTATAATGCGCAACTTTGTACAAAAAAGCTGATATCGAAAA 977
QY 121 TGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAAGACATAATATCTG 180
Db 978 TGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAAGACATAATATCTG 1037
QY 181 TAAACACAACTATCCAGTCACTATGATGAATCAACTACTAGATGCTATTAGTACCTGTA 240
Db 1038 TAAACACAACTATCCAGTCACTATGATGAATCAACTACTAGATGCTATTAGTACCTGTA 1097
QY 241 GTCGACCGACGCTTCCAAATGTTCTTCGGGTGATGCTGCGCAACTTAGTCGACCGACAG 300
Db 1098 GTCGACCGACGCTTCCAAATGTTCTTCGGGTGATGCTGCGCAACTTAGTCGACCGACAG 1157

QY 301 CTTTCCAAATGCTCTCTTCTCAAAACGGAATCGTGTATCGAGCTACTCGCTATTTGCTCTCA 360
Db 1158 CTTTCCAAATGCTCTCTTCTCAAAACGGAATCGTGTATCGAGCTACTCGCTATTTGCTCTCA 1217
QY 361 ATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 420
Db 1218 ATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 1277
QY 421 ACAAAATAAAAACATCTACCTATTATCATATAGCTAGTCTCATAGTCTCTGAAATCATCTG 480
Db 1278 ACAAAATAAAAACATCTACCTATTATCATATAGCTAGTCTCATAGTCTCTGAAATCATCTG 1337
QY 481 CATCAAGAAACAATTTCAACAACCTCTTATATCTTTCTTTACAGTCTGTCGGCTTCATCTG 540
Db 1338 CATCAAGAAACAATTTCAACAACCTCTTATATCTTTCTTTACAAGTCTGTCGGCTTCATCTG 1397
QY 541 GATTTTCAGCTCTATATCTACTTAAACGCTGATGATAAAGTTTCTGTAAATTTCTACTGCTATCGA 600
Db 1398 GATTTTCAGCTCTATATCTACTTAAACGCTGATGATAAAGTTTCTGTAAATTTCTACTGCTATCGA 1457
QY 601 CCTGCAGACCTGCTGTGTATAGGAGGAGCTGACATTTATATTTCCCGCAGAACATCAGGTTA 660
Db 1458 CCTGCAGACCTGCTGTGTATAGGAGGAGCTGACATTTATATTTCCCGCAGAACATCAGGTTA 1517
QY 661 ATGGCGTTTTCATGTCATTTTCGCGGTGCTGAGATGAGCCACTTCTTCCCGGATAACG 720
Db 1518 ATGGCGTTTTCATGTCATTTTCGCGGTGCTGAGATGAGCCACTTCTTCCCGGATAACG 1577
QY 721 GAGACCGGCACACTGCGCCATATCGGTGTCATCATGCGCAGCTTTCATCCCGGATATGC 780
Db 1578 GAGACCGGCACACTGCGCCATATCGGTGTCATCATGCGCAGCTTTCATCCCGGATATGC 1637
QY 781 ACCACCGGCTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGTCACCTGCGCAGGGGG 840
Db 1638 ACCACCGGCTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGTCACCTGCGCAGGGGG 1697
QY 841 ATCACCATCGTCGCGCGGCGGTGTCATTAATATCACTCTGTACATCCACAAACAGACGA 900
Db 1698 ATCACCATCGTCGCGCGGCGGTGTCATTAATATCACTCTGTACATCCACAAACAGACGA 1757
QY 901 TAACGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTC 960
Db 1758 TAACGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTC 1817
QY 961 GTCAGCAAAAGAGCGGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 1818 GTCAGCAAAAGAGCGGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1877
QY 1021 TTCCGCTTTCCAGCGTTCCGCGACGACGACGCGGCTTCATTTCTGATGTTGTGCTTAC 1080
Db 1878 TTCCGCTTTCCAGCGTTCCGCGACGACGACGCGGCTTCATTTCTGATGTTGTGCTTAC 1937
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTTCAGCAACTGATAGCTGTCGCTGCAACT 1140
Db 1938 CAGACCGGAGATATTGACATCATATATGCTTTCAGCAACTGATAGCTGTCGCTGCAACT 1997
QY 1141 GTCAGTAAATACGCTGCTTCATAGCACTCTTTTGGACATACCTTCGGGTA 1193
Db 1998 GTCAGTAAATACGCTGCTTCATAGCACTCTTTTGGACATACCTTCGGGTA 2050

RESULT 12
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001

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; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match      24.4%; Score 1186.6; DB 15; Length 4627;
Best Local Similarity 99.7%; Pred. No. 3e-187;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTCGTTGCAACAAATTGA 60
Db 9 CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTCGTTGCAACAAATTGA 68
QY 61 TGAGCAATGCTTTTATAATGCCAATTTGTACAAAAAGCTGCAACGAGAAACGTAAAA 120
Db 69 TGAGCAATGCTTTTATAATGCCAATTTGTACAAAAAGCTGATATCGAAACGTAAAA 128
QY 121 TGATATAAATATCAATATATAATTTAGATTTTGATATAAATAAAGACAGATACATACTG 180
Db 129 TGATATAAATATCAATATATAATTTAGATTTTGATATAAATAAAGACAGATACATACTG 188
QY 181 TAAACACACACATATCCAGTCATCTATGAATCAACTTCTAGATGGTATTAGTCACTGTA 240
Db 189 TAAACACACACATATCCAGTCATCTATGAATCAACTTCTAGATGGTATTAGTCACTGTA 248
QY 241 GTCGACCGACAGCCTTCCAAATGTTCTTGGGGTATGCTGCCAACTTAGTCGACCGACAG 300
Db 249 GTCGACCGACAGCCTTCCAAATGTTCTTGGGGTATGCTGCCAACTTAGTCGACCGACAG 308
QY 301 CCTTCCAAATGTTCTTCCAAAGGATCGTCTATCCAGCTTACCTGCTATTTGCTCTCA 360
Db 309 CCTTCCAAATGTTCTTCCAAAGGATCGTCTATCCAGCTTACCTGCTATTTGCTCTCA 368
QY 361 ATGCCGATTAATAATCAATAAAGAAATGAAGAAAGAGGTCGAGCCTCTTTTCTGTG 420
Db 369 ATGCCGATTAATAATCAATAAAGAAATGAAGAAAGAGGTCGAGCCTCTTTTCTGTG 428
QY 421 ACAAATATAAACATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAATCATCTG 480
Db 429 ACAAATATAAACATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAATCATCTG 488
QY 481 CATCAAGAACAAATTCACAACTCTATCTCTTCTTACAGTCTGTCGGCTTCACTG 540
Db 489 CATCAAGAACAAATTCACAACTCTATCTCTTCTTACAGTCTGTCGGCTTCACTG 548
QY 541 GATTTTCAGCCTCTATPACTTACTATAACGTATATAAGTTTCTGTAAATTTCTACTGTATCA 600
Db 549 GATTTTCAGCCTCTATPACTTACTATAACGTATATAAGTTTCTGTAAATTTCTACTGTATCA 608
QY 601 CTGCGAGACTGGTGTATAGGAGCCTGCATTTATATCCCGAACATCATCAGTTTA 660
Db 609 CTGCGAGACTGGTGTATAGGAGCCTGCATTTATATCCCGAACATCATCAGTTTA 668
QY 661 ATGGCTTTTGTATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATAAG 720
Db 669 ATGGCTTTTGTATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATAAG 728
QY 721 GAGACCGGACACTGGCCATATCGGTGGTCAATCATCGCCAGCTTTTCATCCCGATATGC 780
Db 729 GAGACCGGACACTGGCCATATCGGTGGTCAATCATCGCCAGCTTTTCATCCCGATATGC 788
QY 781 ACCACGGGTAAAGTTTACGGGAGACTTTATCTGACGACGAGACGTGCATGCGCCAGGGG 840
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Db 789 ACCACGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGG 848
QY 841 ATCACCATCGTCGCCCGGGCGTGTCAATAATATCACTCTGTATACATCCACAAAACAGACGA 900
Db 849 ATCACCATCGTCGCCCGGGCGTGTCAATAATATCACTCTGTATACATCCACAAAACAGACGA 908
QY 901 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTACACAGTCCCTGTCTC 960
Db 909 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTTACACAGTCCCTGTCTC 968
QY 961 GTCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGCGACTAGCCATCCCTTCTGATTT 1020
Db 969 GTCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGCGACTAGCCATCCCTTCTGATTT 1028
QY 1021 TTCCGCTTTCCAGCGTTCGGCACGACGACGCGGGCTTCATTTCTGCATGGTTGTGCTTAC 1080
Db 1029 TTCCGCTTTCCAGCGTTCGGCACGACGACGCGGGCTTCATTTCTGCATGGTTGTGCTTAC 1088
QY 1081 CAGACCGGAGATTTGACATCATATATATGCTTGAGCAACTGATAGCTGCTGCTCAACT 1140
Db 1089 CAGACCGGAGATTTGACATCATATATGCTTGAGCAACTGATAGCTGCTGCTCAACT 1148
QY 1141 GTCACGTGTAATACGCTGCTTCATAGCACACCTCTTTTTCGACATCTTCGGGTA 1193
Db 1149 GTCACGTGTAATACGCTGCTTCATAGCACACCTCTTTTTCGACATCTTCGGGTA 1201

RESULT 13
US-10-151-690-64
; Sequence 64, Application US/10/151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match      24.4%; Score 1186.6; DB 15; Length 4627;
Best Local Similarity 99.7%; Pred. No. 3e-187;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTCGTTGCAACAAATTGA 60
Db 9 CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTCGTTGCAACAAATTGA 68
QY 61 TGAGCAATGCTTTTATAATGCCAATTTGTACAAAAAGCTGCAACGAGAAACGTAAAA 120
Db 69 TGAGCAATGCTTTTATAATGCCAATTTGTACAAAAAGCTGATATCGAAACGTAAAA 128
QY 121 TGATATAAATATCAATATATAATTTAGATTTTGATATAAATAAAGACAGATACATACTG 180
Db 129 TGATATAAATATCAATATATAATTTAGATTTTGATATAAATAAAGACAGATACATACTG 188
QY 181 TAAACACACATATCCAGTCATCTATGAATCAACTTCTAGATGGTATTAGTCACTGTA 240
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Db 189 TAAACACACATATCCAGTCACATATGAATCAACTCTTAGATGGTATTAGTACCTGTGA 248
QY 241 GTCGACGACGAGCTTCCAAATGTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAG 300
Db 249 GTCGACGACGAGCTTCCAAATGTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGAG 308
QY 301 CCTTCGAAATGTCTTCTGAAACGGAATCTGCTATCCAGCTTACTGCTATTGTCTTCA 360
Db 309 CCTTCGAAATGTCTTCTGAAACGGAATCTGCTATCCAGCTTACTGCTATTGTCTTCA 368
QY 361 ATGCGCTATTAAATCATATAAAGAAATAAGAAAGAGGTGCGAGCTCTTTTTTGTGTC 420
Db 369 ATGCGGTATTAAATCATATAAAGAAATAAGAAAGAGGTGCGAGCTCTTTTTTGTGTC 428
QY 421 ACAAATAAATAACATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAATATCTGT 480
Db 429 ACAAATAAATAACATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAATATCTGT 488
QY 481 CATCAAGAACAAATTCACAACTCTTATACCTTTCTCTTCAAGTCTGTTCCGCTTCACTG 540
Db 489 CATCAAGAACAAATTCACAACTCTTATACCTTTCTCTTCAAGTCTGTTCCGCTTCACTG 548
QY 541 GATTTTCAGCTCTATATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 549 GATTTTCAGCTCTATATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA 608
QY 601 CTTGCAGACTGGCTGTGTATAGGAGCCTGACATTTATATCCCGAAGACATCAGGTTA 660
Db 609 CTTGCAGACTGGCTGTGTATAGGAGCCTGACATTTATATCCCGAAGACATCAGGTTA 668
QY 661 ATGCGCTTTTGTATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATAACG 720
Db 669 ATGCGCTTTTGTATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATAACG 728
QY 721 GAGACCGGCACATCGGCCATATCGGTGTGTCATATCGCGCAGCTTTTCATCCCGGATATGC 780
Db 729 GAGACCGGCACATCGGCCATATCGGTGTGTCATATCGCGCAGCTTTTCATCCCGGATATGC 788
QY 781 ACCACCGGTAAAGTTTACCGGAGACTTTATCTGACAGCAGCTGTCAGCTGGCCAGGGG 840
Db 789 ACCACCGGTAAAGTTTACCGGAGACTTTATCTGACAGCAGCTGTCAGCTGGCCAGGGG 848
QY 841 ATCACCATCGCTCGCCCGCGGTGTCATTAATATATCACTCTGTATCATCCACAAACAGACGA 900
Db 849 ATCACCATCGCTCGCCCGCGGTGTCATTAATATATCACTCTGTATCATCCACAAACAGACGA 908
QY 901 TAAAGGCTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTTCAAGTCCCTGTCTC 960
Db 909 TAAAGGCTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTTCAAGTCCCTGTCTC 968
QY 961 GTCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 969 GTCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGATT 1028
QY 1021 TCCGCTTTCCAGCTTCGACGACGACGAGCGGGTTCATCTGATGCTGTGCTTAC 1080
Db 1029 TCCGCTTTCCAGCTTCGACGACGACGAGCGGGTTCATCTGATGCTGTGCTTAC 1088
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAAGCAGCTGATGCTGTGCTCAACT 1140
Db 1089 CAGACCGGAGATATTGACATCATATATGCTTGAAGCAGCTGATGCTGTGCTCAACT 1148
QY 1141 GTCAGCTTAATAGCTGCTTCATAGCACACCTCTTTTGTGATACATTTCCGGGTA 1193
Db 1149 GTCAGCTTAATAGCTGCTTCATAGCACACCTCTTTTGTGATACATTTCCGGGTA 1201
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RESULT 14

US-10-270-176-20/c

; Sequence 20, Application US/10270176

; Publication No. US20040033608A1

; GENERAL INFORMATION:

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; APPLICANT: Wanner, Barry
; APPLICANT: Halldmann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 4782
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-20
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Query Match 18.0%; Score 876.4; DB 13; Length 4782;
Best Local Similarity 71.6%; Pred. No. 1.1e-135;
Matches 1259; Conservative 0; Mismatches 441; Indels 58; Gaps 6;

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QY 1852 TAAGATGATATACGCCGCGTAAAGAGTTCCAACTTTCACCATATGAATAAGATCACTA 1911
Db 4299 TGAGAGCTTGTATCGGCACGTAAGAGGTTCCAACTTTCACCATATGAATAAGATCACTA 4240
QY 1912 CCGGGCGTATTTTGTAGTTATCGAGTTTTCAGAGAGCTTAAGGAAGCTAAATGGAGAAA 1971
Db 4239 CCGGGCGTATTTTGTAGTTATCGAGTTTTCAGAGAGCTTAAGGAAGCTAAATGGAGAAA 4180
QY 1972 AAAATCACTGGATATACCAACCTTGATATATATCCCAATGGCATCGTAAAGAAATTTTGAG 2031
Db 4179 AAAATCACTGGATATACCAACCTTGATATATATCCCAATGGCATCGTAAAGAAATTTTGAG 4120
QY 2032 GATTTTCAGTCTAGTGTCTCAATGTACTATACCAAGCCGTTTACCGGCTTTTATCCAGTCTT 2151
Db 4119 GATTTTCAGTCTAGTGTCTCAATGTACTATACCAAGCCGTTTACCGGCTTTTATCCAGTCTT 4060
QY 2092 TTTTAAAGACCGCTAAAGHAAATTAAGCAACAAGTTTATCCGGCTTTTATCCAGTCTT 2151
Db 4059 TTTTAAAGACCGCTAAAGHAAATTAAGCAACAAGTTTATCCGGCTTTTATCCAGTCTT 4000
QY 2152 GCCCGCTTCAATGCTCATCCGNAATTCCTATGCGAATGAAGACCGTGGTGGT 2211
Db 3999 GCCCGCTTCAATGCTCATCCGNAATTCCTATGCGAATGAAGACCGTGGTGGT 3940
QY 2212 ATATGGATAGTGTTCACCCCTTGTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 2271
Db 3939 ATATGGATAGTGTTCACCCCTTGTACACCGTTTCCATGAGCAAACTGAAACGTTTCA 3880
QY 2272 TGGCTCTGAGTGAATATACCAACGATTTCCGGAGTTTCTACATATATTCGCAAGAT 2331
Db 3879 TGGCTCTGAGTGAATATACCAACGATTTCCGGAGTTTCTACATATATTCGCAAGAT 3820
QY 2332 GTGGGCTGTACGTTGAACACCTGCTTATTCCTTAAGGGTTTATGAGAAATATGTT 2391
Db 3819 GTGGGCTGTACGTTGAACACCTGCTTATTCCTTAAGGGTTTATGAGAAATATGTT 3760
QY 2392 TTCTGCTCAGCAAACTCCCTGGGTGATTTTCACAGTTTGTATTAAGGTGCGCAATATG 2451
Db 3759 TTCTGCTCAGCAAACTCCCTGGGTGATTTTCACAGTTTGTATTAAGGTGCGCAATATG 3700
QY 2452 GACAACTTCTTCGCGCCCGCTTTTCCATGGGCAAAATATATACGAAAGGCGCAAGGTG 2511
Db 3699 GACAACTTCTTCGCGCCCGCTTTTCCATGGGCAAAATATATACGAAAGGCGCAAGGTG 3640
QY 2512 CTGATGCGCTGCGCATTTCAAGTTTCAATCATGCTGCTGATGCTTCCATGTCGCGCAGA 2571
Db 3639 CTGATGCGCTGCGCATTTCAAGTTTCAATCATGCTGCTGATGCTTCCATGTCGCGCAGA 3580
QY 2572 ATGCTTAATGAATTAACAACAGTACTCTGATGAGTGGCAGGGCGGCGGCTAATCGCGTGA 2631
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Db 3579 ATGCTTAATGATATACACAGTACTGCGATGAGTGGCGAGCGGGCGGTAAAT----- 3528
Qy 2632 TCGGGCTTACTAAAGCCAGATAACAGATGCGTATTTGGCGCTGATTTTGGGTATA 2691
Db 3527 -----TTTTTAAAGCAGTTATGCTGCTCACT 3499
Qy 2692 AGATATATATGATATGTCGGGCCCATATAGTAATCTAGCTGGTGTGATGAATATAA 2751
Db 3498 GATTAAGCATGGAATGTCAGACCAAGTTTACTCATATATCTTTAGATGATTTAAA 3439
Qy 2752 TATCAATGATATAAATACTATAGTAAATAAGATAATAATAATAATAATAATAATTTT 2811
Db 3438 ACTTCATTTTAAATTTGGCGCCGAGATCCGGCCACGATGCGTGGCGGTAGAGAT 3379
Qy 2812 ATGATTAATGTTTATATATAATAATAATCTATACCATPACPAATAATTTTATGTTAA 2871
Db 3378 CTGAAGATCAGCAGTCTCAACCTGTGTAGTAGTACGTACTAAGCTCTCATGTTTACGTTACT 3319
Qy 2872 AAGTTAATAATATTTTGTAGAAATTCCAATCTGCTGTGTAATTTATCAATAAACAAT 2931
Db 3318 AAGCTCTCATGTTTAAACGTAATAAGCTCTCATGTTTAAACGAACTAAACCCCTCATGGCTAA 3259
Qy 2932 ATTAATAAACAAGCTAAAGTAACAATAAATAATCAAACTAATAGAAACAGTAATCTAATGT 2991
Db 3258 CGTACTAAGCTCTCATGCTAAACGTACTAAGCTCTCATGTTTACGTACTAAGCTCTCAT 3199
Qy 2992 AACMAACNATAATCTAATGTAATATAAACAAGCGCAAGATCTATCATATTTATATAGTAT 3051
Db 3198 GTTTGAACAA-----TAAATTAATAATAAATCAGCAACTTAAATAGCCTCTAAGGTTTAA 3143
Qy 3052 TATTTTCAATCAACATCTTATTAATTTCTAAATAATACTTGTAGTTTATTAACCTCTA 3111
Db 3142 GTTTTAAAGAAA-----AAGAATATAAAGCTTTTAAAGCTTTTAAAGGTTTAA 3091
Qy 3112 AATGATTTGACTAATTAATTAATGAATTAGTCGAACATGAATTAACAAGGTAAACATGATA 3171
Db 3090 ACGGTTCTGACAAACAAGCCAGGATGTAAAGCACTGGAAGCCCTTAGAGCCTCTCAA 3031
Qy 3172 GATCATGCTATGTTGTTATCATTTGATCTTATCATTTGATTTGATTTGATTTGATTTG 3231
Db 3030 GCAAT-----TTGAGTGACACAGCAACACTTAACGGCTGACATGGGAATTAGCCATGGCA 2975
Qy 3232 GTTCGAATCATGAATGCTTGGATCCTCTAGAGAGCTGACGCTGGATGGCAATTAATGATT 3291
Db 2974 TCACAGTATCGTGTATGACAGGCGAGGATGGGACAAATTTGAA-ATCAATTAATGATT 2916
Qy 3292 TTATTTGACTGATAGTGACCTGTTGTTGCAACAAATTTGATTAAGCAATGCTTTCTTTATA 3351
Db 2915 TTATTTGACTGATAGTGACCTGTTGTTGCAACAAATTTGATTAAGCAATGCTTTTTTATA 2856
Qy 3352 ATGCCAATTTGTACAGAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATA 3411
Db 2855 ATGCCAATTTAGTATAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATA 2796
Qy 3412 TTAATTTAGATTTTGCATAAATAACAGACTACATAATCTGTAATAACACAAC--ATATCC 3469
Db 2795 TTAATTTAGATTTTGCATAAATAACAGACTACATAATCTGTAATAACACAACATATATGC 2736
Qy 3470 AGTCATATGAATCAACTACTTAGATGATTAAGTACCTGTAGTCGACTAAGTTGGCAG 3529
Db 2735 AGTCATATGAATCAACTACTTAGATGATTAAGTACCTGTAGTCGACTAAGTTGGCAG 2676
Qy 3530 CATCACCGGCGACTTTGGCCCAATAAATACCTGTGACGGAAGATCATCTGCAGAAAT 3589
Db 2675 GGTGATTTTGTCTTCTGTGGCTAATTTTTTGTATCAAAACCTGTGCACTCCAGAGAAG 2616
Qy 3590 AAATAAATCTCTGGTGTCC 3607
Db 2615 CACAAGCCTCGCAATCC 2598
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RESULT 15

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US-10-270-176-19/c
; Sequence 19, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanney, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 6742
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-19
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Query Match 18.0%; Score 876.4; DB 13; Length 6742;
Best Local Similarity 71.6%; Pred. No. 1.3e-135;
Matches 1259; Conservative 0; Mismatches 441; Indels 58; Gaps 6;

Qy 1852 TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACCATATGAAATAGATCACTA 1911
Db 6259 TGAGAGCTTGATCGGCACGTAAAGAGTTCCAACTTTCCACCATATGAAATAGATCACTA 6200
Qy 1912 CCGGGCGTATTTTGGATTTATCGAGATTTTCAGGAGCTAAGAAAGCTAAATGGAGAA 1971
Db 6199 CCGGGCGTATTTTGGATTTATCGAGATTTTCAGGAGCTAAGAAAGCTAAATGGAGAA 6140
Qy 1972 AAAATCAGTGGATATACCCGCTTGATATATCCCATGCGATCGTAAAGACATTTTGAG 2031
Db 6139 AAAATCAGTGGATATACCCGCTTGATATATCCCATGCGATCGTAAAGACATTTTGAG 6080
Qy 2032 GCATTTTCAGTCAGTTGCTCAATGTAATCTAATAACAGACCGTTTCAGCTGGATATTACGGCC 2091
Db 6079 GCATTTTCAGTCAGTTGCTCAATGTAATCTAATAACAGACCGTTTCAGCTGGATATTACGGCC 6020
Qy 2092 TTTTAAAGACCGTAAAGAAAATAAGACAAGTTTATCCGGCTTTTATTCACATCTTT 2151
Db 6019 TTTTAAAGACCGTAAAGAAAATAAGACAAGTTTATCCGGCTTTTATTCACATCTTT 5960
Qy 2152 GCCGCGCTGATGAATGCTCATCCGGAATTCGATGCGAATGAAGACGCTGAGCTGGTG 2211
Db 5959 GCCGCGCTGATGAATGCTCATCCGGAATTCGATGCGAATGAAGACGCTGAGCTGGTG 5900
Qy 2212 ATATGGATAGTTTTCACCCCTGTTACACCGTTTTCATGAGCAAACTGAAACGTTTTC 2271
Db 5899 ATATGGATAGTTTTCACCCCTGTTACACCGTTTTCATGAGCAAACTGAAACGTTTTC 5840
Qy 2272 TCCTCTGGAGTGAATACCAAGAGATTTCCGGCAGTTTCTACATATATTTCGCAAGAT 2331
Db 5839 TCCTCTGGAGTGAATACCAAGAGATTTCCGGCAGTTTCTACATATATTTCGCAAGAT 5780
Qy 2332 GTGGCGTTTACCGTGAACACCTGGCTATTTCCCTAAAGGGTTTATTCAGATATGTTT 2391
Db 5779 GTGGCGTTTACCGTGAACACCTGGCTATTTCCCTAAAGGGTTTATTCAGATATGTTT 5720
Qy 2392 TTCCTCTCAGCCAAATCCCTGGGTGAGTTTTCACCGAGTTTTCATTTAAACGTTGCAATATG 2451
Db 5719 TTCCTCTCAGCCAAATCCCTGGGTGAGTTTTCACCGAGTTTTCATTTAAACGTTGCAATATG 5660
Qy 2452 GACAACTTCTTCGCCCGCTTTTTCACATGGGCAATATATACGCAAGCGCAAGGTG 2511
Db 5659 GACAACTTCTTCGCCCGCTTTTTCACATGGGCAATATATATACGCAAGCGCAAGGTG 5600
Qy 2512 CTGATCGCGTGGCGATTTCAGGTTTCATCATCGCGTCTGTCATGCTTCCATGTCGCGAGA 2571
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Db 5599 CTGATGCGCTGGCGATTTCAGGTTTCATCATGCCGTCTGTGATGGCTTCCATGTGCGGAGA 5540
QY 2572 ATGCTTTAAATCAATTAACAAGTACTGCGATGAGTGGCAGGGCGGGGTAATCGCTGGA 2631
Db 5539 ATGCTTTAAATCAATTAACAAGTACTGCGATGAGTGGCAGGGCGGGGTAAT 5488
QY 2632 TCCGGCTTACTAAAGCCAGATAACAGTATGCCGTAATTTGGCGCTGATTTTCCGGTATA 2691
Db 5487 -----TTTTTAAGGCAGTTATTGGTGCTCACT 5459
QY 2692 AGAATATATATGATGTCGGGCCCATATAGTAATCTTAGCTGGTTGATCAATTA 2751
Db 5458 GATTAAGCATTTGGTAATCTGTACAGCCAAAGTTTACTCATATATATCTTTAGATTGATTAA 5399
QY 2752 TATCAATGATAAAATACTATAGTAAATAAATAAGAAATAAATAAATAAATAAATAAATAA 2811
Db 5398 ACTTCATTTTAAATTTTGGGGCGCAAGATCCGGCCACGATGGTCCGGCGTAGAGGAT 5339
QY 2812 ATGATTAATAGTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2871
Db 5338 CTGAAGATCAGCATTCACAGCTGTGTAGTAGTACTAAGCTCTCATGTGTTTCACTACT 5279
QY 2872 AAGTTAATAAATAATTTTGTAGAAATCCAAATCTGCTTGTAAATTTATCAATAACAAAT 2931
Db 5278 AAGCTCTCATGTTTAAAGTACTAAGCTCTCATGTGTTTCACTACTAAGCTCTCAT 5219
QY 2932 ATTAAATAACAAGCTAAAGTAACAATAATAATCAAACTAATAGAAACAGTAATCTAATGT 2991
Db 5218 CGTACTAAGCTCTCATGGCTAAAGTACTAAGCTCTCATGTGTTTCACTACTAAGCTCTCAT 5159
QY 2992 AACAAACATTAATCTAATGCTAATAATAACAAGGGCAAGATCTATCATTTTATATAGTAT 3051
Db 5158 GTTTGAACAA-----TAAATTAATAATAAATCAGCAACTTAAATAGCCTCTAAGGTTTTAA 5103
QY 3052 TATTTTCAATCAACATTTCTTAAATTTCTAATAATAATACTTTAGTTTAACTTCTA 3111
Db 5102 GTTTTATAAGAAAA-----AAGAATAATAATAGGCTTTTAAAGCTTTTAAAGTTTA 5051
QY 3112 AATGGATGTACTAATAATAATGAATTAAGTGAACATGAATAAACAAGGTAAACATGATA 3171
Db 5050 ACGGTTGTGACAAACAAGCCAGGATGTAACGCACATGAGAAGCCCTTAGAGCCTCTCAA 4991
QY 3172 GATCATGCTCATTTGGTTATCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3231
Db 4990 GCAATT-----TTGAGTGACACAGAACACTTAACGGCTGACATGGGAATTAGCCATGGCA 4935
QY 3232 GTTCGAATCGATAAGCTTGATCTCTAGAGAGCTGCAGCTGGATGGCAAAATAATGATT 3291
Db 4934 TCACAGTATCGTGATGACAGAGCAGGAGTGGACAAAATTGAA-ATCAATAATGATT 4876
QY 3292 TTATTTTGACGTAGTAGCTGTTGCTGGACAAATTTGATTAAGCAATGCTTTCTTATA 3351
Db 4875 TTATTTTGACGTAGTAGCTGTTGCTGGACAAATTTGATTAAGCAATGCTTTCTTATA 4816
QY 3352 ATGCCAACTTTGTACAAAGAGCTGAACGAGAAACGTAATAATGATATAAATAATCAATATA 3411
Db 4815 ATGCCAACTTTAGTATAAATAAGCTGAACGAGAAACGTAATAATGATATAAATAATCAATATA 4756
QY 3412 TTAATTTAGATTTTGCATAAATAAACAAGACTACATAATCTGTAAACACAAC-ATATCC 3469
Db 4755 TTAATTTAGATTTTGCATAAATAAACAAGACTACATAATCTGTAAACACAACATATATGC 4696
QY 3470 AGTCACTATGATCAACTACTAGTATGATGTTAGTACCTGTAGTGCAGTAAGTTGGCAG 3529
Db 4695 AGTCACTATGATCAACTACTAGTATGATGTTAGTACCTGTAGTGCAGTAAGTTAGCGCAA 4636
QY 3530 CATCACCGGCGCACTTTGGCGCGCAATAAATACCTGTGACGGAAGATCACTTCGCAGAA 3589
Db 4635 GGTGATTTTGTCTTCTTGGCTTAATTTTGTGTCATCAACCTGTGCTGCTCCAGAGAAG 4576
QY 3590 AATAAATCTCTGTGTCC 3607
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7540.15 Seconds

(without alignments)

19251.609 Million cell updates/sec

Title: US-10-055-001B-13_COPY_13040_17900

Perfect score: 4861

Sequence: 1 cgggccccaaaataatgattt.....atcattatttggggcccgag 4861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_estc.*

10: gb_estc2.*

11: gb_estc3.*

12: gb_estc4.*

13: gb_est5.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_man.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	732	15.1	782	28	BH242215
C 2	712	14.6	939	28	CC219264
C 3	697.4	14.3	783	28	BZ069663
C 4	697.4	14.3	812	28	BZ071317

C	5	697.4	14.3	848	28	BZ067942
C	6	697.4	14.3	903	28	BZ569330
C	7	697.2	14.3	789	28	BZ086476
C	8	696.4	14.3	799	28	BZ070237
C	9	695.4	14.3	794	28	BZ070076
C	10	695.2	14.3	719	28	BZ057486
C	11	695.2	14.3	785	28	BZ077741
C	12	694.8	14.3	792	28	BZ070235
C	13	694.8	14.3	797	28	BZ069987
C	14	693.8	14.3	797	28	BZ070648
C	15	693.6	14.3	725	28	BH960653
C	16	693.4	14.3	762	28	BZ077280
C	17	693	14.3	811	28	BZ070474
C	18	692.8	14.3	799	28	BZ085150
C	19	692.6	14.2	885	28	BZ084529
C	20	691.6	14.2	892	28	BZ083912
C	21	691.2	14.2	746	28	BZ064939
C	22	690	14.2	790	28	BZ070298
C	23	689.6	14.2	751	28	BZ069698
C	24	688.2	14.2	794	28	BZ243026
C	25	687.4	14.1	800	28	BZ069387
C	26	687	14.1	930	28	BZ056540
C	27	686	14.1	800	28	BZ070618
C	28	685.8	14.1	743	28	BZ042047
C	29	683.6	14.1	831	28	BH239118
C	30	682.2	14.0	792	28	BZ069550
C	31	681.2	14.0	780	28	BZ085923
C	32	681.2	14.0	785	28	BZ086527
C	33	681.2	14.0	799	28	BZ069940
C	34	681.2	14.0	799	28	BZ070540
C	35	680.2	14.0	689	28	BH936398
C	36	679.2	14.0	766	28	BZ085715
C	37	679.2	14.0	767	28	BH920449
C	38	678.6	14.0	775	28	BZ063552
C	39	678.6	14.0	876	28	BZ056481
C	40	678	13.9	914	28	BZ056494
C	41	677.6	13.9	863	28	BZ076353
C	42	676.4	13.9	735	28	BH951002
C	43	674.4	13.9	780	28	BZ041037
C	44	674.4	13.9	842	28	BZ038229
C	45	674.2	13.9	741	28	BZ071068

ALIGNMENTS

RESULT 1
BH242215/c
LOCUS
DEFINITION
ATZFD43TF ATZF Arabidopsis thaliana genomic clone ATZFD43, genomic survey sequence.
ACCESSION
BH242215
VERSION
BH242215.1
GI:16917233
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 782)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V., Feldhym, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T20G10
Unpublished (2001)
COMMENT
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1370. Caution: the DNA in this BAC may be from some non-Arabidopsis source
Seq primer: TP

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Class: sheared ends.
Location/Qualifiers
1. .782
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="ATZFD43"
/notes="Vector: pBAC2.1; Site 1: BstXI; 2-3 kb sheared BAC
DNA inserted into pBAC2.1 using BstXI linkers"

ORIGIN
Query Match 15.1%; Score 732; DB 28; Length 782;
Best Local Similarity 98.4%; Pred. No. 8.6e-122;
Matches 760; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1852 TAAGTATATACGGCGGTAAAGAGTTCCAACTTTCCACCATATGAATAAGATCACTA 1911
DB 775 TGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 716
QY 1912 CCGGCGGTATTTTGAAGTATCGAGATTTTCAGAGCTAAGGAAGCTAAATAGGAGAA 1971
DB 715 CCGGCGGTATTTTGAAGTATCGAGATTTTCAGAGCTAAGGAAGCTAAATAGGAGAA 656
QY 1972 AAATCATCTGATATACACCGTTGATATATCCCAATGGCATCTGAAGACATTTTGAG 2031
DB 655 AAATCATCTGATATACACCGTTGATATATCCCAATGGCATCTGAAGACATTTTGAG 596
QY 2032 GCATTTCACTGAGTTGCTCAATGTACCTATATAACAGACCGTTTCAGCTGGATATACCGCC 2091
DB 595 GCATTTCACTGAGTTGCTCAATGTACCTATATAACAGACCGTTTCAGCTGGATATACCGCC 536
QY 2092 TTTTAAAGACCGTAAAGAAAAAATGAACAAAGTTTATCCGGCTTTATTCACATCTT 2151
DB 535 TTTTAAAGACCGTAAAGAAAAAATGAACAAAGTTTATCCGGCTTTATTCACATCTT 476
QY 2152 GCGGCGTGTGAATGCTCATCCGGAATTCGGTATGGCAATGAAGAGCGTGAGCTGTG 2211
DB 475 GCGGCGTGTGAATGCTCATCCGGAATTCGGTATGGCAATGAAGAGCGTGAGCTGTG 416
QY 2212 ATATGGGATAGTTTCACTTGTATACACCGTTTTCATAGCAAACTGAAACGTTTCA 2271
DB 415 ATATGGGATAGTTTCACTTGTATACACCGTTTTCATAGCAAACTGAAACGTTTCA 356
QY 2272 TCGCTCTGGAGTGAATACCAAGCAATTTCCGGAGTTTCTACATATATTCGCAAGAT 2331
DB 355 TCGCTCTGGAGTGAATACCAAGCAATTTCCGGAGTTTCTACATATATTCGCAAGAT 296
QY 2332 GTGGCGTGTAGCGTGAAGAACTGGCCCTATTTCCCTAAAGGTTTATTTGAGAAATATGTT 2391
DB 295 GTGGCGTGTAGCGTGAAGAACTGGCCCTATTTCCCTAAAGGTTTATTTGAGAAATATGTT 236
QY 2392 TTCTGCTCAGCCAAATCCCTGGGTGAGTTTCAACAGTTTGAATTTAAACGTTGCCAAATG 2451
DB 235 TTCTGCTCAGCCAAATCCCTGGGTGAGTTTCAACAGTTTGAATTTAAACGTTGCCAAATG 176
QY 2452 GACAACTTCTTCCGCGCGTTTTCACCATGGCAATATATACCAAGGCGCAAGGTG 2511
DB 175 GACAACTTCTTCCGCGCGTTTTCACCATGGCAATATATACCAAGGCGCAAGGTG 116
QY 2512 CTGATGCGCTGGCGATTCAGGTTTCATCATGCGCTGTGTGAGGCTT-CCATGTCGGCAG 2570
DB 115 CTGATGCGCTGGCGATTCAGGTTTCATCATGCGCTGTGTGAGGCTTCCATGTCGGCAG 56
QY 2571 AATGCTT-AATGAATTAACAGTACTGCGATGAGTGGCAGGCGGGGGGTA 2621
DB 55 AATGCTTAAATGAATTAACAGTACTGCGATGAGTGGCAGGCGGGGGGTA 4

RESULT 2
CC219264/c 939 bp DNA linear GSS 12-MAY-2003
LOCUS
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DEFINITION

CH261-114B11_Sp6.1 CH261 Gallus gallus genomic clone CH261-114B11,

genomic survey sequence.

ACCESSION

CC219264

VERSION

CC219264.1 GI:30541330

KEYWORDS

GSS.

SOURCE

Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 939)

AUTHORS

Kremitzki, C., Higginsbotham, J., Wylie, K., Carter, J., McPherson, J.,

Warren, W., Graves, T., Mardis, E. and Wilson, R.

TITLE

Gallus gallus BAC End Reads

JOURNAL

Unpublished (2003)

COMMENT

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@wustl.edu

Insert Length: 182000 Std Error: 0.00

Seq primer: Sp6 ATTAGGTGACACTATAG

Class: BAC ends

High quality sequence start: 36

High quality sequence stop: 800.

Location/Qualifiers

1. .939

/organism="Gallus gallus"

/mol_type="genomic DNA"

/strain="Red Jungle Fowl"

/db_xref="taxon:9031"

/clone="CH261-114B11"

/sex="female"

/cell_line="UCD001, inbred 256"

/clone_lib="CH261"

/notes="Vector: pBAC2.1; Site 1: EcoRI; Site 2: EcoRI;

CH261 Female Chicken library - for library and clone

ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 14.6%; Score 712; DB 28; Length 939;

Best Local Similarity 97.7%; Pred. No. 3.2e-118;

Matches 733; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

QY 1876 GGTTCACAACTTCCACCAATGAATAA--GATCACTACCGGGGATATTTTTCAGTTAT 1933

DB 918 GTTCCCAATTTCCCTTATGAATAAAGATCACTTCCCGGGGATATTTTTCAGTTAT 859

QY 1934 CGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCAACG 1993

DB 858 CGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCAACG 799

QY 1994 TTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCTGCTCAAT 2053

DB 798 TTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCTGCTCAAT 739

QY 2054 GTACCTATAACCAACGACCTTCAGCTGGATATACGCGCTTTTAAAGACCGTAAGAAAA 2113

DB 738 GTACCTATAACCAACGACCTTCAGCTGGATATACGCGCTTTTAAAGACCGTAAGAAAA 679

QY 2114 ATAAGCAACAGTTTATCCGCGCTTTATTCACATTTTCCCGCTGATGATGCTCATC 2173

DB 678 ATAAGCAACAGTTTATCCGCGCTTTATTCACATTTTCCCGCTGATGATGCTCATC 619

QY 2174 CGGAATTCGCTATGGCAATGAAGACGCTGAGCTGGTGATATGGGATAGTGTTCACCTT 2233

DB 618 CGGAGTTCCGCTATGGCAATGAAGACGCTGAGCTGGTGATATGGGATAGTGTTCACCTT 559

QY 2234 GTTACACCGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACG 2293

DB 558 GTTACACCGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACG 499

QY 2294 ACGATTTCCGCGAGTTTTCACATATATTCGAAGATGTCGCGTGTGTACCGTGAACACC 2353

Db 498 ACAGTTCCGGCAGTTCTACACATATATTCGCAAGATGGCGGTACGGTGAAACC 439
 QY 2354 TGGCTTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAAATCCCTGGG 2413
 Db 438 TGGCTTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAAATCCCTGGG 379
 QY 2414 TGGTTTCCACAGTTTGTATTAAGCGTGGCCAAATATGGAACACTTTTCGCCCGCGTTT 2473
 Db 378 TGAGTTTCCACAGTTTGTATTAAGCGTGGCCAAATATGGAACACTTTTCGCCCGCGTTT 319
 QY 2474 TCACCAATGGGCAATATATTACCCAGGCGCAAGGTGCTGTGATGCGCGTCCGCGATTTCAGG 2533
 Db 318 TCACCAATGGGCAATATATTACGACAGGCGCAAGGTGCTGTGATGCGCGTCCGCGATTTCAGG 259
 QY 2534 TTCAATATGCGCGTCTGTGATGCGTTTCCATGTCGGCAGATGCTTAATGAATTAACAAGT 2593
 Db 258 TTCAATATGCGCGTCTGTGATGCGTTTCCATGTCGGCAGATGCTTAATGAATTAACAAGT 199
 QY 2594 ACTGCGATGAGTGGCAGGGCGGGCGGTAAT 2623
 Db 198 ACTGCGATGAGTGGCAGGGCGGGCGGTAAT 169

RESULT 3

BZ069663/c 783 bp DNA linear GSS 10-OCT-2002
 LOCUS 1jt36e08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.

ACCESSION BZ069663

VERSION BZ069663.1 GI:23685962

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 783)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1jt36 row: e column: 08

Seq primer: -21UPPOT forward

Class: shotgun

High quality sequence start: 8

High quality sequence stop: 551.

FEATURES

source Location/Qualifiers

1. .783

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/note=Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T01000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

ORIGIN

Query Match 14.3%; Score 697.4; DB 28; Length 783;
 Best Local Similarity 97.8%; Pred.No. 1.5e-115;
 Matches 707; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGGTATTTTTCAGTATTCGAGATTTCAGGAGCTAAGGAAGCTAAA 1962

Db 752 AGCTTATCATCGATAAGCTTTTAATGAGTATTCGAGATTTCAGGAGCTAAGGAAGCTAAA 693

QY 1963 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAGAA 2022
 Db 692 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAGAA 633
 QY 2023 CATTTTGGAGGCAATTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGAT 2082
 Db 632 CATTTTGGAGGCAATTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGAT 573
 QY 2083 ATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCAAAAGTTTATCCGGCCTTTATT 2142
 Db 572 ATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCAAAAGTTTATCCGGCCTTTATT 513
 QY 2143 CACATTTCTTCCCGCTGATGATGCTCATCCGGAATCCGATGCGAATGAAGACCGT 2202
 Db 512 CACATTTCTTCCCGCTGATGATGCTCATCCGGAATCCGATGCGAATGAAGACCGT 453
 QY 2203 GAGCTGCTGATATGGGATAGTGTTCACCCCTTGTTCACCCGTTTCCATGAGCAAACTGAA 2262
 Db 452 GAGCTGCTGATATGGGATAGTGTTCACCCCTTGTTCACCCGTTTCCATGAGCAAACTGAA 393
 QY 2263 AGTTTTCATGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTTACATATAT 2322
 Db 392 AGTTTTCATGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTTACATATAT 333
 QY 2323 TCGCAGATGTGGCGTGTACCGTGAAACCTGGCCTATTTCCTAAAGGTTTATTGAG 2382
 Db 332 TCGCAGATGTGGCGTGTACCGTGAAACCTGGCCTATTTCCTAAAGGTTTATTGAG 273
 QY 2383 AATATGTTTTTCTCTCAGCCCAATCCCTGGGTGAGTTTTCACAGTTTGTGATGCTTCCAT 2442
 Db 272 AATATGTTTTTCTCTCAGCCCAATCCCTGGGTGAGTTTTCACAGTTTGTGATGCTTCCAT 213
 QY 2443 GCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAAATATTATAGCAAGGC 2502
 Db 212 GCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAAATATTATAGCAAGGC 153
 QY 2503 GACAAAGTGTGATGCGGTGGCGATTTCAGTTTCATCATGCGCTGTGATGCTTCCAT 2562
 Db 152 GACAAAGTGTGATGCGGTGGCGATTTCAGTTTCATCATGCGCTGTGATGCTTCCAT 93
 QY 2563 GTCGGAGCAATGCTTAATGAATTTACAAAGTACTGCGATGAGTGGCAGGCGGGCGCTAA 2622
 Db 92 GTCGGAGCAATGCTTAATGAATTTACAAAGTACTGCGATGAGTGGCAGGCGGGCGCTAA 33
 QY 2623 TCG 2625
 Db 32 TTG 30

RESULT 4

BZ071317/c

LOCUS 812 bp DNA linear GSS 10-OCT-2002

DEFINITION B.oleracea002 Brassica oleracea genomic, genomic survey sequence.

ACCESSION BZ071317

VERSION BZ071317.1 GI:23688254

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 812)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1jul3 row: g column: 05

Seq primer: -21UPPOT forward

Class: shotgun		High quality sequence start: 8		High quality sequence stop: 551.	
Location/Qualifiers		1. .812		/organism="Brassica oleracea"	
source		/mol_type="genomic DNA"		/db_xref="taxon:3712"	
ORGANISM		Brassica oleracea		/clone_lib="B.oleracea002"	
REFERENCE		Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.		Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."	
AUTHORS		Contact: Richard K. Wilson		Genome Sequencing Center	
TITLE		Washington University School of Medicine		Email: submissions@wustl.edu	
JOURNAL		Plate: ljt37 row: a column: 10		Seq primer: -28RPpOT reverse	
COMMENT		Class: shotgun		High quality sequence start: 16	
FEATURES		High quality sequence stop: 551.		Location/Qualifiers	
source		1. .848		/organism="Brassica oleracea"	
source		/mol_type="genomic DNA"		/db_xref="taxon:3712"	
source		/clone_lib="B.oleracea002"		/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."	
ORIGIN		Query Match		14.3%; Score 697.4; DB 28; Length 848;	
ORIGIN		Best Local Similarity		97.8%; Pred. No. 1.4e-115;	
ORIGIN		Matches		707; Conservative 0; Mismatches 16; Indels 0; Gaps 0	
ORIGIN		Qy		1903 AGATCACTACCGGGCGGTATTTTTCGAGTTATCGAGATTTTCAGGAGCTTAAGGAAGCTAAA 1963	
ORIGIN		Db		804 AGCTTATCATCGATAGCTTTAATGAGTTTTCGAGTTTTCGAGAGCTTAAGGAAGCTAAA 745	
ORIGIN		Qy		1963 ATGGAGAAAAAATCACTGGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022	
ORIGIN		Db		744 ATGGAGAAAAAATCACTGGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAA 685	
ORIGIN		Qy		2023 CATTTTGAGCATTTCAGTCAGTTGCTCAATGATCTATACACGACCGTTTCAGCTGGAT 2082	
ORIGIN		Db		684 CATTTTGAGCATTTCAGTCAGTTGCTCAATGATCTATACACGACCGTTTCAGCTGGAT 625	
ORIGIN		Qy		2083 ATTACGGCCCTTTTAAAGACCGTAAAGAAAAATAAGCAACAGTTTTCACCGCCCTTTATT 2142	
ORIGIN		Db		624 ATTACGGCCCTTTTAAAGACCGTAAAGAAAAATAAGCAACAGTTTTCACCGCCCTTTATT 565	
ORIGIN		Qy		2143 CACATCTTTCGCCGCTGATGAATGCTCATCCGGAATTCCTCGATTCGGCAATGAAGACCGT 2202	
ORIGIN		Db		564 CACATCTTTCGCCGCTGATGAATGCTCATCCGGAATTCCTCGATTCGGCAATGAAGACCGT 505	
ORIGIN		Qy		2203 GAGCTGGTGAATGGGATAGTGTTCACCCCTGTTACACCGTTTTCATCGAGCAAACTGAA 2262	
ORIGIN		Db		504 GAGCTGGTGAATGGGATAGTGTTCACCCCTGTTACACCGTTTTCATCGAGCAAACTGAA 445	
ORIGIN		Qy		2263 ACGTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCCGGAGTTTTCACACATATAT 2322	
ORIGIN		Db		54 TTG 52	

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Db      444  AGCTTTTCATCGCTCTGGAGTGAATACCCAGAGATTTCCGGCAGTTTCTACACATATAT 385
QY      2323  TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCTAAAGGGTTTATTGAG 2382
Db      384  TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCTAAAGGGTTTATTGAG 325
QY      2383  ATATATGTTTTCGTCCTCAGCAATCCCTGGGTGAGTTTCAACAGTTTGTATTAACAGTG 2442
Db      324  AATATGTTTTCGTCCTCAGCAATCCCTGGGTGAGTTTCAACAGTTTGTATTAACAGTG 265
QY      2443  GCCAATATGACAACTTCTTCGCCCGCTTTTCACCATGGGCAAAATATTATACGCAAGGC 2502
Db      264  GCCAATATGACAACTTCTTCGCCCGCTTTTCACCATGGGCAAAATATTATACGCAAGGC 205
QY      2503  GACAAGGTGCTGATGCGCTGGCGATTCAGGTTTCATCATGCCGTCTGTGATGGCTTCCAT 2562
Db      204  GACAAGGTGCTGATGCGCTGGCGATTCAGGTTTCATCATGCCGTCTGTGATGGCTTCCAT 145
QY      2563  GTGGCAGAAATGCTTAATGAATTAACACAGTACTGGGATGAGTGGCAGGGCGGGCGTAA 2622
Db      144  GTGGCAGAAATGCTTAATGAATTAACACAGTACTGGGATGAGTGGCAGGGCGGGCGTAA 85
QY      2623  TCG 2625
Db      84  TTG 82

RESULT 6
BZ569330
LOCUS      903 bp      DNA      linear      GSS 17-DEC-2002
DEFINITION pacs2-164_8345.x1 pacs2-164 Pseudomonas aeruginosa genomic clone
ACCESSION BZ569330
VERSION   BZ569330.1 GI:27203786
KEYWORDS  GSS.
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 903)
AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
          Burns,J.L., Kaul,R. and Olsen,M.V.
          Whole-Genome-Sequence variation among multiple isolates of
          Pseudomonas aeruginosa library
          J. Bacteriol. (2002) In press
          Contact: Chris K. Raymond
          Genome Center
          University of Washington
          Box 352145, Seattle, WA 98105-2145, USA
          Tel: 2062216954
          Fax: 2066857244
          Email: craymond@u.washington.edu
          Class: shotgun.
FEATURES   Location/Qualifiers
            source          1..903
                           /organism="Pseudomonas aeruginosa"
                           /mol_type="genomic DNA"
                           /strain="2-164"
                           /db_xref="taxon:287"
                           /clone="pacs2-164_8345"
                           /clone_lib="pacs2-164"
                           /note="Clinical isolate 2-164 Whole genomic shotgun
                           library."
ORIGIN
Query Match 14.3%; Score 697.4; DB 28; Length 903;
Best Local Similarity 96.6%; Pred. No. 1.4e-115;
Matches 744; Conservative 0; Mismatches 22; Indels 4; Gaps 3;
QY 1854 AGATGATATACGGCGGTAAAGGTTCCAACTTTCCACATAATGAATAAGATCACTACC 1913
Db 117 AGACGTTGATCGGCACGTAAAGAGGTTCCAACTTTCCACATAATGAATAAGATCACTACC 176

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QY      1914  GGGCGTATTTTGTGAGTTATCGAGATTTTTCAGAGCTAAGGAAGCTAAATCGAGAAAA 1973
Db      177  GGGCGTATTTTGTGAGTTATCGAGATTTTTCAGAGCTAAGGAAGCTAAATCGAGAAAA 236
QY      1974  AATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC 2033
Db      237  AATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC 296
QY      2034  ATTTCAGTCAGTTGCTCAATGATACCTATTAACAGACCGTTTCAGCTGGATATTACGCGCTT 2093
Db      297  ATTTCAGTCAGTTGCTCAATGATACCTATTAACAGACCGTTTCAGCTGGATATTACGCGCTT 356
QY      2094  TTTAAAGCCGTAAAGAAAATAAGCACAAAGTTTATCCGGCTTTTATTCACATCTTTCG 2153
Db      357  TTTAAAGCCGTAAAGAAAATAAGCACAAAGTTTATCCGGCTTTTATTCACATCTTTCG 416
QY      2154  CCGCCTGATGAATGCTCATCCGGAATTCGATGGCAATTCGAAAGACGGTGAGTGTGAT 2213
Db      417  CCGCCTGATGAATGCTCATCCGGAATTCGATGGCAATTCGAAAGACGGTGAGTGTGAT 476
QY      2214  ATGGGATGATGTTTACCCCTTGTATACCGTTTTCATGAGCAAACTGAAACGTTTTCATC 2273
Db      477  ATGGGATGATGTTTACCCCTTGTATACCGTTTTCATGAGCAAACTGAAACGTTTTCATC 536
QY      2274  GCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGT 2333
Db      537  GCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGT 596
QY      2334  GGCGTGTACGGTGAACAACTCGCCCTATTTCCTAAAGGGTTTATTGAGAATATGTTTTT 2393
Db      597  GGCGTGTACGGTGAACAACTCGCCCTATTTCCTAAAGGGTTTATTGAGAATATGTTTTT 656
QY      2394  CGTCTCAGCCAAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAACGTTGCCCAATATGA 2453
Db      657  CGTCTCAGCCAAATCCCTGGGTGAGTTTACCAGTTTGTATTTAAACGTTGCCCAATATGA 716
QY      2454  CAACTTCTTCGCCCGCTTTTACCACATGGCAATATTATACCAAGGCGCAAGGTGCT 2513
Db      717  CAACTTCTTCGCCCGCTTTTACCACATGGCAATATTATACCAAGGCGCAAGGTGCT 776
QY      2514  GATCGCGTGGCGATTCAGGTTTCATCATGCCGTCTGTGATGGTTCCATGTCGGCAGAT 2573
Db      777  GATCGCGTGGCGATTCAGG-TCATCATGCCGTCTGTGATGGTTCCATGTCGGCAGAT 834
QY      2574  GCTTAATGAATTACACAGTACTGCGATGATGGCGAGGGCGGGCGGCTAAT 2623
Db      835  GCTTA--TGAATTACACAGTACTGCGATGATGGCGAGGGCGGGCGGCTAAT 882

RESULT 7
BZ086476/c
LOCUS      lk194b10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BZ086476
VERSION   BZ086476.1 GI:23718434
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
REFERENCE 1 (bases 1 to 789)
AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
          Nash,W., Rabinowicz,P.D. and Wilson,R.K.
          Whole genome shotgun reads from Brassica oleracea
          Unpublished (2002)
          Contact: Richard K. Wilson
          Genome Sequencing Center
          Washington University School of Medicine
          Email: submissions@watson.wustl.edu
          Plate: lk194 row: b column: 10

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Seq primer: -21UpPOT forward
Class: shotgun
High quality sequence start: 20
High quality sequence stop: 551.
High quality sequence stop: 551.
Location/Qualifiers
1. .789
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."
ORIGIN
Query Match 14.3%; Score 697.2; DB 28; Length 789;
Best Local Similarity 97.4%; Pred. No. 1.6e-115;
Matches 708; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1903 AGATCACTACCGGCGTATTTTGGCTATTCGAGATTTTCAGGAGCTAAGGAGCTAAA 1962
Db 743 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAA 684
QY 1963 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022
Db 683 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCNCATGCGATCGTAAAGAA 624
QY 2023 CATTTGAGGATTTAGTCAGTTGCTCAATGTCACCTATTAACGACCGTTCAGCTGGAT 2082
Db 623 CATTTGAGGATTTAGTCAGTTGCTCAATGTCACCTATTAACGACCGTTCAGCTGGAT 564
QY 2083 ATTACGGCTTTTAAAGACCGTAAAGAAAAATAGCACAGTTTATTCGGCGCTTTATT 2142
Db 563 ATTACGGCTTTTAAAGACCGTAAAGAAAAATAGCACAGTTTATTCGGCGCTTTATT 504
QY 2143 CACATTCCTGCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGT 2202
Db 503 CACATTCCTGCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGT 444
QY 2203 GAGCTGGTATGGGATAGTGTTCACCTGTGTTACACCGTTTCCATGACCAACTGAA 2262
Db 443 GAGCTGGTATGGGATAGTGTTCACCTGTGTTACACCGTTTCCATGACCAACTGAA 384
QY 2263 ACCTTTTTCATCGCTCTGAGTGAATACCACGACGATTTTCGGCAGTTTCTACACATATAT 2322
Db 383 ACCTTTTTCATCGCTCTGAGTGAATACCACGACGATTTTCGGCAGTTTCTACACATATAT 324
QY 2323 TCGCAAGATGGGGGTGTACGGTGAATAACCTGGCCTATTTCCCTAAAGGGTTATTGAG 2382
Db 323 TCGCAAGATGGGGGTGTACGGTGAATAACCTGGCCTATTTCCCTAAAGGGTTATTGAG 264
QY 2383 AATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTCCAGTTTGAATTAACGCTG 2442
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QY 2443 GCCAATATGGAACAATCTTCTCGCCCGCGTTTTCACCATGGGCAATATATACGCAAGGC 2502
Db 203 GCCAATATGGAACAATCTTCTCGCCCGCGTTTTCACCATGGGCAATATATACGCAAGGC 144
QY 2503 GACAAAGTCTGATCGCGTGGCGATTTCAGTTTCATATGCGCTGTGTGATGGCTTCCAT 2562
Db 143 GACAAAGTCTGATCGCGTGGCGATTTCAGTTTCATATGCGCTGTGTGATGGCTTCCAT 84
QY 2563 CTCGGCAGAACTCTTAATCAATACAAAGTACTGCGATGAGTGGCAGGCGGGCGTAA 2622
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QY 2623 TCGCGTG 2629
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Db 23 TTGGGCG 17

RESULT 8
BZ070237/c
LOCUS
DEFINITION
BZ070237.1 GI:23686536
Accession
Version
Keywords
Source
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 799)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: lkj38 row: a column: 06
Seq primer: -21UpPOT forward
Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
1. .799
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 14.3%; Score 696.4; DB 28; Length 799;
Best Local Similarity 97.6%; Pred. No. 2.2e-115;
Matches 706; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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Db 748 AGCTTATCATCGATAAGCTTTAATGAGTTATTCGAGATTTTCAGGAGCTAAGGAGCTAAA 689
QY 1963 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022
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QY 2023 CATTTGAGGATTTAGTCAGTTGCTCAATGTCACCTATTAACGACCGTTCAGCTGGAT 2082
Db 628 CATTTGAGGATTTAGTCAGTTGCTCAATGTCACCTATTAACGACCGTTCAGCTGGAT 569
QY 2083 ATTACGGCTTTTAAAGACCGTAAAGAAAAATAGCACAGTTTATTCGGCGCTTTATT 2142
Db 568 ATTACGGCTTTTAAAGACCGTAAAGAAAAATAGCACAGTTTATTCGGCGCTTTATT 509
QY 2143 CACATTCCTGCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGT 2202
Db 508 CACATTCCTGCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAGACGGT 449
QY 2203 GAGCTGGTATGGGATAGTGTTCACCTGTGTTACACCGTTTCCATGACCAACTGAA 2262
Db 448 GAGCTGGTATGGGATAGTGTTCACCTGTGTTACACCGTTTCCATGACCAACTGAA 389

QY 2263 AGTGTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGCTTCTACACATATAT 2322
 DB |||||
 QY 388 AGCTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGCTTCTACACATATAT 329
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 QY 2323 TCGCAAGATGTGGCGTGTACCGTGAACACCTGGCCCTATTTCCCTAAAGGGTTTATTGAG 2382
 DB |||||
 QY 328 TCGCAAGATGTGGCGTGTACCGTGAACACCTGGCCCTATTTCCCTAAAGGGTTTATTGAG 269
 DB |||||
 QY 2383 AATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTCACCAAGTTTGAATTAACAGTG 2442
 DB |||||
 QY 268 AATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTCACCAAGTTTGAATTAACAGTG 209
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 QY 2443 GCCAATATGCAACACTTCTTCGCCCGCTTTTACCATGGCAAAATATTATACGCAAGC 2502
 DB |||||
 QY 208 GCCAATATGCAACACTTCTTCGCCCGCTTTTACCATGGCAAAATATTATACGCAAGC 149
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 QY 2503 GACAAGGTGCTGATGCCGTGGCGATTCAGGTTTCATCGCCGTCTGTGATGGCTTCCAT 2562
 DB |||||
 QY 148 GACAAGGTGCTGATGCCGTGGCGATTCAGGTTTCATCGCCGTCTGTGATGGCTTCCAT 89
 DB |||||
 QY 2563 GTCCGAGAAATGCTTAATGAATTAACAACAGTACTGCGATGAGTGGCAGGCGGGCGTAA 2622
 DB |||||
 QY 88 GTCCGAGAAATGCTTAATGAATTAACAACAGTACTGCGATGAGTGGCAGGCGGGCGTAA 29
 DB |||||
 QY 2623 TCG 2625
 DB |||||
 QY 28 TTG 26
 DB |||||

RESULT 9
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 LOCUS 1kf64d08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.
 ACCESSION BZ070076
 VERSION BZ070076.1 GI:23686375
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 794)
 AUTHORS Delehaenty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 JOURNAL Whole genome shotgun reads from Brassica oleracea
 COMMENT Unpublished (2002)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Plate: lkf64 row: d column: 08
 Seq primer: -21UPpOT forward
 Class: shotgun
 High quality sequence start: 24
 High quality sequence stop: 551.

FEATURES
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_lib="B.oleracea002"
 /note="Vector; pOTw13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea T01000D3 buds provided by
 Thomas Osborn at the University of Wisconsin. Genomic
 DNA was provided by Pablo Rabinowicz (CSHL) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

ORIGIN

Query Match 14.3%; Score 695.4; DB 28; Length 794;
 Best Local Similarity 99.1%; Pred. No. 3.3e-115;

Matches 699; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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 DB |||||
 QY 787 TTTATGAGTTTATCGAGATTTCAGGAGCTAAAGAGCTAAATCGAGAAAAATCACT 728
 DB |||||
 QY 1981 GGATATACACCGTGTGATATATCCCAATGGCATCTGAAGAACATTTTGGAGCAATTCAG 2040
 DB |||||
 QY 727 GGATATACACCGTGTGATATATCCCAATGGCATCTGAAGAACATTTTGGAGCAATTCAG 668
 DB |||||
 QY 2041 TCAGTTGTCTAATGATACCTATAAACACGACCGTTACGTGGATATATACGCGCTTTTAAAG 2100
 DB |||||
 QY 667 TCAGTTGTCTAATGATACCTATAAACACGACCGTTACGTGGATATATACGCGCTTTTAAAG 608
 DB |||||
 QY 2101 ACCGTAAAGAAAAAAGCACAAAGTTTATCCGGCTTTTATTCACATTTCTCCCGCCCTG 2160
 DB |||||
 QY 607 ACCGTAAAGAAAAAAGCACAAAGTTTATCCGGCTTTTATTCACATTTCTCCCGCCCTG 548
 DB |||||
 QY 2161 ATGAATGCTCATCCGGAATTCGGTATGGCAATGAAAGACGGTGAATGATGGGAT 2220
 DB |||||
 QY 547 ATGAATGCTCATCCGGAATTCGGTATGGCAATGAAAGACGGTGAATGATGGGAT 488
 DB |||||
 QY 2221 AGTGTTCACCTTTGTATACCGTTTCCATGAGCAACTGAAACGTTTTCATCGCTCTCG 2280
 DB |||||
 QY 487 AGTGTTCACCTTTGTATACCGTTTCCATGAGCAACTGAAACGTTTTCATCGCTCTCG 428
 DB |||||
 QY 2281 AGTGAATACACGACGATTTCCGGCAGTTTTCACACATATATTCGCAAGATGTGGCTGT 2340
 DB |||||
 QY 427 AGTGAATACACGACGATTTCCGGCAGTTTTCACACATATATTCGCAAGATGTGGCTGT 368
 DB |||||
 QY 2341 TACGTTGAAAACTCGCTTATTTCCCTAAAGGGTTTATTGAAATATGTTTTTGTCTCA 2400
 DB |||||
 QY 367 TACGTTGAAAACTCGCTTATTTCCCTAAAGGGTTTATTGAAATATGTTTTTGTCTCA 308
 DB |||||
 QY 2401 GCAATCCCTGGTGTGATTTTCCAGTTTGTATTAACGTCGCCAATATGACACTTC 2460
 DB |||||
 QY 307 GCCAATCCCTGGTGTGATTTTCCAGTTTGTATTAACGTCGCCAATATGACACTTC 248
 DB |||||
 QY 2461 TTCGCCCCCGTTTTTACCATGGCAATATTTATACGAAGGCGACAAAGTGTGATGCCG 2520
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 QY 247 TTCGCCCCCGTTTTTACCATGGCAATATTTATACGAAGGCGACAAAGTGTGATGCCG 188
 DB |||||
 QY 2521 CTGGCGATTCAAGTTTCATCGCGCTGTGATGGCTTCCATGTCGCGAGAAATGCTTAAT 2580
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 QY 187 CTGGCGATTCAAGTTTCATCGCGCTGTGATGGCTTCCATGTCGCGAGAAATGCTTAAT 128
 DB |||||
 QY 2581 GAATTACACACTGCTGCTGATGAGTGGCAGGCGGGCGGTAATTCG 2625
 DB |||||
 QY 127 GAATTACACACTGCTGCTGATGAGTGGCAGGCGGGCGGTAATTG 83
 DB |||||

RESULT 10
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 LOCUS 1kg74cl0.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.
 ACCESSION BZ057486
 VERSION BZ057486.1 GI:23665427
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 719)
 AUTHORS Delehaenty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 JOURNAL Whole genome shotgun reads from Brassica oleracea
 COMMENT Unpublished (2002)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu

RESULT 11
BZ077741/c
LOCUS
DEFINITION
BZ077741
ACCESSION
BZ077741
VERSION
BZ077741.1
GI:23701053
KEYWORDS
SOURCE
ORGANISM
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica
1 (bases 1 to 785)
Delehaunty, K., Fewell, G., Fulton, L., McComb, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Plate: lk118 row: f column: 05
Seq primer: -21UpOT forward
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1. .785
/organism="Brassica oleracea"
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/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

Query Match 14.3%; Score 695.2; DB 28; Length 719;
Best Local Similarity 99.6%; Pred. No. 3.7e-115;
Matches 697; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1926 TGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATCGAGAAATCACTCGATA 1985
718 TGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATCGAGAAATCACTCGATA 659
1986 TACCACCGTTGATATATCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGT 2045
658 TACCACCGTTGATATATCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGT 599
2046 TGCTCAATGTACCTATTAACAGACCGTTCAGTCAGTATTAACAGACCGT 2105
598 TGCTCAATGTACCTATTAACAGACCGTTCAGTCAGTATTAACAGACCGT 539
2106 AAAGAAAAATTAAGACAACTTTTACCGCTTTTACCACTTCTCCGCGCTGATGAA 2165
538 AAAGAAAAATTAAGACAACTTTTACCGCTTTTACCACTTCTCCGCGCTGATGAA 479
2166 TGCTCATCCGGAATTCGGTATGGCAATGAAGACGGTGAGTGGTATGGGATAGTGT 2225
478 TGCTCATCCGAGTTCGGTATGGCAATGAAGACGGTGAGTGGTATGGGATAGTGT 419
2226 TCACCCCTGTGTACCGCTTTTCCATGAGCAACTGAAACGTTTTCATCGCTCTCGAGTGA 2285
418 TCACCCCTGTGTACCGCTTTTCCATGAGCAACTGAAACGTTTTCATCGCTCTCGAGTGA 359
2286 ATACCACGACGATTTCCGCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGG 2345
358 ATACCACGACGATTTCCGCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGG 299
2346 TGAAACCTGGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTTCGCTCTAGCCAA 2405
298 TGAAACCTGGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTTCGCTCTAGCCAA 239
2406 TCCCTGGGTGAGTTTACAGCTTTTGAATTAACCTGGCCATATGGAACAATCTCTCGC 2465
238 TCCCTGGGTGAGTTTACAGCTTTTGAATTAACCTGGCCATATGGAACAATCTCTCGC 179
2466 CCCCGTTTTACATGGGCAATATATACGCAAGCGCAAGGTGCTGATGCCCTGGC 2525
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2526 GATTCAGGTTCATATGCGCTGTGATGGCTTCCATGTCCGAGATGCTTAATGAAT 2585
118 GATTCAGGTTCATATGCGCTGTGATGGCTTCCATGTCCGAGATGCTTAATGAAT 59
2586 ACAAAGTACTCGATGAGTGGCAGGCGGGCGTAAATCG 2625
58 ACAAAGTACTCGATGAGTGGCAGGCGGGCGTAAATCG 19

2346 TGAACCTGCGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTCCTCTCAGCCAA 2405
 Db
 363 TGAACCTGCGCTATTTCCCTAAAGGTTTATTGAGAAATATGTTTTCCTCTCAGCCAA 304
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 2406 TCCTGGGTGAGTTTACCAAGTTTGTGATTTAAAGCTGGCCAAATATGACAACTTCTTCGC 2465
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 303 TCCTGGGTGAGTTTACCAAGTTTGTGATTTAAAGCTGGCCAAATATGACAACTTCTTCGC 244
 Qy
 2466 CCCGTTTTTACCAATGGGCAAAATATATAGCAAGGCGCAAGGTCGTGATGCGCTGGC 2525
 Db
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 2526 GATTGAGTTTCATCATGCGCTCTGTGATGCTTCCATGTCGCGAAGTCTTAATGAATT 2585
 Db
 183 GATTGAGTTTCATCATGCGCTCTGTGATGCTTCCATGTCGCGAAGTCTTAATGAATT 124
 Qy
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 123 ACAACAGTACTGCGATGAGTGGCAGGCGGCGCGTAATG 84

RESULT 12
 BZ070235/c
 LOCUS
 DEFINITION BZ070235 792 bp DNA linear GSS 10-OCT-2002
 1kj38a04.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 sequence.

ACCESSION BZ070235
 VERSION BZ070235.1 GI:23686534
 KEYWORDS GSS.

SOURCE
 ORGANISM

Brassica oleracea
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 1 (bases 1 to 792)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,

Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

CONTACT: Richard K. Wilson

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1kj38 row: a column: 04

Seq primer: -21upPOT forward

Class: shotgun

High quality sequence start: 16

High quality sequence stop: 551.

FEATURES

source

1..792

/organism="Brassica oleracea"

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/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/note="vector: pOTw13; whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea TO100DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

ORIGIN

Query Match 14.3%; Score 694.8; Db 28; Length 792;

Best Local Similarity 97.5%; Pred. No. 4.3e-115;

Matches 705; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1903 AGATCACTACCGCGCTATTTTGTGATTCAGATTTTTCAGAGCTAAGGAGCTAAA 1962

Db 748 AGCTTATCATCGATAGCTAAATAGTATTATCAGATTTTTCAGAGCTAAGGAGCTAAA 689

Qy 1963 ATGGAGAGAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022

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 2023 CATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATTAACAGACCGTTTCAGCTGGAT 2082
 Db
 628 CATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATTAACAGACCGTTTCAGCTGGAT 569
 Qy
 2083 ATTACGGCCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTATCCGGCTTTATT 2142
 Db
 568 ATTACGGCCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTATCCGGCTTTATT 509
 Qy
 2143 CATTTTTCGCCCTCTGATGATGCTCATCCGGAATCCGTTATGGCAATGGAAGACGGT 2202
 Db
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 Qy
 2203 GAGCTGTGATATGGGATAGTGTTCACCTTGTGTACACCGTTTTCATAGCAAACTGAA 2262
 Db
 448 GAGCTGTGATATGGGATAGTGTTCACCTTGTGTACACCGTTTTCATAGCAAACTGAA 389
 Qy
 2263 ACCTTTTTCATCGCTCTCGAGTGAATACACGACGATTTCCGGCAGTTTCTACATATAT 2322
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 Qy
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 2383 AATATGTTTTTCGTCCTCAGCCAATCCCTGGGTGAGTTTCCACGATTTTGAATTTAAACGTG 2442
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 268 AATATGTTTTTCGTCCTCAGCCAATCCCTGGGTGAGTTTCCACGATTTTGAATTTAAACGTG 209
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 Qy
 2563 GTCGGCAGAAATGCTTAATGAATTACACAGTACTGCGATGAGTGGCAGGGGCGGCGTAA 2622
 Db
 88 GTCGGCAGAAATGCTTAATGAATTACACAGTACTGCGATGAGTGGCAGGGGCGGCGTAA 29
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 2623 TCG 2625
 Db
 28 TTG 26

RESULT 13

BZ069987/c

LOCUS

DEFINITION

1kf31c12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey

sequence.

ACCESSION BZ069987

VERSION BZ069987.1 GI:23686286

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 797)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,

Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

CONTACT: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1kf31 row: c column: 12

Seq primer: -28RPOT reverse

Class: shotgun

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High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
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/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

FEATURES
source
1. .797
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 14.3%; Score 694.8; DB 28; Length 797;
Best Local Similarity 97.5%; Pred. No. 4.3e-115;
Matches 705; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGGATTTTGGAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAA 1962
Db 761 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAA 702

QY 1963 ATGGAGAAAAAATCACTGGATATACACCGTTGCATATATCCCAATGGCATCGTAAAGAA 2022
Db 701 ATGGAGAAAAAATCACTGGATATACACCGTTGCATATATCCCAATGGCATCGTAAAGAA 642

QY 2023 CATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTATTAACAGACGTTTCAGCTGGAT 2082
Db 641 CATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTATTAACAGACGTTTCAGCTGGAT 582

QY 2083 ATTACGGCCTTTTAAAGACGTTAAAGAAAAATAGCAAGTTTATCCGGCCTTTATT 2142
Db 581 ATTACGGCCTTTTAAAGACGTTAAAGAAAAATAGCAAGTTTATCCGGCCTTTATT 522

QY 2143 CACATCTTCGCCGCTCATGAATCTCATCCGGAATTCCTATGGCAATGAAGAAGCGGT 2202
Db 521 CACATCTTCGCCGCTCATGAATCTCATCCGGAATTCCTATGGCAATGAAGAAGCGGT 462

QY 2203 GAGCTGGTGATATGGGATAGTTTCCACCCCTTGTATACCGTTTCCATGAGCAAACTGAA 2262
Db 461 GAGCTGGTGATATGGGATAGTTTCCACCCCTTGTATACCGTTTCCATGAGCAAACTGAA 402

QY 2263 AGCTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATAT 2322
Db 401 AGCTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATAT 342

QY 2323 TCGCAAGATGTGGCGTGTACGGTGAAACCTGGGCTTATTTCCCTAAAGGGTTTATTGAG 2382
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QY 2383 AATATGTTTTTCGTCTACGCCAATCCCTGGGTGAGTTTCCACAGTTTGAATTAACGCTG 2442
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QY 2503 GACAAGTGCTGATGCGGTGGCGAATTCAGGTTTCATCATGCCGCTCTGTGATGGCTCCAT 2562
Db 161 GACAAGTGCTGATGCGGTGGCGAATTCAGGTTTCATCATGCCGCTCTGTGATGGCTCCAT 102

QY 2563 GTCGGCAGATGCTTATGAAATTAACAACAGTACTGCGATGAGTGGCAGCGCGGGGTAA 2622
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QY 2623 TCG 2625
Db 41 TTG 39
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RESULT 14
BZ070648/c
LOCUS
DEFINITION
BZ070648
BZ070648.1 GI:23687090
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 797)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: lkh33 row: h column: 10
Seq primer: -28RPPOT reverse
Class: shotgun
High quality sequence start: 22
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flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 14.3%; Score 693.8; DB 28; Length 797;
Best Local Similarity 99.0%; Pred. No. 6.4e-115;
Matches 698; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1921 TTTTTCGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAATCACT 1980
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Db 725 GGATATACCCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCCAG 666

QY 2041 TCAGTTGCTCAATGTACCTATTAACAGACCGTTTCAGCTGGATATTACGGCCTTTTAAAG 2100
Db 665 TCAGTTGCTCAATGTACCTATTAACAGACCGTTTCAGCTGGATATTACGGCCTTTTAAAG 606

QY 2101 ACCGTAAAGAAAAATAAGCAAGTTTATCCGGCCTTTATTCACATTTCTGCGCCGCTG 2160
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QY 2281 AGTGAATACACGACGATTTTCGGGAGTTTTCACATATATTCGACAGATGCGGCTG 2340
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Db 425 AGTGAATACCAACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGT 366
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Db 365 TACGGTGAAGAACTGCGCCATATTCCTAAAGGTTTATTGAGAATATGTTTTTCGTCTCA 306
QY 2401 GCCATCCCTGGGTGAGTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTC 2460
Db 305 GCCATCCCTGGGTGAGTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTC 246
QY 2461 TTGCCCCCGTTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTC 2520
Db 245 TTGCCCCCGTTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTCACCACTTTTC 186
QY 2521 CTGGCAGTTCAGTTTCATCATGCGCTTGTGATGGCTTCCATGTCGGCAGAAATGCTTAAT 2580
Db 185 CTGGCAGTTCAGTTTCATCATGCGCTTGTGATGGCTTCCATGTCGGCAGAAATGCTTAAT 126
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RESULT 15
BH960653/c
LOCUS odh64a12.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BH960653
VERSION BH960653.1 GI:23441879
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 725)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odh64 row: a column: 12
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 22
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flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T0100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

FEATURES
source
1..725
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T0100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 14.3%; Score 693.6; DB 28; Length 725;
Best Local Similarity 99.4%; Pred. No. 7.2e-115;
Matches 696; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 725 GAGTATCGAGATTTTCAGGAGCTAGGAAGCTAAATGGAGAAAAATCACTGATAT 666

QY 1987 ACCACGCTGTATATATCCCAATGGCATCGTAAGAACAATTTTGAAGCAATTCAGTCAGTT 2046
Db 665 ACCACGCTGTATATATCCCAATGGCATCGTAAGAACAATTTTGAAGCAATTCAGTCAGTT 606
QY 2047 GTCATATGTACCTATAACACAGACCGTTTCAGCTGGATATTTACGGCCTTTTAAAGACCGTA 2106
Db 605 GTCATATGTACCTATAACACAGACCGTTTCAGCTGGATATTTACGGCCTTTTAAAGACCGTA 546
QY 2107 RAGAAAAATAACACAGAAAGTTTATCCGGCTTTTATTCACATTCCTGCCCGCCTGATGAAT 2166
Db 545 RAGAAAAATAACACAGAAAGTTTATCCGGCTTTTATTCACATTCCTGCCCGCCTGATGAAT 486
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QY 2227 CACCTTGTACACCGTTTTCATGAGCAAACTGAAACCGTTTTCATCGCTCTGAGTGAA 2286
Db 425 CACCTTGTACACCGTTTTCATGAGCAAACTGAAACCGTTTTCATCGCTCTGAGTGAA 366
QY 2287 TACCACGAGATTTCCGGCAGATTTCTACACATATATTCGCAAGATGTGGCTGTACGGT 2346
Db 365 TACCACGAGATTTCCGGCAGATTTCTACACATATATTCGCAAGATGTGGCTGTACGGT 306
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